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8	KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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721 CAGGAGCATCACCACACCTCCCTACCCCCCCCTCCTCCCCCCCTCGCTGC 721 CAGGAGCATCACCACCTCCTCCTCCCCCCCCCCCCCCCC	1021 TAGGCCAGAACTTCCCAACTGTGAGGGGGAAGAGCTGGGGGACAAGCTCCTCCCTG.	AF030100  Muss musculus TWEAK mRNA, complete cds.  AF030100.2 GI:33348855  Mus musculus (house mouse)  Mus musculus  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Butele  Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murin  (Chicheportiche,Y., Bourdon,P.R., Xu,H., Hau,Y.M., Scott,H.  Hessian,C., Garcia,I. and Browning,J.L.  TWEAK, a new secreted ligand in the tumor necrosis factor  TWEAK, a new secreted ligand in the tumor necrosis factor  TWEAK, a new secreted ligand in the tumor necrosis factor  TWEAK, a new secreted ligand in the tumor necrosis factor  TWEAK, a new secreted ligand in the tumor necrosis factor  TWEAK, a new secreted ligand in the tumor necrosis factor  TWEAK, a new secreted ligand in the tumor necrosis factor  J. Biol. Chem. 272 (51), 32401-32410 (1997)  9405449  Chicheportiche,Y., Bixler,S., Tizard,R. and Browning,J.  Direct Submission  Submitted (14-OCT-1997) Cell Biology, Biogen, 12 Cambridge  Cambridge, MA 02142, USA  Sequence update by submitter  On Jul 30, 2003 this sequence version replaced gi:2707220.  Location/Qualifiers  Cambridge, MA 02142, USA  Sequence update by submitter  On Jul 30, 2003 this sequence version replaced gi:2707220.  Location/Qualifiers  Cambridge, MA 02142, USA  Sequence update by submitter  On Jul 30, 2003 this sequence version replaced gi:2707220.  Location/Qualifiers  On Jul 30, 2003 this sequence  Call Expe="maxMa"   Most Aref="maxMa"   Most Aref=
3     3     4     3     4     3     4     3     4     4     4     3     4 <td><u>ኞ</u>ብ ኞብ ኞብ</td> <td>RESULT 2 AF030100 LOCUS DEPINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL REMARK COMMENT FEATURES SOURCE</td>	<u>ኞ</u> ብ ኞብ ኞብ	RESULT 2 AF030100 LOCUS DEPINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL REMARK COMMENT FEATURES SOURCE
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901 CAAAGCCCTACTTATCCCTGACTCCCCACCCACCCGACCACGTGTTTATTC Db 972 CAAAGCCCTACTTATCCCTGACTCCCCCACCCCACCCGACCACGTGTTTATTC OY 961 TTGTGCACCAGGCACTGAGTGGCTGGACCTGGTGGAGCCTGGTGTTTATTC Db 1032 TTGTGCACCAGGCACTGAGATGGGCAGGAGCCTGGTGGAGCCTGGGAGCCTGGTGTGTGT	ACCESSION Mus musculus chromosome 11 clone RP23-168P5, WORKING DRAFT SCUENCE, 7 unordered pieces.  ACCESSION ACC69459 ACC69459.23 GI:14547768 REFWORDS HIGH HTGS PHABEI; HTGS_DRAFT; HTGS_FULLTOP. MUS musculus (house mouse) ORGANISM Mustazoa; Chordata; Craniata; Vertebrata; Eutelec Mammalia; Eutheria; Rodentia; Sciurcognathi; Muridae; Murinic (hoases 1 to 203083) AUTHORS Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwnonu, G., Carner, T., Addison, S., Pace, A., Williams, G., Chen, G., Cox, C., Dausc, C., Dauston, D., Proremandez, C., Partsaguto, D., Fernandez, C., Ding, Y., Dugan-Rocha, S., Fernandez, C., Diu, W., Loulseged, H., Lozado, R.J., Martii Massey, E., McLeod, M.P., Mei, G., Moore, S., Moorgan, M., Morriit Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morriit Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morriit	Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Ogul, M., Parish, Perez, L., Reiter, D., Say, J., Shen, H., Wasquez, L., Watlinger Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A., Muzly, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, Morley, K. and Gibbs, R.  TITLE Direct Submission  DUPLISHED  TITLE Direct Submission  AUTHORS Worley, K.C.  TITLE Direct Submission  TITLE Direct Submission  OURNAL Dispublished  AUTHORS Worley, K.C.  TITLE Direct Submission  TOURNAL Dispublished  AUTHORS Worley, K.C.  TITLE Direct Submission  TOURNAL Dispublished  BAJOR Plaza, Houston, TX 77030, USA  COMMENT On Jun 25, 2001 this sequence version replaced gi:12621364  Center code: BCM  Web Site: http://www.hgsc.bcm.tmc.edu/  Conter: Baylor College of Medicine  Center code: BCM  Web Site: http://www.hgsc.bcm.tmc.edu/  Contert: Baylor College of Medicine  Center project Information  Center project Information  Center project name: RAFO  Center project
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This is a "working draft' sequence. It currently ists of 7 contigs. The true order of the pieces ot known and their order in this sequence record is trary. Gaps between the contigs are represented as of N, but the exact sizes of the gaps are unknown.

record will be updated with the finished sequence.
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Pearce, A. Direct Submission

Direct Submission

Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, F. Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.on Nov 20, 2001 this sequence version replaced gi:16605765 During sequence assembly data is compared from overlapping. Where difference are found these are annotated as variation together with a note of the overlapping clone name. Note the variation annotation may not be found in the sequence submoorresponding to the overlapping clone, as we submit seque only a small overlap as described above.

This sequence was finished as follows unless otherwise not regions were either double-stranded or sequenced with an a chemistry or covered by high quality data (i.e., phred que 30); an attempt was made to resolve all sequencing problem as compressions and repeats, all regions were covered by a one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The followir abbreviations are used to associate primary accession numt in the feature table with their source databases: Em:, EME SWISSPROT; IT:, TREMBL; Wp:, WORMPEP; Information on the W database can be found at AL603707 234182 bp DNA linear ROD 17 Mouse DNA sequence from clone RP23-422L16 on chromosome 11 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murir 1 (bases 1 to 234182) http://www.sanger.ac.uk/Projects/C\_elegans/wormpep RP23-42
from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.k 42539 AAAGCCCCTACTTATCCCTGACTCCCCCACCCACTCACCCGACCACGTGTTTATTG 42479 rerecaccadecacreagaresecresaceresesesesesaseaasecas 42419 AGGCCAGAAGTTCCCAACTGTGAGGGGAAGAGCTGGGGACAAGCTCCTCCCTGGP TGTGGATTTTTGAAAGATACTATTTTTATTATTATTGTGACAAAATGTTAAATGGA 42359 IGTGGATTTTGAAAGATACTATTTTTATTATTATTGTGACAAATGTTAAATGG TGTGCACCAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTG 1022 AGGCCAGAAGTTCCCAACTGTGAGGGGAAGAGCTGGGGACAAGCTCCTCCCTGG This sequence is the entire insert of clone RP23-422L16. U)

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H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Crowley, C., Currell, B., Deuel, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Chui, C., Crowley, C., Gur, O., Hass, P.B., S.S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Leds, E., Seshagiri, S., Simmon, E., Sanchez, C., Simchez, C., Simchez, C., Simchez, C., Simchi, V., Simchi, V., Simchi, V., N.J., Vages, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, X., G., Wood, W.I. and Godowski, P. Wand, V. Shang, M., Zhang, M., Creted Protein Discovery Initiative (SPDI), a Large-Scale creted Protein Discovery Initiative (SPDI), a Large-Scale to Identify Novel Human Secreted and Transmembrane Proteins:
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--ACAGACGTATCCTTGCTCTTCTTAACATCCCATCCCACCACAACTATCCACCTC 891
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ia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                          ---TTATCCCTGACTCCCCCACCACT
                                             <u>AAÁTÁCAGTATTÓCCACTCTTATCTTÁCAACTCCCCCACCCCCACTCTCCACCTC</u>
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Res. 13 (10), 2265-2270 (2003)
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/mol_type="mRNA"
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58. .807
/locus_tag="UNQ181"
/note="PRO207"
                                                                                             GCTCCCAAAGCCCCTAC----
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/product="Apo-3 Ligand"
/protealn_id="AAQ9229.1"
/db_xref="[d1:3718288]
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XYLXYCQYHFDBGRAVYLKLDLLVDGYLALRCLEEFSATAASSLGPQLRI
RPGSSLRIRTLPWAHLKAAPFLITYFGLFQVH"
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Pred. No. 2.1e-155;
0; Mismatches 219;
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Best Local Similarity 76.2%;
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s,S.A., Sheridan,J.P., Pitti,R.M., Brush,J., Goddard,A. and
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function="binds to the death-domain-containing receptor
\(\frac{1}{2}\) DR3"
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1) Eutheria, Primates, Catarrhini, Hominidae, Homo.
18 1 to 1368)
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Submission
ed (DS-MAR-1998) Molecular Oncology, Genentech, 1 DNA Way,
an Francisco, CA 94080, USA
Location/Qualifiers
                     TTATCCCTGACTCCCCCCCCCCCT
                                                                                                                                                                                 PAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGACTAG
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product="Apo3/DR3 ligand"
                                                                                                   SACCACGIGITIAITGACTITGIGCAC-
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein id="AAC39724.1"
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QY         242 CGAGCTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACGGAC	542 704 602 662 682 722 722 884 884 939 939 939 1119	QY         1024 GCCAGAACTTCCCAACTGTGAGGGGAAGAGCTGGGGACAAGCTCCTCCCTC	RESULT 9 AF030099 LOCUS . AF030099 DEFINITION Homo sapiens TWEAK mRNA, complete cds.
CCCCCAGGTCATTGTGTTCACTGTACTCTGTGGCCAAGGATGGGTCCAGAAGACCC 1144  -CAGGCACTGAGATGGCTGGACCTGGTGGCAAGGAACCTGGCACTAG 1023	ligand polypeptide.  ligand polypeptide.  22.1 GI:22636562 152284-A7.  apiens (human)  pta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  la; Eutheria; Primates; Catarrhini; Hominidae; Homo.  ses 1 to 1421)  azi,A.J., Marsters,S.A. and Pitti,R.  ligand polypeptide  : JP 200152284-A1 120-NOV-2001;  ECH INC  como sapiens (human)  P 200152284-A1 20-NOV-2001;  ECH INC  como sapiens (human)  P 200152284-A1  0-NOV-201  9-CCT-1997 US 60/062037,17-DEC-1997 US 60/06962 PI  ASHKENAZI,SCCT A MARSTERS,ROBERT PITTI  12N15/09,A61X38/00.COTK14/705,COTK16/24,CI2N15/00,A61X37/02  polypeptide  corruption (human)  location/Qualifiers  1. 1421  Location/Qualifiers  1. 1421  Location/Qualifiers  1. 1421  Abre="Momo sapiens"  (mol_type="Momo sapiens")  (mol_total)  (mol_total		AACAACTAGTCCGGCCTCGAAGAGTGCTCCTAAAGGCCGGAAGGCGCGGCCTCGC 241

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1 (bases 1 to 1373)
Chicheportiche, Y. and Browning, J.L.
A tumor necrosis factor related ligand
Patent: JP 2011505407-A 2 24-APR-2001;
BIOGEN INC, THE FACULTY OF MEDICINE OF THE UNIVERSITY OF GE
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RAKALAHVEVHPREPQDGAQAGVOTYVSGWEBARINSSSPLRYNRQIGEFIYTRAGL
YYLYCQVHFDBGKAYYLKLDLLVDGYLALRCIEFSATAASSLGPQLRLCQVSGLLAL
RPGSSERIRTLDWAHLKAAPFLLYFGLPQVH"
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| translation="MAARRSQRRRGREGEFGTALLVPLALGLGLALACLGLLLAVVSL
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Location/Qualifiers
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                                                                                                                                             ta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
a, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                            ortiche,Y., Bourdon,P.R., Xu,H., Hau,Y.M., Scott,H.,
.C., Garcia,I. and Browning,J.L.
arew secreted ligand in the tumor necrosis factor family
akly induces apoptosis
.Chem. 272 (51), 32401-32410 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.4%; Score 624; DB 9; Length 1306; 76.0%; Pred. No. 3.4e-154; ive 0; Mismatches 220; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                   es 1 to 1306)
.P., Hession, C., Tizard, R. and Browning, J. Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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18. 767
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/product="TWEAK"
                            GI:2707218
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16 ပ 953 GCTCCAGACCTGCCCTCCTAGAGGCTGCCTGGGCCTGTTCACGTGTTTTCCA Wiley, S.R. Member of the TNF family useful for treatment and diagnosi -----cricgacacacriticragacaccacaccccrcraccccaccacacac 781 GGTCCAGTCCTGTCTCTCC--TCAAAGGCAGCCAGAGCTTGTTCACATGTTTCCAT 1013 ACATAAATACAGTATTCCCACTCTTATCTTACAACTCCCCCCACCGCCACTCTCCA 892 ACTAGCTCCCAAAGCCCCTAC-------TTATCCCTGACTCCCCCACC 1073 ACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGATCTCGACTCCCCCTG ----CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAAACCTGGGA 2 GTGCTGAGCCTGGGCGTGGCCTGCCTTGGCCTCCTGCTGGTGGTCGTGGTCAG 193 gaccaggaccegregaacrgaareeceagacagaagaagaagaagaageeceee TTGGAACAACTAGTCCGGCCTCGAAGAAGTGCTCCTAAAGGCCGGAAGGCGCGGCC 722 AGGAGCATCACCACACCTCCCTACCCCACCCCCACTCCTCCACCCCCTC-GCTGC1 122 CGCCGGGAGCCCCCTGAACTGAATCCCCAGAGAGGAAAGCCAGGATGTGGTACC 1312 cergregarrirraaaacagararrarrirrirarrarrarregagaaarerrea CCTGTGGATTTTGAAA--AGATACTATTTTTATTATTATTGTGACAAAATGTTAA 1024 GCCAGAAGTTCCCAACTGTGAGGGGAAGAGCTGGGGACAAGCTCCTTGGA PAT Length 1236; linear Indels Query Match 51.2%; Score 597.8; DB 6; Best Local Similarity 75.2%; Pred. No. 3e-147; Matches 879; Conservative 0; Mismatches 222;

361 432 421 492 481 552 541 612 601 672 661 732 721 792 780 847 837 907 891 967

GGATTTTGAAAGATACTATTTT 1108 GGATTTTTAAAACAGATATTATTT 1235

AAGTICCCAACTGIGAGGGGAAGAGCTGGGACAAGCTCCTCCTGGA----TC 1079

CAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAG

CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGACTAG

CCCCAGGGCATTGTGTTCACTGTACTGTGGGCAAGGATGGGTCCAGAAGACCC 1087

GACCACGIGITITATIGACITIGICAC

936

1236 bp DNA linear PAT 27-AUG-2002 tnf family useful for treatment and diagnosis of GI:22602730 the 7. 4. 5. 1. 34 of

CGGATCCGCACCTCCCCTGGGCTCATCATAAGGCTGCCCCTTCCTAACTTACTACTTT

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelen Bammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

B. 1 (1968).

Miley,S.R.

Member of the tnf family useful for treatment and diagnosi:
Patent: JP 2001513626-A 1 04-SEP-2001;
ABBOTT LABORATORIES

PN JP 200153626-A/1

PP 12-FEB-1998 JP 1998535077

PR 12-FEB-1999 US 08/798692,10-FEB-1998 US 09/02171

STEVEN WILEY

PC C1201/68,112N15/63,C07K14/525,C07K16/28,G01N33/50,G011

PC A61K38/19

CC Strandedness: Single;

CC Topology: Linear;
FH Key GGTGTGCTGGCCTGCGCTGCCTGGAGAATTCTCAGCCACTGCGGCGAGTTCCCT GTGCTGAGCCTGGGCCTGGCGCTGGCCTTGGCCTTGCCTGCTGGTCGTGGTCAG GGGAGCCGGCCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGCTGGTGGTGCAGA TTGGAACAACTAGTCCGGCCTCGAAGAAGTGCTCCTAAAGGCCGGAAGGCGCGGCC CTGAACCGACTAGTTCGGCCTCGAAGAAGTGCACCTAAAGGCCGGAAAAACAGGGC CGAGCTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACA 313 AGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGACGAGACGACCCA CGCTACGACCGCCAGATTGGGGGAATTTACAGTCATCAGGGCTGGGGCTCTACTACCTA CGCTACAACCGCCAGATCGGGGGGTTTATAGTCACCGGGCTGGGCTCTACTACTCTC TGTCAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGT TGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGT GGTGTGCTGGCCTTGCGTTGGAAGAATTCTCAGCCACAGAGCAGCAAGCTCTCC cecchaerrecentrangechaererengaeerarraceeeraegeenarie CCCCAGCTCCGCCTCTGCCAGGTGTCTGGGCTGTTGGCCCTGCGGGCCAGGGTCCTC GGGAGCTGGGCAACGCTGTCTGCCCAGGAGCCTTCTCAGGAGGAGCTGACAGCAGA 122 CGCCGGGAGCCCCCTGAACTGAATCCCCAGACAGAGAAAGCCAGGATGTGGTACC GGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAAATCAACAGCTCCAGCCC GGTGTGGACGGGACAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCC Length 1236; Query Match
Best Local Similarity 75.2%; Pred. No. 3e-147;
Matches 879; Conservative 0; Mismatches 222; Indels /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" Location/Qualifiers
1. .1236 JP 2001513626-A/1. Homo sapiens (human) Homo sapiens 133 182 253 242 433 493 62 N 302 373 422 482 553 542 613 362 source SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL KEYWORDS FEATURES COMMENT ORIGIN ò 임 ò q à 임 ò d à 셤 ò d ð 셤 ò d à g ò 셤

1116,A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., 1ey, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., J., Haghighi, P., Han, J., Hansen, M., Ho, S.-L., Hu, P., B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q., i.R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., i.B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., I.A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D. 5 130254 bp DNA linear HTG 06-JUN-2003 norvegicus clone RP31-258K6 strain Brown Norway, WORKING CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGGACTAG 1023 GAAGTICCCAACTGTGAGGGGGAAGAGCTGGGGACAAGCTCCTCCTGGA----TC 1079 derecechárecergáceerrreageeeeegagaareregacreeeeega 1027 ccccchagaccarrangererationary TCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAG 1147 GGAGTTCCCAAATGTGAGGGGGGGAA-AACAAGACAAGCTCCTCCCTTGAGAATTC 1206 GCTCCCAAAGCCCCTAC------TTATCCCTGACTCCCCACCACT 936 recaegiricacidasesesecerisarerecesesereseceaseseseseseseseseses 792 CCTCGACAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCACCCTCAGCCGCTCTTT 847 CAGTCCTGTCTCTCC--TCAAAGGCAGCCAGAGCTTGTTCACATGTTTCCATTCC- 837 cadaccirccerceradadecreceredecerericacereritates -- ACAGACGTATCCTTGCTCTTCTTAACATCCCATCCCACCACCACTATCCACCTC 891 AAATACAGTATTCCCACTCTTATCTTACAACAACCCCACGCCCACTCTCCACCTC 967 ICCGCACCCICCCCIGGGCCCAICICAAGGCIGCCCCCIICCTCACCIACIICGGA 732 ITCAAGITCACIGAGGGGCCTIGCICICCCAGAITCCTIAAACITTCCCIGGCICC 721 ota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; ia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Submission (30-0CT-2002) NIH Intramural Sequencing Center, 8717 ant Circle, Galthersburg, MD 20877, USA GCATCACCACACCTCCCTACCCCACCCCCACTCCTCCACCCCTC-GCTGCTCCTT TGGATTTTGAAAGATACTATTTT 1108 TGGATTTTTAAACAGATATTATTT 1235 CGACCACGTGTTTATTGACTTTGTGCAC-SEQUENCE, 12 ordered pieces. IGS\_PHASE2; HTGS\_DRAFT. norvegicus (Norway rat) GI:31442440 uses 1 to 130254) ises 1 to 130254) ses 1 to 130254) norvegicus Submission ished

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with a phrap-derived quality score.

Sequencing vector: plasmid; n/4; 100% of reads
Sequencing vector: plasmid; n/4; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 128169 bases at least Q40
Consensus quality: 128674 bases at least Q30
Consensus quality: 128972 bases at least Q30
Insert size: 150000; agarose-fp
Insert size: 129184; sum-of-contigs
Quality coverage: 10.78x in Q20 bases; sum-of-contig;
                                                                                                                                                                                                                                                                                                 The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicat order and orientation of each sequence contigl has been established using one or more of the following: read-pair data from individual subclones, overlaps with neaghboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is believed to be correct as given, however the sizes of the gaps between them are based on estimates that happrovided by the submitter.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 10521: contig of 10521 bp in length 10522 13327: contig of 2706 bp in length 10522 13327: contig of 2706 bp in length 13328 13427: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : contig of 15497 bp in length agap of unknown length contig of 10177 bp in length contig of 2605 bp in length contig of 2605 bp in length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 7366 bp in length

gap of unknown length

contig of 16500 bp in length

contig of 3721 bp in length

contig of 3721 bp in length

contig of 7318 bp in length

contig of 7318 bp in length

gap of unknown length
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Location/Qualifiers
1. 130254
/mol type="genomic DNA"
/mol type="genomic DNA"
/strāin="Brown Norway"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown length
of 7366 bp in length
                                                                                                   Center: NIH Intramural Sequencing Center
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gap of unknown leng
                                                                                                                                                Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
Center project name: dcf
Center clone name: 258K06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
                                                                                                                                Center code: NISC
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Rattus.

Rat
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murina
72937 TCCCAAAGCCCCCACGTA-CCCGACTACCCCGCCCCAACCCTGGGACCCTGTTTT1
                                                                                                                                                                                                                   73056 GACTAGGCCAGAAAGTTCCCAAATGTGAGGGAAAGAGAAGAGATGGAGACAAGCTCCCC
                                                                                                                                                                                                                                                                                                   1078 TCCCTGTGGATTTTGAAAAGATACTATTTTTATTATTATTGTGACAAAATGTTAAA
                                                                                                                                                                                                                                                                                                                                               73116 TCCCTGTGGATTTTTGAAAAGATACTATTTTTTATTATTATTGTGAAAATGTTAAA
                                                                                                           72996 ACTATGTGCATCAGGCATCAAGATAGGCTGGACCTGGTGGCAGGAAGCCAAAGAAC
                                                                                                                                                                             GACTAGGCCAGAAGTTCCCAACTGTGAGGGGGAAAGAGCTGGGGACAAGCTCCTCCC
                                                        ACTITIGEGEACCAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAAC
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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AC119115/c
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KEYWORDS
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117864. 130254
/note="clone overlaps with GenBank Accession Number
AC134317 clone RP31-421B16 (center project name dce)"
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missing T7 clone end on 3' end of insert"
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42007. .70095
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94262. .97982
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                                                            clone_lib="RP31"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111613 GCTCCAGTCCTGTCTTCCAAGGCAGCCAGGGCTGATGTTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      839 CAGACGIATCCTIGCTCTTCT-TAACAICCCATCCCACACCACAACTATCCACCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         958 ACTTTGTGCACCAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAAA
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organism="Rattus norvegicus"
                                                                                      1. .2103
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/note="clone_boundary
clone_end:T7
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ted (06-NOV-2001) Human Genome Sequencing Center, Department ecular and Human Genetics, Baylor College of Medicine, One

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Submitted (10-MAY-2003) Human Genome Sequencing Center, Del of Molecular and Human Genetics, Baylor College of Medicinn Baylor Plaza, Houston, TX 77030, USA on May 10, 2003 this sequence version replaced gi:25008075 on May 10, 2003 this sequence version replaced gi:25008075 on May 10, 2003 this sequence version of BAC bases and whole genome shotgun sequencing reads assembled using, (http://www.hgsc.bem.tmc.edu/projects/rak/). Each contig din the feature table below represents a scaffold in the Atlassembly (a 'contig-scaffold'), Within each contig dindividual sequence contigs are ordered and oriented, and by sized gaps filled with Ns to the estimated size. The semmy extend beyond the ends of the clone and there may be sized gaps filled with Ns to the calinated size. The semmy extend beyond the ends of the clone and there may be sizence shotgun sequence reads. Both end sequences and whole shotgun sequence only contigs will be indicated in the fea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: Atlas 3.0;
Consensus quality: 214785 bases at least Q40
Consensus quality: 216906 bases at least Q20
Consensus quality: 218593 bases at least Q20
Estimated insert size: 227169; sum-of-contigs estimati
Quality coverage: 7x in Q20 bases; sum-of-contigs esti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: Estimated insert size may differ from sequence len (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_da * NOTE: This is a "working draft' sequence. It currently * consists of a contists The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 CAGGIGCACTITIGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAA
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89.1%; Pred. No. 1.1e-138;
ive 0; Mismatches 74;
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site:EcoR1
end_sequence:RWBBO08TJB"
3 (bases 1 to 223877)
Rat Genome Sequencing Consortium.
Direct Submission
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/note="wgs_contig"
complement (217607.
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TIGGCCTGCGCTGCCTGGAAGATTCTCAGCCACCAGCAGCTCTCCTGGGCCC 544 JAAGTTGACTGAGGGGCCTTGCTCCCAGATTCCTTAAACTTTCCC----TGGGTC 720 ITGTGCACCAGGCACTGAATGGCTTGGACCTGGTGGCAGGAAGCCAGAAGCTGG 1017 838 957 604 GCACCCTCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTACTTTGGACTC 664 897 TCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCAGGTCTTCCCTTCGG MANAGCCCCTACTIATCCCTGACTCCCCCACTCACCCGACCACGTGTTTATTG AAAGAGAATAAATCATGATTTCTCTTC 1168

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GenCore version 5.1.6 opyright (c) 1993 - 2004 Compugen Ltd.	c search, using sw model	il 7, 2004, 17:30:19; Search time 2831.52 Seconds (without alignments) 12318.149 Million cell updates/sec	09-245-198A-1	gtgctgagcctgggcctggataaatcatgatttctcttc 1168	NTITY NUC OP 10.0 , Gapext 1.0	13289 seqs, 14931090276 residues	s satisfying chosen parameters: 55026578	th: 0 th: 200000000	nimum Match 0% Ximum Match 10% Aimum Match 100	3611	em_estba:*	em_estin: em_estin:* em estin:*	em_estov:*	em cacta: em cacta:	em ntc:* gb_est:.* .b ort:.*	gb_htc:* gb_htc:*	gb_cg gb_est4:* qb_est5:*	em_estfun:* em_estom:*	em_gss_hum:* em_gss_inv:*	em_gss_pln:* em_gss_vrt:*	ည်ည် အီးရာ အီးရာ	em_gss_pro:* em_gss_rod:*	em_gss_phg:*	gb_gssI:* gb_gss2:*	the number of results predicted by chance to have a than or equal to the score of the result being printed, d by analysis of the total score distribution.	SUMMARIES	ry ch Length DB ID Description	.7 1033 11 AK020909 AK020909 Mus muscu .0 892 14 CB204861 CB204861 AGENCOURT 6 918 10 BRC77781 BEC77781	665 13 BY742288 BY742288

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1, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., T., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., co, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., ce, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., i, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. integrated sequence analysis (RISA) system--384-format cing pipeline with 384 multicapillary sequencer.
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KEN Genome Exploration Research Group Phase II Team and the nal annotation of a full-length mouse cDNA collection 409, 685-690 (2001) Consortium.

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is of the mouse transcriptome based on functional annotation 770 full-length cDNAs 420, 565-573 (2002) ses 1 to 1033) J. Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., AT. Bono, H., Carninnci, P., Fukuda, S., Fukunishi, Y., M. Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., a.T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., a.T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., K., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., H., Saito, R., Sakai, C., Sakai, K., Sano, H., Saaski, D., a., K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., H., Taqama, M., Taqawa, A., Takahashi, F., Tanaka, T., Yamamura, T., Yaunishi, A., Yoshida, K., M., Marana, T., Yamamura, T., Yaunishi, A., Yoshida, K., Consortium and the RIKEN Genome Exploration Research 9 I & II Team. Phase MOIN

al and Chemical Research (RIKEN), Laboratory for Genome ation Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, wa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, 1p://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, ted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of o, M., Muramatsu, M. and Hayashizaki, Y. Submission

visit our web site (http://genome.gsc.riken.go.jp/) for

of sequence [5,

amHI and XhoI. Vector: a modified pBluescript KS(+) after xcision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' amHI Host: DH10B. Retnina RNA was provided by Stefano cich (Department of Neurobiology, Harvard Medical School, 220 od Ave., Boston, MA 02115, USA) whose assistance is ully acknowledged.

RNA was provided by Stefano Gustincich (Department of RNA was pravided by Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA USA) whose assistance is gratefully acknowledged. SAGATICTCGAGTIAATIAAATIAATCCCCCCCCCCC 3']. cDNA was cleaved

Location/Qualifiers .1033

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/mol\_type="mRNA" /strain="C57BL/6J"

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99.4%; Pred. No. 1.9e-219;
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c1. .433
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                                                                                                                                                                                                                                                                                    match=787)"
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/lab_host="DH10B (phage-resistant)"
/lab_host="NH40E:30140199"
/lab_host="Wilth MGC 135"
/done lib="Wilth MGC 135"
/note="Vector: pCWVSport6.1; Site 1: BcoRV; Site 2: Not1;
Normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5,
14.5, and 15.5 (size selected for the 0.5-1 kb fragments)
Cloned directionally, priming method: Oligo-dr. cDNA enrichment: >1k bp, Average insert size 1.6k bp.
Normalization (Cot value): 7.5 kb. Priming sequence:
5'GACTAGTTCTAGATCGCGAGCGCCCC(T)3' Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                              ITGAAAAGATACTATTTTTATTATTATTGTGACAAAATGTTAAATGGATATTAAA 1144
                                                                                                                                                                                                                                                                                                                           EST 05-FEB-2003
                                                         AGTICCCAACTGTGAGGGGGAAGAGCTGGGGACAAGCTCCTCCTCCTGGAICCCTGT 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367
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                                                                                                                                                               INGAAAAGAIACIAITITIIIAITIAITIAITGIGACAAAAIGIIAAAIGGAIAITAAA 901
9
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a, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Procurement: Dr. David Rowe ibrary Preparation: Invitrogen Corp ibrary Preparation: Invitrogen Corp ibrary Arrayed by: The I.M.A.G.E. Consortium (LLNL) quencing by: Agencourt Bioscience Corporation distribution: MGC clone distribution information can be hrough the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov NDAM045 row: n column: 16 ality sequence stop: 611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACAGTGAGTGGCTGGGAAGAGCCAAAATCAACAGCTCCAGCCCTCTGCGCTAC
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                                                                                            AGTICCCAACTGIGAGGGGGAAGAGCTGGGGACAAGCTCCTCCTGGATCCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 724.4; DB 14; Length 892;
Pred. No. 7.9e-178;
0; Mismatches 19; Indels 10;
                                                                                                                                                                                                                                                                                                                     1 892 bp mRNA linear ES;
RT 11289277 NIH MGC 135 Mus musculus cDNA clone
0140199 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism≈"Mus musculus"
/mol_type="mRNA"
/db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robert Strausberg, Ph.D.
                                                                                                                                                                                                  DAMATCATGATTTCTCTTC 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                    raaarcargarircrerre 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                    culus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                 GI:28242661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.0%;
96.6%;
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Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murin; 1 (bases 1 to 918) NIH-MGC http://mgc.nci.nih.gov/ NIH-ional Institutes of Health, Mammalian Gene Collection (Nupublished (1999) 602092080F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:42( 241 CTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCAGGGTCTTCCCTTCGC cecaccercecercescrearerrassecrececerrecrasecracerrasecre CAAGITCACIGAGGGCCTIGCICICCCAGAITCCIIAAACIITICCCIGGCIGCAGG CAAGTTCACTGAGGGGCCTTGCTCTCCCAGATTCCTTAAACTTTCCCTGGCTCCAGG TCCTGTCCTCTCCTCAAAGGCAGCCAGAGCTTGTTCACATGTTTTCCACAG GCCCCTACTTATCCCTGACTCCNCCACCCACTCACCCGAACACGTTTATTGACTT 661 GCACCANGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGACT 721 ccagaagricccaacrerdageeegaaaagacreeegacaacaacreecreecreearr G--TGGATTTTGAAAAGATACTATTTT---ATTATTATTGTGACAAAATGTTAAAT GGTGGAATTTTGAAAAGAACNAATTTTGTAATTATATTGGTGACAAAATGTTTAA GTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAACGG GTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAACGGT CTGGCCCTGCGCTGCAAGAATTCTCAGCCACAGCAAGCTCTCCTGGGCCC crescerrecereceresaasaarrereaseeacaseaaserereereseee ATCACCACACCTCCCTACCCCACCCCCACCTCCTCCACCCCCTCGCTGCTCCTTGGT ATCCTTGCTCTTC-TTAACATCCCATCCCACCACCACTATCCACCTCACTAGCTCCC Arccirigerretriaacareceareceaecaecaecaecaecreereaecreeree GCCCCTACTTATCCCTGACTCCCCCACCCACTCACCCGACCACGTGTTATTGACT GCACCAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGACT CCAGAAGTTCCCAACTGTGAGGGGG-AAGAGCTGGGGACAAGCT-CCTCCCTGGAT( CGCACCCTCCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTACTTTGGACT

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/lab_host="DHIOB (TI phage-resistant)"
/clone lib="WOI CGAP Cod4"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGAGCCTTCTCAGGAGGAGCTGACAGAGAGGACCGCCGGGAGCCCCCTGAACT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caddadccirrcroadaddadcroacaddaddadccccccadadcr 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STICATCCTCGGCCAGGACAGGATGGAGCACAAGCAGGTGTGGATGGGACAGTGAG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGAAGAGACCAAAATCAACAGCTCCAGCCCTCTGCGCTACGACCGCCAGATTGG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGGGCTGTTGCCGCTGCGGCCAGGGTCTTCCCTTCGGATCCGCACCCTCCCCTG 621
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                                                                                      equencing by: Incyte Genomics, Inc.
distribution: MGC clone distribution information can be
through the I.M.A.G.E. Consortium/LINL at:
//mage.lln.gov
LLAM9767 row: p column: 20
uality sequence start: 17
uality sequence start: 724.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAAGTGCTCCTAAAAGGCCGGGAGCGCGGGCCTCGCCGAGCTATTGCAGCCCATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGAATTCTCAGCCACAGCAGCAAGCTCTCCTGGGCCCCCAGCTCCGTTTGTGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
Procurement: Jeffrey E. Green, M.D.
Library Preparation: Life Technologies, Inc.
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 918;
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99.2%; Pred. No. 4.7e-152;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
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Sokazaki, Y., Costo, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tarana, Y., Hasegawa, H., Yamanaka, I., Schombach, C., Gojobori, T. Maldarelli, R., Hill, D. P., Bult, Riyosawa, H., Yagi, K., Tasgagawa, Y., Hill, D. P., Bult, Hume, D.A., Quackenbush, J., Schriml, L. M., Kanapin, A., Swist, C., Gorbani, L. E., Eract, T. Bradt, D. Bradt, D. P., Bult, Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kar Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konag Kurcohkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D. Mallais, L., Marchiouni, L., McKenzie, L., Miki, H., Nagashime Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrosky, N., Pillai, R., Pontius, J.U., Qi, D., Randandrar Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Rings Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, Sultana, R., Takenaka, Y., Taylor, M., St., Marchabe, Y. Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, L., Yang, L., Yang, Y., Watanabe, Y. Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizaw Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Inotani, K., Itoh, M., Kagawa, T., Miyazaki, A., Sahai, K., Saski, D., Shingswa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lanč Rogers, J., Birney, E. and Hayashizaki, Y.

Rogers, J., Birney, E. and Hayashizaki, Y.

Radiysis of the mouse transcriptome based on functional an of 660,770 full-length connermance of 60,770 full-length connermance of 60,770 full-length connermance of 66,770 full-leng
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Conteact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Ge
Sciences Center(GSC), Yoshoman Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-004
Tel: 81-45-503-922
Fax: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                   BY742288 RIKEN full-length enriched, adult retina Mus musc
clone A930030D13 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computational Analysis of Full-Length Mouse cDNAs Compare
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDN
prepare full-length cDNA libraries for rapid discovery of
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-for
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muriz
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY742288.1 GI:27167686
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682 GGCCT 686
                                                                                                                  GGCCT 662
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PUBMED
                                                                                                                                                                                                                                                                                      RESULT 4
BY742288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
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ing pipeline with 384 multicapillary sequencer. Genome Res., 1757-171 (2000)
er-based methods for the mouse full-length cDNA pedia: real-time sequence clustering for construction of andant cDNA library. Genome Res. 11 (2), 281-289 (2001) ibrary was prepared and sequenced in Mouse Genome Spedia Project of Genome Exploration Research Group in Riken Sciences Center and Genome Science Laboratory in RIKEN. n of Experimental Animal Research in Riken contributed to mouse tissues

οŧ RNA was provided by Dr. Stefano Gustincich (Department of ology, Harvard Medical School, 220 Longwood Ave., Boston, USA) whose assistance is gratefully acknowledged. visit our web site (http://genome.gsc.riken.go.jp) for details.

organism="Mus musculus" /mol\_type="mRNA" /db\_xref="taxon:10090" /clone="A930030D13" /tissue\_type="retina" Location/Qualifiers .665

contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCATCCAAGAGCTCTTTTTTTTTTTTVN 3'], cDNA was dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="RIKEN full-length enriched, adult retina"

/clone\_lib="Site 1: Sall; Site 2: BamH1; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken

367 121 61 AGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACAAGCAGGTGTG AGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACAAGCAGGTGTG GACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCCCTCTGCGCTAC GACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCCCTCTGCGCTAC 2; Gaps 22; Indels Score 605.6; DB 13 Pred. No. 7.7e-147; 0; Mismatches 22; 51.8%; 96.4%; nservative

DB 13; Length 665;

427 181 487 241 547 301 CCAGATTGGGGAATTTACAGTCATCAGGGCTGGGCTCTACTACTGTGTCAG ccadarregegaarrracagrearcagegeregegereracracergracrege CTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAACGGTGTG CTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAACGGTGTG CCTGCGCTGCCTGGAAGAATTCTCAGCCACAGCAGCAGCTCTCCTGGGCCCCCAG CCTGCGCTGCAAGAATTCTCAGCCACAGCAAGCAAGCTCTCCTGGGCCCCAG

302 CTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCAGGGTCTTCCCTTCGC caadricacreagescerrecreeceaarrecriaaacrireceresere 482 ATCACCACACCTNTCTACCCCACCCTCACTCCTCCACCCCCTAGCTGCTCCTTGGT TCCTGT-CTCTCCTCAAAGGCAGCCAGAGCTTGTTCACATGTTTCCATTCCACAGA( recrerererereanagecagacagecrigicacargnitricarecacada TCCTTGCTCTT-CTTAACATCCCATCCCACCACAACTATCCACCTCACTAGCTCCC TCCTTGCTTCTTTACATTCCATTCCACCACAACTATTCACCTTACTAGCTCCAC CGCACCCTCCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTACTTTGGACT 362 cecaccerecerresercarentasecreceerrecerrectasecraringaer CCC 908 CCC 664 422 847 608 542 602 899 728 788 906 RESULT 5 AK044387 ð 셤 g ð g à 임 ð à à

DEFINITION

AK044387 linear HTC 20-Mus musculus adult retina cDNA, RIXBN full-length enriched clone:4930010H34 product:tumor necrosis factor (ligand) superfamily, member 12., full insert sequence. AK044387

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina Mus musculus (house mouse) GI:26336423 HTC; CAP trapper Mus musculus AK044387.1 ACCESSION VERSION KEYWORDS ORGANISM

Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Weth. Enzymol. 303, 19-44 (1999) 99279253 .0349636 AUTHORS TITLE REFERENCE JOURNAL PUBMED

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, I Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of r Genome Res. 10 (10), 1617-1630 (2000) 1042159 AUTHORS JOURNAL PUBMED REFERENCE TITLE

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carr Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., I Sumi, N., Ishli, Y., Nakamura, S., Hazama, M., Nishine, T., Harr Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashi, Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watal Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., I Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizak: RIKEN integrated sequence analysis (RISA) system--384-form Genome Res. 10 (11), 1757-1771 (2000) JOURNAL

Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) The RIKEN Genome Exploration Research Group Phase II Team FANTOM Consortium. AUTHORS REFERENCE

PUBMED REFERENCE

TITLE

JOURNAL

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(1) (1) Length 2237;

Score 549; DB 11; Pred. No. 8.2e-132;

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OST189654, genomic survey sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Muril
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                                                                               GGTGCTGAGCCTGGGCCTGGCGCTGGCCTTGCCTTGGCCTCCTGCTGGTCGTGGT
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Mismatches
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information ca
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAML12034 row: b column: 07
High quality sequence stop: 728.
Location/Qualifiers
1...731
                                                                                                                                                                                                                                                                                                      /clone="IMAGE:5405478"
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/tissue_type="adenocarcinoma, cell line"
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/clone_lib="NIH MGC 90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_l:
Site_2: Sall, cloned unidirectionally; oligo-dT p
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Techno
Note: this is a NIH_MGC Library."
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85.2%; Pred. No. 2.7e-124;
iive 0; Mismatches 101;
                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
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604; Conservative
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ia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2 http://mgc.nci.nih.gov/.
31 Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                      Score 533.4; DB 29; Length 543;
Pred. No. 5.2e-128;
0; Mismatches 6; Indels 0;
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                                                                                                                                                              /db_xref="taxon:10090"
/clone="0821186564"
/cloll_type="embryonic stem cell"
/clone_lib="www musculus 1298v/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: Robert Strausberg, Ph.D. cgapbs-r@mail.nih.gov
Procurement: ATCC
                                                                                            /organism="Mus musculus"
                                                                                                                  /mol_type="genomic DNA"
/strain="129SV/EV"
                          Gene Trap.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CONA Library Preparation: Life Technologies, Inc.

CONA Library Preparation (LINE)

CONA Library Preparation (LINE)

CONA Library Limitation of Cona Contaction (LINE)

High quality sequence stop: 728.

High quality sequence stop: 728.
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/tissue_type="adenocarcinoma, cell line"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NHH MGC 90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1
Site_2: Sall; Cloned unidirectionally; oligo-dT ]
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Techn
Note: this is a NIH_MGC Library."
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603395641F1 NIH_MGC_90 Home sapiens cDNA clone IMAGE;54054
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection Unpublished (1999)
366 GACTOTTICAMGITCACTGAGGGGCCTTGCTCCCCAGATTCCTTAACTTTCC
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/db xref="taxon:10090"
/clone="IMAGE:3155633"
/tissue type="tumor, gross tissue"
/tissue type="tumor, gross tissue"
/dev stage="10 months"
/lab_host="DH10B"
/lab_host="DH10B"
/clone lib="NCI CGAP_Mam3"
/note="Organ: mammar, vector: pCMV-SPORT6; Site
Site 2: Not1; Cloned unidirectionally. Primer: O
Library constructed by Life Technologies. Investi:
providing samples: Lothar Hennighausen/Chu-Xia De:
Reference for transgenic model: Xu et al., Nature
22, 37-43 (1999)."
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murin
1 (bases 1 to 533)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE628951 53 bp mRNA linear EST 25 uu30c03.yl Soares mammary gland NMLMG Mus musculus cDNA cl IMAGE:3373444 5' similar to TR:054907 054907 TNF-RELATED W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 CCGAGCTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 AGGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 AGGTGTGGATGGGACAGTGAGTGCCTGGGAAGAGACCAAAATCAACAGCTCCAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTGCTGAGCCTGGCCTGGCCTGCCTTGGCCTCCTGCTGGTCGTGGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 43.2%; Score 504; DB 10; Local Similarity 99.8%; Pred. No. 2.5e-120; nes 504; Conservative 0; Mismatches 1;
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                        organism="Mus musculus"
mol_type="mENA"
gtrain="129,C57BL/6J,FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 CGGTGTGCTGCCCTGCCTG 505
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E: Robert Strausberg, Ph.D.
cgapbs.remail.nih.gov.
Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
Library Preparation: Life Technologies, Inc.
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
equencing by: Washingron University Genome Sequencing Center
distribution: NCI-CGAP clone distribution information can be
through the I.M. A.G.E. Consortium/LLNL at:
llnl.gov/image/html/iresources.shtml
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/lab_host="NHIOB"
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/note="Vector: pt7f3D-pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pf773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
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al Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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lone is available royalty-free through LLNL ; contact the
Consortium (info@image.llnl.gov) for further information.
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    .533
/organism="Mus musculus"

                                                                                                                                                                                                                  t: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uality sequence stop: 437.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3373444"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     imer: -40RP from Gibco
                                                                                                                                                                ished (1997)
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/organism="Mus musculus"
/mol type="mRNA"
/db_xref="taxon:10090"
/clone="InfAGB:4527038"
/tissue_type="retina"
/lab bost="nBIAD (phage-resistant)"
/clone lab bost="NBIAD (phage-resistant)"
/clone lab=NUH_MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Note=: his is a NIH_MGC Library."
                                                                                                                                                                                                       Mus musculus
Mukaryota: Metazoa; Chordata; Craniata; Vertebrata; Eutele
Bukaryota: Butheria; Rodentia; Sciurognathi; Muridae; Murin
1 (bases 1 to 650)
                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (
                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Copko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information cafound through the I.M.A.G.E. Consortium/LLNL at:
http://image.lihl.gov
Plate: LLAM10435 row: h column: 15
BG404836 650 bp mRNA linear EST 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACCCCATTCAGGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGAGACCAAAATCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 468.
Location/Qualifiers
1..650
                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                      BG404836.1 GI:13298284
                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                  mRNA sequence.
                                                                                                BG40483
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            LOCUS
                                                                                                                                                                                                             ORGANISM
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VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
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/dev stage="ADDIA"
//dev stage="ADDIA"
//dev stage="ADDIA"
//lab_host="DH10B (Life Technologies)"
//clone_lib="ULI-R-EPO"
//clone_lib="ULI-R-EPO"
//clone_lib="Uli-R-EPO"
//note="Vector: pT7130-Pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: Eco RI; UI-R-EPO is a
subtracted cDNA library constructed according to Bonaldo,
Lennon and Soares, Genome Research, 6:791-806, 1996. First
strand cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an Eco R I adaptor digested with Not I, and cloned
directionally into pT773-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tags for this
library are: distal colon, GAAGTGCTCC; osteoblast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 687 bp mRNA linear EST 02-MAY-2002 00-coc-1-22-0-UI.sl UI-R-EPO Rattus norvegicus cDNA clone 0-coc-1-22-0-UI 3', mRNA sequence.
                                                               503
                                                                                                                                  ICCTIGGICCAGICCIGI-CICICCICAAAGGCAGCCAGAGCITGIICACAIGII 829
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nuence contained an oligo-dT track that was present in the
cloctide that was used to prime the synthesis of first
cDNA and therefore this may represent a bonafide poly A
he sequence tag present in the cDNA between the NotI site
coligo-dT track served to identify it as a clone from the
cased duodenum library cDNA Library Preparation: M.B. Soares
me distribution: clones will be available through Research
s (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      norvegicus
Aa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
a; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                ',M.F., Lennon,G. and Soares,M.B. zation and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                       --CCAAAGAGTATACTAGATCTACTTAAATAGCCATGCAAAAAAATATACACA 619
GGCTCCAGGAGCATCACCACACCTCCCTACCCCACCCCCACTCCTCCACCCCTC
                                                    MEBRF, Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : Soares, MB
lated Laboratory for Computational Genomics
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/clone="UI-R-BP0-coc-l-22-0-UI"
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/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     norvegicus (Norway rat)
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ton Road , 4156 N
.9 335 8250
.9 335 9565
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murin
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8
                                                                                                                                    Length 687;
                                                                                                                                                                      Indels
                                                                                                                                Score 488.8; DB 13;
Pred. No. 2.6e-116;
0; Mismatches 73;
AAGATATCAA, cell line R3327 5A, R3327 5P, CACGTGAGAT; duodenum,
                                                 TAG_TISSUE=duodenum
TAG_LIB=UI-R-EP0
                                                                                   TAG SEQ = TGTGGTTCAT"
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ilarity 87.9%;
Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murin
1 (bases 1 to 939)
                                                                                                                                                                  CB849011 939 bp mRNA linear EST 01
MRA-0673 MOUSE ADULT RETINA Mus musculus cDNA 5', mRNA seq
CB849011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Annotation and analysis of 10,000 expressed sequence tags developing mouse eye and adult retina Genome Biol. 4 (10), R65 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 ACAGCTCCAGCCCTCTGCGCTACGACCGCCAGATTGGGGGAATTTACAGTCATCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 ACAGCTCCACCCTCTGCGCTACGACCGCCAGATTGGGGAATTTACAGTCATCAG
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542 AGCCAGNGCTTGATGACATGTTTTCCATTCCACAGACATATTC 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Swaroop, A. Department of Ophthalmology and Visual Sciences Kellogg Eye Center, University of Michigan 540 KEC, 1000 Wall St., Ann Arbor, MI 48105, USA Tel: 734 615 2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="retina"
/clone_lib="MOUSE_ADULT_RETINA"
/note="Vector: pSPORT1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: swaroop@umich.edu.
    Location/Qualifiers
    1. .939
                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
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liver, embryo, heart, muscle, spleen"
/lab host="SOLR"
/clone_lib="Rat gene index, normalized rat, norvegicus,
lento Soares"
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Xho1; Estimated insert size approx.1 kb"
                                                              H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., age, A.R. and Adams, M.D. nome Project: Generation of a Rat EST (REST) Catalog & Rat
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stitute for Genomic Research
Medical Center Drive, Rockville, MD 20850,
3011-838-529
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lone is available through the ATCC,
3-365-2700 for further information
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/db_xref="taxon:10116"
/clone="RGIEF49"
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## SUMMARIES

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Description	Aav18599 Mus muscu	Adc97713 Murine FL	Aax23425 Mouse TNR	Aaa49717 Human PRO	Abk40255 cDNA enco	Aax56000 Human tum	Acc57587 Polynucle	Acc57901 Human TWE	Adc35205 Human cDN	Abk34881 Human cDN	Aav18600 Homo sapi	13 TNF re	Aad04350 Human TRE	Aax23424 Human TNR	Aas03964 Expressio	Adb56326 Toxicity-	Abx37032 Bovine ES	90 Human	9540 Colon	Ach34013 Human end	Abn55975 Mouse spl	Abt09678 Human PAL	Abx52254 Bovine ES
ΙD	A.	ADC97713	AAX23425	AAA49717	ABK40255	AAX56000	ACC57587	ACC57901	ADC35205	ABK34881	AAV18600	AAV47613	AAD04350	AAX23424	AAS03964	ADB56326	ABX37032	AAT22190	ABK29540	ACH34013	ABN55975	ABT09678	ABX52254
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Length	1	1239		S	35	1421	30	1306	30	ß	37	1236	1236	1030	868	412	408	282	195	493	65	1064	264
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Ada71938 Ric Adc8668 Hur Adc86738 Hur Aad30228 Hur Aat94101 Hur Aat18551 Hur Aat18551 Hur Aat18551 Hur Aat18658 Hur Abt60682 Hur	2484 2484	3631	388	3843	\$529	0254 R26	200	NTS					related ligand (TRELL) gene.	ligand; tnf; treatment; cancumulation; suppression;				s factor related ligand"								<ul> <li>useful for, e.g. treating</li> <li>es to tissue grafts.</li> </ul>		tumour necrosis factor related can be included with a carrier
7 ADA71938 9 ADC86688 6 ADC86738 6 AAD30228 2 AAT94101 2 AAT18551 2 AAT94108 6 ABT09682	ADC8673 ADC8673 AAZ1726 AAA0248	ADC8/06 ABK9863	ACD1388 ABK9859	ACD1384	ABL3452	ABL7025	AAH0500	ALIGNMENT		1168 BP.			factor	related stem; sti			ion/Qualifiers	umour necrosis			945.	41P. 15P. 20P.	ry medicine.	ng JL;		related ligand - u immune responses	; English.	encoding mouse tu ive fragments car
2000 1117 0 3133 0 53522 0 53526 0 53577 0 53577	5452 5452 9 1337 8 1000	8 3163 8 12733	8 12733 8 12739	8 12739	7 16167	7 16167	7 720			CDNA;		irst entry)	tumour necrosis	U Wa	ש		h t	/*tag= a /note= "ti			97WO-US013	96US-002354 96US-002851 97US-004083	EN INC. GENEVA FACULTY	Y, Browning	9/13.	factor ease and	5-46; 69pp	that or act
0 4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6		s. e.	m m	8.	o. 9.	.6	4. C.			AAV18599 standard;	18599;	-JUL-1998 (£	musculus	; tumour mmune di	ft rejection;	musculus.			WO9805783-A1.	-FEB-1998.	AUG-1997;	-AUG-1996; -OCT-1996; -MAR-1997;	(BIOJ ) BIOGEN (UYGE-) UNIV GE	Chicheportiche	1; 1998-14561 PSDB; AAW4752	Tumour necrosis auto-immune dis	aim 2; Page 4	The sequence is (TRELL). TRELL
0 0 0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	, w w w c	a) (a)	0 38 39	4.	44	4 4	* 4 * 3		RESULT 1		AC AAV18	21	XX DE Mus		KW graft XX	OS Mus	FH Key			12	- 40	PR 07- PR 18-		-	34 7		បី	•
				-																								

CAGGAGCATCACCACACCTCCCTACCCCACCCCCACTCCTCCACCCCCTCGCTGCT Treating a TWEAK-related condition, e.g. liver, gastrointestinal "FL-TWEAK" Location/Qualifiers Ė BP Murine FL-TWEAK coding sequence. Zheng ADC97713 standard; cDNA; 1239 09-APR-2003; 2003WO-US011350 09-APR-2002; 2002US-0371611P (first entry) /product= ಡ À, 1. .750 /\*tag= Burkly L, Jakubowski WPI; 2003-845256/78. (BIOJ ) BIOGEN INC P-PSDB; ADC97712 WO2003086311-A2 15-JAN-2004 23-OCT-2003 1141 ADC97713; 721 781 1021 781 901 901 961 196 1081 Mus sp RESULT 2 Д g 9 ð ð 셤 ઠે à à 셤 à du ₹ cl compositions to treat cancer, autoimmune diseases or uses to tissue grafts, or to stimulate or suppress the immune useful to screen for TRELL receptors, by labelling with a bel and screening compositions for binding. Agents ith TRELL-receptor binding can also be screened for, can instered, optionally with interferon-gamma, to induce cell t, suppress or alter immune responses (especially involving recinoma cells) involving a signal pathway between TRELL and The DNA sequence can be used in gene therapy for TRELLö ders in mammals (especially humans), e.g. tumours, difflammatory diseases or inherited genetic disorders, by nto cells, and expressing, therapeutically effective amounts e.g. a virus comprising a gene encoding TRELL. It may also the preparation of prepare probes for screening etic DNAs for TRELL-encoding sequences and for antisense 780 120 120 180 180 240 240 300 300 360 360 420 420 480 480 540 540 900 600 099 999 720 720 09 9 SATCCGCACCCTCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTACTTTGG SATCCGCACCCTCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTACTTTGG CTGAGCCTGGGCCTGGCCTGCCTTGGCCTCCTGCTGGTCGTGGTCAGCCT CTGAGCCTGGGCCTGGCGCTGGCCTGCCTTGGCCTCCTGCTGGTCGTGGTCAGCCT AGCTGGGCAACGCTGTCTGCCCAGGAGCCTTCTCAGGAGGAGCTGACAGAGGAGA AGCTGGGCAACGCTGTCTGCCCAGGAGCCTTCTCAGGAGGAGGAGCTGACAGCAGAGGA CGGGAGCCCCCTGAACTGAATCCCCAGACAGAAAGCCAGGATGTGGTACCTTT CGGGAGCCCCCTGAACTGAATCCCCAGACAGAGGAAAGCCAGGATGTGGTACCTTT GAACAACTAGTCCGGCCTCGAAGAGTGCTCCTAAAGGCCGGAAGGCGGCGCCTCG GCTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACAAGC GCTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACAAGC GTGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCCCTCT GTGGATGGGACAGTGGCTGGCAAGAGACCAAAATCAACAGCTCCAGCCCTCT TACGACCGCCAGATTGGGGGAATTTACAGCTCATCAGGGCTGGGGCTCTACTACTGTA TACGACCGCCAGATTGGGGAATTTACAGTCATCAGGGCTGGGGCTCTACTACTGTA CAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAA caderecacriridareadedaaadecrerererereadecregacrifecregidaa GTGCTGGCCCTGCGCTGCCTGGAAGAATTCTCAGCCACAGCAGCAAGCTCTCCTGG GTGCTGGCCTGCCTGGAAGAATTCTCAGCCACAGCAGCAGCTCTCCTGG CAGCTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCAGGGTCTTCCCT CAGCTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCAGGGTCTTCCCT TICAAGITCACTGAGGGGCCTTGCTCCCAGALTCCTTAAACTTTCCCTGGCTC Tricaagircacigaggggcirgciciccagariccriaaacrirgciggcic BAGCATCACCACCTCCCTACCCCACCCCCACTCCTCCACCCCCTCGCTCCTTT 0; Gaps Length 1168; 242 A; 360 C; 298 G; 268 T; 0 U; 0 Other; 0; Indels DB 2; ; Score 1168; DB 2; ; Pred. No. 8.6e-306; 0; Mismatches 0; 100.0%; Conservative BP;

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TNF; Tumour Necrosis Factor; TWEAK; fibrosis; cardiac disease; liver disease; lung disease; kidney disease; skin disease; skin disease; skin disease; skin disease; skeletal muscle disease; adipose tissue disease; gastrointestinal tract disease; pancreatic disease; errorative organ disease; pancreatic disease; bone disease; connective tissue disease; callular death; hepatot: dermatological; gastrointestinal; osteopathic; gene; ss. GACGTATCCTTGCTCTTAACATCCCATCCCACCACAACTATCCACCTCACTAC cadascocorractratocorgaorococoacocorocogacoacororraria TTGTGCACCAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTC THETGCACCAGGCACTGAGTGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTC 1021 TAGGCCAGAAGTTCCCAACTGTGAGGGGGAAGAGCTGGGGACAAGCTCCTCCCTG TAGGCCAGAAGTTCCCAACTGTGAGGGGGGAAGAGGCTGGGGACAAGCTCCTCCTCCTG 1081 CIGIGGAITITGAAAAGAIACIATITITTATTATTATTGIGACAAAIGTTAAATG FL-TWEAK; TNF relatedness and weak ability to induce cel GGTCCAGTCCTGTCTCTCAAAGGCAGCCAGAGCTTGTTCACATGTTTCCATT GACGTATCCTTGCTCTTCTTAACATCCCATCCCACCACTATCCACCTCACTA CAAAGCCCCTACTTATCCCTGACTCCCCACCCACTCACCCGACCACGTGTTTAT GGTCCAGTCCTCTCTCCTCAAAGGCAGCCAGAGCTTGTTCACATGTTTCCATT χ, TAAAGAGAATAAATCATGATTTCTCTTC 1168 1141 TAAAGAGAATAAATCATGATTTCTCTTC 1168 Hahm

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Tumour necrosis factor receptor; signal transducer molecule; TNF; developmental abnormality; gestational abnormality; prostate ca ApOs; APOS; TOS; TNRL-1; TNRL-3; diagnosis; treatment; therapy; cytoplasmic domain; immunogen; antibody preparation; breast carci apoptosis; mouse; ss. New Tumor Necrosis Factor family receptor polypeptides and ligand useful for diagnosis and treatment of prostate cancer and develop or gestational abnormalities. GGTCCAGTCCTGTCTCTCCTCAAAGGCAGCCAGAGCTTGTTCACATGTTTCCATTC GACGTATICCTTGCTCTTTAACATCCCATCCCACCACAACTATCCACCTCACTAG GACGIAICCITGCICITGIAACAICCCAICCCACCACAACIAICCACCICACIAG TTGTGCACCAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAAACCTG 1032 rrerecaccacacreagareserresercresersesassassassassas 1021 TAGGCCAGAAGTTCCCAACTGTGAGGGGGAAAGAGCTGGGGACAAGCTCCTCCTGG 1092 TAGGCCAGAAGTTCCCAACTGTGAGGGGAAGAGCTGGGGACAAGCTCCTCCCTGG 1081 CTGTGGATTTTGAAAAGATACTATTTTTATTATTATTGTGACAAAATGTTAAATGG GGTCCAGTCCTGTCTCTCTCAAAGGCAGCCAGACCTTGTTCACATGTTTCCATTC CAAAGCCCCTACTTATCCCTGACTCCCCACCCACTCACCCCGACCACGTGTTTATT 972 CAAAGCCCCTACTTATCCCTGACTCCCCCACCCACTCACCCGACCACGTGTTTATT 1141 TAAAGAGAATAAATCATGATTTCTCTTC 1168 1212 TAAAGAATAAATCATGATTTCTCTTC 1239 Example VII; Fig 13B; 156pp; English. Location/Qualifiers 1. .636 /product= "TNRL3" ВР 97US-00924634. 98WO-US018393 AAX23425 standard; DNA; 701 (first entry) rd ı. .630 /\*tag≕ (UNIW ) UNIV WASHINGTON WPI; 1999-205191/17. P-PSDB; AAW93591. DNA. Chaudhary PM; WO9911791-A2 04-SEP-1998; 05-SEP-1997; 18-JUN-1999 Mouse TNRL3 11-MAR-1999 AAX23425; 852 901 961 781 841 912 Mus sp RESULT 3 g d g g g à d à ò ð à ò 셤 equence is the coding sequence for murine transmembrane FL-atedness and weak ability to induce cell death, where TNF sosis Factor. TWEAK is a member of the TNF family. TWEAK itagonists are useful for treating a TWEAK-related y. fibrosis; cardiac disease; liver disease; lung disease; is kin disease; skeletal muscle disease; adipose tissue cointestinal tract disease; pancreatic disease; reproductive ineural disease; cartilage disease; bone disease; sue disease; cellular death, and a pathological condition opressing a TWEAK receptor. 120 180 240 480 540 600 099 720 780 851 311 300 371 360 431 420 551 611 671 731 791 131 191 251 491 9 ATCCGCACCCTCCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTATGG AGCATCACCACACCTCCCTACCCCACCCCCACTCCTCCACCCCCTCGCTGCTCTT TGAGCCTGGCCTGGCCTGGCCTTGGCCTCCTGCTGGTGGTCGTGGCCT AGCTGGGCAACGCTGTCTGCCCAGGAGCCTTCTCAGGAGGAGCTGACAGCAGAGGA scrarrigcagecearrargagerrearecregeceaggaeggageageage stegateggacagregoreggaagagaccaaaarcaacaccecerer raccaccacacarracacarrracacrcarcacacracacacrcacarracacara 2AGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAA SAGCTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCAGGGTCTTCCCT ATCCGCACCCTCCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTACTTTGG rtrcaagtrcacrgaggggccrrgcrcccagarrccrraaacrrrccrggcrc AGCATCACCACACCTCCCTACCCCACCCCCACTCCTCCACCCCCTCGCTGCTCCTT TRAAGCCTGGGCCTGGCCTGCCTTGGCCTCCTGCTGGTCGTGGTCAGCCT GCTGGGCAACGCTGTCTGCCCAGGAGCCTTCTCAGGAGGAGCTGACAGCAGAGGA GGGAGCCCCCTGAACTGAATCCCCAGACAGAAAGCCAGGATGTGGTACCTTT BAACAACTAGTCCGGCCTCGAAGAAGTGCTCCTAAAGGCCGGAAGGCGCGGCCTCG SCTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACAAGC STGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAAATCAACAGCTCCAGCCCTCT STGCTGGCCCTGCCTGCCTGGAAGAATTCTCAGCCACAGCAGCAAGCTCTCCTGG CAGCTCCGTTTGTGCCAGGTGTCTGGGCTTGTTGCCGCTGCGGCCAGGGTCTTCCCT TTTCAAGTTCACTGAGGGCCTTGCTCTCCCAGATTCCTTAAACTTTCCCTGGCTC GGGAGCCCCCTGAACTGAATCCCCAGACAGGAAAGCCAGGATGTGGTACCTTT ic, cartilage or neural tissue condition in a subject nistering to the subject a TWEAK agonist or antagonist Gaps 0 100.0%; Score 1168; DB 9; Length 1239; 100.0%; Pred. No. 8.8e-306; BP; 249 A; 386 C; 331 G; 273 T; 0 U; 0 Other; Indels 0; 0; Mismatches 2; 120pp; English. nservative ON GI ?

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n describes isolated Tumor Necrosis Factor (TNF) family peptides: APO4, APO6, APO8 and APO9 or their active d'isolated TWP related ligands in and 3 (TNRL1 and TNRL3) or fragments. APO4 is useful for diagnosing prostate cancer by evels of APO4 is useful for diagnosing prostate cancer by APO4 selective binding agents linked to a therapeutic polypeptides are also useful for identifying selective solveptides are also useful for identifying selective solveptides are also useful for identifying selective solveptide/active fragment which is extracellular, or the cell surface. The binding is preferably performed in lypeptides/ active fragments are also useful for screening and antagonists by binding and observing the changer in APO4 ective pharmacological agente useful in diagnosis or disease are also identified using APO4 polypeptides/ active I APO4 signal transducer molecules that specifically interact asmic domain of APO4 and detecting a change in level of APO4 is method is performed in vivo or in vitro. APO polypeptides is anosis/treatment of developmental or gestational duced apoptosis

BP; 139 A; 210 C; 203 G; 149 T; 0 U; 0 Other;

ö 540 103 163 120 223 180 283 240 343 300 403 360 463 420 523 480 583 643 600 09 TGACAGCAGAGGACCGCCGGGAGCCCCCCTGAACTGGAATCCCCCAGACAGGAAAGC TCGTGGTCAGCCTGGGGAGCTGGGCAACGCTGTCTGCCCAGGAGCCTTCTCAGGAG #TCGTGGTCAGCCTGGGGAGCTGGGCAACGCTGTCTGCCCCAGGAGCCTTCTCAGGAG ATGLEGIACCTTTCTTGGAACAACTAGTCCGGCCTCGAAGAAGAGTGCTCCTAAAGGC AGGCGCGCCTCGCCGAGCTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGA CAAGCTCTCCTGGGCCCCCAGCTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTG CAGGGTCTTCCCTTCGGATCCGCACCCTCCCCTGGGCTCATCTTAAGGCTGCCCCC ATGTGGTACCTTTCTTGGAACAACTAGTCCGGCCTCGAAGAAGAGTGCTCCTAAAGGC AGGCGCGCCTCGCCGAGCTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGA ATGGAGCACAAGCAGGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATC GCTCCAGCCCTCTGCGCTACGACCGCCAGATTGGGGGAATTTACAGTCATGGGGT GCTCCAGCCCTCTGCGCTACGACCGCCAGATTGGGGGAATTTACAGTCATCAGGGCT TCTACTACCTGTACTGTCAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAG rcractactractgractgracagracacrirraargagggaaaggcrgrcraccrgaag \*ACTTGCTGGTGAACGGTGTGCTGGCCCTGCGCTGCCTGGAAGAATTCTCAGCCACA SACTTGCTGGTGAACGGTGTGCTGGCCCTGCGCTGCCTGGAAGAATTCTCAGCCACA caddencircecircearecedaecerecerecereaererraadecreeee 0; Gaps 59.9%; Score 699.4; DB 2; Length 701; 99.9%; Pred. No. 5.8e-179; ive 0; Mismatches 1; Indels 0; onservative

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ã 24 ä The present sequence is that of cDNA clone DNA30879-1152 (ATCC 20 encoding human PRO207 (see AAY95338), which shows homology to ser members of the tumour necrosis factor family, especially human [ymphotoxin (23.4%). The CDNA was identified in a foetal kidney (library following identification of an expressed sequence tag will homology to human Apo-2 ligand. A claimed method for inhibiting (growth of a tumour call comprises exposing the tumor cell to PRO: PRO207, PRO30, PRO219, PRO221, PRO224, PRO328, PRO301, PRO526, PRO356, PRO356, PRO310, PRO219, PRO219, PRO224, PRO328, PRO311, PRO526, C polypeptides incorporating them. The tumour is especially a cance selected from breast, ovarian, renal, colorectal, uterine, prostic lung, bladder and central nervous system cancer, melanoma and len Nucleic acids encoding PRO179 etc. are used in the recombinant p:

703 99

TAACCTACTTTGGACTCTTTCAAGTTCACTGAGGGGCCTTGCTCCCAGATTCCT TAACCTACTTTGGACTCTTTCAAGTTCACTGAGGGCCTTGCTCTCCCAGATTCCT

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Novel composition to inhibit neoplastic cell growth or for treat: in mammal comprises polypeptides PRO179, PRO307, PRO320, PRO219, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO569 or PRO866

Claim 20; Fig 3; 172pp; English.

Marsters SA

Godowski PJ, Gurney AL,

Goddard A, Godov

Pitti RM,

Ashkenazi AJ,

Napier MA,

WPI; 2000-442668/38. P-PSDB; AAY95338.

(GETH ) GENENTECH INC

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PRO207; human; antitumour; tumour; therapy; cytostatic; breast carovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; central nervous system cancer; melanoma; leukaemia; neoplasm; ss
        661 TARACTTTCCCTGGCTCCAGGAGCATCACCACACCTCCCTA 701
704 TAAACTTTCCCTGGCTCCAGGAGCATCACCACACCTCCCTA
                                                                                                Human PRO207 cDNA clone DNA30879-1152.
                                                                                                                                                                   Location/Qualifiers
58. .807
                                                    AAA49717 standard; cDNA; 1353
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polypeptides	
; 25/ A; 443 C; 389 G; 264 T; U U; U CENEK; 53.8%; Score 628.6; DB 3; Length 1353;	
Pred. No. 1.2e-159; 0; Mismatches 219; Indels 73; Gaps 10;	1145
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GACAGCAGAGGAC 12	1080 CCTGTGGATTTTGAAAAGATACTATTTTTATTATTGTGACAAAATGTT)
CCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGCTGGTGGCAGGAGGAG 249 QY GGAGCCCCTGAACTGAATCCCCAGACAAGCCAGGATGTGGTACCTTTC 181	1135 GGATATTAAAGAGAATAATCATGA 1159
rccrececcrrrc 309	1324 (GGATATTAAATAGAATAAGTCATAA 134
.ACAACTAGTCCGGCCTCGAAGAAGTGCTCCTAAAGGCGGGAAGGCGGGCTCGC 241	SULT 5 K40255 ABK40255 standard; cDNA; 1353 BP.
XX XATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGGACAGAGA 301 AC	ABK40255;
CGGAGCGCAGGCA 429	15-JUL-2002 (first entry)
GGATGGGACAGTGAGTGGGTGGGAAGAGCCAAAATCAACAGCTCCAGCCCTCTG 361 DE DE LI	cDNA encoding human PRO20
crecadecerere 489	Human; PRO; benign tumour leukaemia; neuronal disor
П "	inflammato gene thera
CINCINCTIGIAL 343	Homo sapiens.
1000	WO200153486-A1.
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	11-FEB-2000; 2
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729	11-MAY-1999; 02-JUN-1999;
AACCTACTTTGGA 661	22-JUN-1999; 22-JUN-1999;
789	20-JUL-1999; 26-JUL-1999;
TCAAGTTCACTGAGGGGCTTGCTCTCCAGATTCCTTAAACTTTCCCTGGCTCC 721	28-000-1999; 17-AUG-1999; 31-AUG-1999;
849	01-SEP-1999; 15-SEP-1999;
SCATCACCACCCCCACCCCCACTCCTCCACCCCCTC - GCTGCTCCTT 780 PR	30-NOV-1999; 99W0-US028313. 01-DEC-1999; 99W0-US028301.
904	01-DEC-1999; 05-JAN-2000; 2
AGRICIGATITICCTCAAAGGGAGCCAGAGCTIGITICCATICC83/ A	(GETH ) GENENTECH INC.
891	Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ; Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM; Watanabe CK, Wood WI;
Tacacaaccac	WDI; 2002-205567/26. P-PSDB; AAU86129.
3CTCCCCAATCCCTTTGAGGCCCCCAGTGATCTCGACTCCCCCTGGCCA 1084 PT 3GACCACGTGTTTATTGACTTTGTGCAC	Thirty five nucleic acids encoding PRO polypeptides, useful for the benign or malignant tumors, leukemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders.

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Human; tumour necrosis factor; Apo-3 ligand; lymphotoxin; apopto NF-kappaB-dependent transcription; JNK/SAPK-dependent response; 965 ACATAAATACAGTATTCCCACTCTTATCTTACAACTCCCCCACCGCCCACTCTCC -----TTATCCCTGACTCCCCCAC 1025 ACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGATCTCGACTCCCCT 1085 chgaccccchochrandigricachcharcrcraggegeargagrecagaa 1145 CACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGG 1205 gecaggagireceaaargreaggegegaga-aacaagacaagcreerecerreag Human tumour necrosis factor Apo-3 ligand polynucleotide sequenc -----CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGG CCTGTGGATTTTGAAA--AGATACTATTTTTTATTATTGTGACAAAATGT---GCCAGAGAGTTCCCAACTGTGAGGGGGAAGAGCTGGGGACAAGCTCCTCCTGGA

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                                                                                                                                                                                                                                                                                                                                    19
mologue designated Apo-3 ligand. Apo-3 ligand has ivity. Apo-3 ligand can be used to induce apoptosis in er cells, to induce NF-kappaB-dependent transcription and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTCCTGTCTCTCC--TCAAAGGCAGCCAGAGCTTGTTCACATGTTTCCATTCC-
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                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                         73;
                                                                                                                                                                                                           Score 628.6; DB 2; Length 1421;
Pred. No. 1.2e-159;
0; Mismatches 219; Indels 73;
                                                                                                                                                     BP; 281 A; 464 C; 404 G; 272 T; 0 U; 0 Other;
                                                                                             SAPK-dependent responses in mammalian cells
                                                                                                                                                                                                              53.8%;
76.2%;
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The present sequence is that of a polynucleotide encoding a non-R member of the tumour necrosis factor (TMP) superfamily. The inven provides non-naturally-occurring proteins that contain one or more external surface loops of RANKL (see ABR42066-70) in combination terrorlogus protein core obtained from a non-RANKL member of the superfamily. Also provided are polynucleotides encoding such protein core obtained some superfamily. Also provided are polynucleotides encoding such protein bind to RANK, acting as mimics of RANKL. They can be obtained bone formation by either inhibiting bone resorption or in costeogenesis, thus providing treatment for diseases or conditions characterised by loss of bone mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New RANKL mimic comprising a core, and at least one external loop for enhancing processes of bone formation or inhibiting bone reso thus providing treatments for disease or condition characterized.
1059 ACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGATCTCGACTCCCCCTG
                                                                                                                                                                  CAGACCCCCAGGTCATTGTGTTCACTGTACTCTGTGGGCCAAGGATGGGTCCAGAAG
                                                                                                                                                                                                                                                     ----CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGA
                                                                                                                                                                                                                                                                                                                                1179 CACTICAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTGTGGATTTTGAAA - - AGATACTATTTTTTATTATTATTGTGACAAAATGT - - - T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     necrosis factor superfamily member
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                                                                                                                                                                                                                                                                                                                                                                                                                   GCCAGAAGTTCCCAACTGTGAGGGGGAAGAGCTGGGGACAAGCTCCTCCCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; RANKL; tumour necrosis factor; osteopathic; bone; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 1306 BP; 247 A; 434 C; 368 G; 257 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 624; DB 7; I
Pred. No. 2.1e-158;
                                                                              CACCCGACCACGTGTTTATTGACTTTGTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATATTAAATAGAATAAGTCATAA 1382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Teitelbaum SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
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76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACC57587 standard; DNA; 1306
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ACC57901 standard; cDNA; 1306
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73; Gaps
0; Mismatches 220; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGACCACGTGTTTATTGACTTTGTGCAC----
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The present sequence is that of a polynucleotide encoding human. The invention relates to compositions comprising heterotrimeric of tumour necrosis factor (TNF) ligand family members, and their the detection, prevention and treatment of disease. In one embod the heterotrimeric complex comprises full-length or extracellular portions of TWEAK and full-length or extracellular portions of oligand family members, preferably VEGI or VEGI-SV. The heterotrim complexes of the invention are useful for treating an autoimmune cancer or osteoporosis, and particularly for inhibiting cancer or proliferation, increasing B cell proliferation, or inducing apop T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New heteromultimeric complex having a first polypeptide member o tumor necrosis factor (TNF) ligand family, and a second differen of TNF ligand family, useful for treating cancer, osteoporosis o
                                                      GCCAGGAGTTCCCAAATGTGAGGGCGAGA-AACAAGAAAAGCTCCTTGAGA
                                                                                                                                                                    CCTGTGGATTTTGAAA--AGATACTATTTTTATTATTGTGACAAAATGT---1
                                                                                                                                                                                                                                                           ccrerecarititraaaacacaratratratratratratrereacaaaarerreat
GCCAGAAGTTCCCAACTGTGAGGGGAAGAGCTGGGGACAAGCTCCTCCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1306 BP; 247 A; 434 C; 368 G; 257 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWEAK; tumour necrosis factor; ligand; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 367-368; 388pp; English.
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                                                                                                                                                                                                                                                                                                                                                      GGATATTAAAGAGAATAAATCA 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                         GGATATTAAATAGAATAAGTCA 1305
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Query Match 53.4%; Score 624; DB 9; Length 1306; Best Local Similarity 76.0%; Pred. No. 2.1e-158; Matches 929; Conservative 0; Mismatches 220; Indels 7: Sequence 1306 BP; 247 A; 434 C; 368 G; 257 T; 0 U; 0 Other; ص ص RESULT 9 g ò g ð rcagecactaagagggectggacctggcggcaggagccaaagagactgggcctag 1164 screcechárecergácerrrangececegagareregéricececeges 1044 CCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCC 1104 629 689 749 809 780 891 SCICCCAAAGCCCCTAC------TIAICCCIGACTCCCCACCCACT 936 301 541 661 721 241 601 CTGGGCAACGCTGTCTGCCCAGGAGCCTTCTCAGGAGGAGGTGACAGCAGAGGAC 121 181 GGACCCGTCGGAACTGAATCCCCAGACAGAAGAAAGCCAGGATCCTGCGCCTTTC 269 ccgactractroccocrocadaacrocaraaaccoccaaaaacaccoccoca 329 garcecaececarrargaagrrearecaegaecregaegaegaegegegeea 389 GGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCCCTCTG 361 CGACCGCCAGATTGGGGAATTTACAGTCATCAGGGCTGGGCTCTACTACTGCTGTAC 421 GGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAAC 481 61 recrescerrecerrecerses as a recresce con a contra de cont Agenececenchece Agenenéra de de la respectación de descripción de la respectación de l SCATCACCACACCTCCCTACCCCACCCCCACTCCTCCACCCCCTC-GCTGCTCCTT AGTCCTGTCTCC--TCAAAGGCAGCCAGAGCTTGTTCACATGTTTCCATTCCadaccidececitecereradadecidecidadecidireacereritecaree -- ACAGACGTATCCTTGCTCTTAACATCCCATCCCACCACAACTATCCACCTC CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGGACTAG CAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGGCTCTACTACTGTAC egrecacriricareagegaaagergreraccreaagergaacrigergegar AGCICCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCAGGGTCTTCCCTT rececaecereceregeerearerrangeerececerrecrangement PTCAAGTTCACTGAGGGCCTTGCTCTCCCAGATTCCTTAAACTTTCCCTGGCTCC cereaacacerereaacacecearecererececeacecereacererer GCTGGCCCTGCGCTGCCTGGAAGAATTCTCAGCCACCAGCAGCAAGCTCTCCTGGG gaccongacconaccanaccinaccinaccinacinaciaccidandina GGAGCCCCTGAACTGAATCCCCAGACAGGAAAGCCAGGATGTGGTACCTTTC TATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACAAGCA GAGCCTGGGCCTGGCCTGCCTTGGCCTCCTGCTGGTCGTGGTCAGCCTG CGACCACGTGTTATTGACTTTGTGCAC

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The invention relates to an isolated nucleic acid molecule encoditumour necrosis factor family ligand. A composition comprising the isolated antibody or its fragment is used for treating an individual need of decreased level of endokine alpha activity. The endokine polypeptide present in a heterotrimeric complex is used for treat individual having a disorder associated with excessive bone resonerg. Osteoporosis, Paget's disease or arterial calcification. Treindividual having a disorder associated with insufficient bone recomprises administering an endokine alpha antagonist, which is the antibody that binds specifically to endokine alpha antagonist, which is the present sequence represents a cDNA encoding a tumour necrosis fac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Endokine alpha gene useful for preparing a composition for tr disease associated with excessive or insufficient bone resorption osteoporosis, Paget's disease or arterial calcification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; gene; human; tumour necrosis factor; TNF ligand; endokine alp excessive bone resorption disorder; osteoporosis; Paget's disease
                                                    1224 CCIGIGGATITITAAAACAGATATIATITITIATITATITGIGACAAAATGITGAT.
1024 GCCAGAAGTTCCCAACTGTGAGGGGGAAGAGCTGGGGACAAGCTCCTCCCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA encoding TNF ligand family member #12.
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                                                                                                                                                                                                                                                       GGATATTAAAGAGAATAAATCA 1156
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ROSEN C A.
NARDELLI B.
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P-PSDB; ADC35206.
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NI J.
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(ROSE/) F
(NARD/) N
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Five hundred and ninety two polynucleotides derived from a varie human tissue sources which encode secreted proteins, useful for immune deficiencies and disorders such as autoimmune disorders. 29-MAR-2001; 2001WO-US010224. 06-APR-2000; 2000US-0195582P WPI; 2002-179321/23. WO200177288-A2 Homo sapiens. 18-OCT-2001 g ò ద ð AGAAGTICCCAACTGTGAGGGGGAAGAGCTGGGGACAAGCTCCTCCCTGGA----TC 1079 --CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGGACTAG 1023 Agenceccannecentra de commande de consecuentes de consecuención de deserción de de deserción de de de deserción 4CCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCC 1104 449 689 749 780 936 896 149 209 181 241 329 301 389 361 421 509 481 569 541 629 601 199 721 809 864 837 924 891 984 61 Accededa Tecenore de Centra de Contra de Contr acceactactrescrescrescresastrescresastrescresasascresser STGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCCCTCTG AGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAAC \*AGCTCCGCCTCTGCCAGGTGTCTGGGCCTGTTGGCCCTGCGGCCAGGGTCCTCCCTG AGCATICACCACACCTCCCTACCCCACCCCCACTCCTCCACCCCCTC - GCTGCTCCTT ccharactracercercaradaderacerdederatracerarinaearee TGAGCCTGGGCCTGGCCTGCCTTGGCCTCCTGCTGGTCGTGAGCCTG :nogeccinedeceredeceredecinedericedecinecinecereceredecerederical GCTGGGCAACGCTGTCTGCCCAGGAGCCTTCTCAGGAGGAGCTGACAGCAGAGGAC ?AGGACCCGTCGGAACTGAATCCCCAGACAGAAAGCCAGGATCCTGCGCCTTTC AACAACTAGTCCGGCCTCGAAGAAGTGCTCCTAAAAGGCCGGGAAGGCGGGGCCTCGC CTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACAAGCA carreceaecearrargaagrrearceaeaecreeaeaeaeaeaeaeeae Progradadacadrandacradandanacandantandacadaracadacaratra :ACGACCGCCAGATTGGGGGATTTACAGTCATCAGGGCTGGGCTCTACTACCTGTAC Aggrecactricalgaegegaagecretchaccreaagcregactrecregaear FIGCTGGCCCTGCGCTGCCTGGAAGAATTCTCAGCCACAGCAGCAAGCTCTCCTGGG riccreeccrecereceresasaarrereaseeacreeseeacreese AGCTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGCGCCAGGGTCTTCCCTT TCCGCACCCTCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTACTTTGGA rececacereceradeseccarereaasecreceerrecreaeraceraceraceraceraceresea TICAAGIIICACIGAGGGCCTIGCICICCCAGAIICCIIAAACIIIICCCIGGCICC riccaggircacigagggccciggichccccaggresicerccaggcrecggercc - cerica de de contra de de contra d CAGTCCTGTCTCC--TCAAAGGCAGCCAGAGCTTGTTCACATGTTTCCATTCC-- ACAGACGTATCCTTGCTCTTGTTAACATCCCATCCCACCACAACTATCCACCTC PAATACAGTATTCCCACTCTTATCTTACAACTCCCCCACCGCCCACTCTCCACCTC GCTCCCAAAGCCCCTAC-------TTATCCCTGACTCCCCACT CCGACCACGTGTTTATTGACTTTGTGCAC------

Human; secreted protein, gene, ss; nutritional supplement, haemoy viral infection; bacterial infection; fungal infection; diabetes autoimmune disorder; rheumatoid arthritis; multiple sclerosis; thautoimmune thyroiditis; allergic reaction; neurodegenerative distance disease; Parkinson's disease; liver fibrosis; cancer coagulation disorder; inflammatory disorder; Crohn's disease; tissue regeneration; wound healing; burn; haematopoiesis; myeloid cell deficiency; lymphoid cell deficiency. CCTGTGGGATTTTTAAAACAGATATTATTTTATTATTATTATTGTGACAAAATGTTGA' CCTGTGGATTTTGAAA--AGATACTATTTTTTATTATTATTGTGACAAAATGT---Human cDNA encoding secreted protein #19. GGATATTAAAGAGAATAAATCA 1156 1284 GGATATTAAATAGAATAAGTCA 1305 BP ABK34881 standard; cDNA; 1364 (first entry) 08-MAY-2002 ABK34881; 1080 1224 1135 RESULT 10 ABK34881 ID ABK

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SH, Howes Agostino MJ, Ж, Fechtel (GEMY ) GENETICS INST INC Clark HF, Fe K, Graham JR; Wong GG, C. Gulukota K,

Claim 1; Page 82; 372pp; English.

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a variety of human tissue sources and which encode novel secrete proteins. The polynucleotides can be used as probes for the identification and isolation of full length cDNA and genomic DNA polynucleotides and proteins can also be used as nutritional sup. The proteins are useful in the treatment of various immune defice and disorders such as viral infections, bacterial infections, fur. infections, autoimmune thyroiditis and diabetes) and allergic read and conditions (e.g. asthma). They are also useful for treating concodencerative diseases (e.g. Alzheimer's disease, Parkinson' disease), liver fibrosis, coagulation disease) and tumours. They useful for tissue regeneration, for wound healing and in the tree burns, incisions and ulcers, the proteins are also useful for resting cuseful for tissue regeneration, for wound healing and in the tree burns, incisions and ulcers. The proteins are also useful for rehamenatopolsesis and cortering myeloid or lymphoid cell deficie Sequences ABK34863-ABK35454 represent polymucleotides of the inv The invention relates to 592 polynucleotides which have been der

Sequence 1364 BP; 246 A; 461 C; 394 G; 263 T; 0 U; 0 Other;

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The sequence is that encoding human tumour necrosis factor related (TRELL). TRELL or active fragments can be included with a carrier pharmaceutical compositions to treat cancer, autoimmune diseases immune responses to tissue grafts, or to stimulate or suppress the system. It is useful to screen for TRELL receptors, by labelling v detectable label and screening compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for then be administered, optionally with interferon- gamma, to induce death or treat, suppress or alter immune responses (especially inhuman adenocarcinoma cells) involving a signal pathway between TRI its receptor. The DNA sequence can be used in gene therapy for TRI related disorders in mammals (especially humans), e.g. tumours,
                                                                                                                                                          TRELL; tumour necrosis factor related ligand; tnf; treatment; cand autoimmune disease; immune system; stimulation; suppression;
                                                                                                                                                                                                                                    CCTGTGGATTTTGAA--AGATACTATTTTTATTATTGTGTGACAAATGT---TP
----CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGA
                                                 1173 CACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour necrosis factor related ligand - useful for, e.g. treating auto-immune disease and immune responses to tissue grafts.
                                                                                                               GCCAGAAGTTCCCAACTGTGAGGGGAAAGAGCTGGGGACAAGCTCCTCCCTGGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens tumour necrosis factor related ligand (TRELL) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "tumour necrosis factor related ligand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOJ ) BIOGEN INC.
(UYGE-) UNIV GENEVA FACULTY MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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엄 dd ð 셤 8 ò g à à CAGACCTGCCCTCCCTCTAGAGGCTGCCTGGCCTGTTCACGTGTTTTCCATCCC 1012 δ 891 777 837 721 897 780 952 837 657 541 717 601 661 237 GGGAGCCCCCTGAACTGAATCCCCAGACAGAAAGCCAGGATGTGGTACCTTTC 181 357 241 ACCGACTAGITCGGCCTCGCAGAAGIGCACCTAAAGGCCGGAAAACACGGGCTCGA 417 cgarcecaecccarrargaagrrcarccacgaccregacaggacggaggggagaga 477 TGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTG 537 ACGACCGCCAGATTGGGGAATTTACAGTCATCAGGGCTGGGCTCTACTACTGTAC 421 acaacceccagarcegegagriraragreaccegegeregecreracracererac 597 AGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAAC 481 GCTGGGCAACGCTGTCTGCCCAGGAGCCTTCTCAGGAGGAGCTGACAGCAGGAC 121 accesacarcacraticacccasasccraceccasascracerasascas CTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACAAGCA 301 TGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCCCTCTG 361 61 AGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGAT --ACAGACGTATCCTTGCTCTTGTTAACATCCCATCCCACCACAACTATCCACCTC AACAACTAGTCCGGCCTCGAAGAAGTGCTCCTAAAGGCCGGGAAGGCGCGGCCTCGC TGCTGGCCCTGCCTGCAAGAATTCTCAGCCACAGCAAGCTCTCCTGGG recrescocrecerscoresassarrorcascoresesecastrocores AGCTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCAGGGTCTTCCCTT Actroceconoriscos de production de la composición del composición de la composición d TCCGCACCCTCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTACTTTGGA recececercecraegecearcreagecreecerrecreecearcraerregga TICAAGIICACIGAGGGGCCTIGCICICCCAGAIICCIIAAACIIIICCCIGGCICC recaggireacteaddegeeeergerereeeeagaegreereergeegeergee AGCATCACCACACCTCCCTACCCCACCCCCACTCCTCCACCCCTC-GCTGCTCCTT - cerceacacercricaegeacecercercricaececercaececercrir CAGTCCTGTCTCCC - TCAAAGGCAGCCAGAGCTTGTTCACATGTTTCCATTCC-TGAGCCTGGGCCTGGCGTGGCCTTGCCTCCTGCTGGTCGTGGTCAGCCTG aggacccgrcggaacrgaarccccagacagaagaaagaagcaggarccrgcgccrrrc Gaps 70; Score 614.6; DB 2; Length 1373; Pred. No. 7.4e-156; O; Mismatches 219; Indels 70; BP; 247 A; 462 C; 394 G; 270 T; 0 U; 0 Other; 52.6%; 75.8%; onservative

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The TNF-related endothelium proliferative agent (TREPA), or its activators or agonists, are used to treat a deficit of TREPA, e.g promote wound healing or tissue grafting, by promoting vascularis also to induce apoptosis for treating cancer and eliminating autor T cells, as an adjunct to cancer chemotherapy or antiviral treat TREPA peptides can also be used to target cytotoxic agents or for affinity isolation of the corresponding receptor, the nucleic ac affinity isolation of the corresponding receptor, the nucleic acresponsive to TREPA and to screen for TREPA mimics. Ribozymes, a RNA, antibodies or peptides, are used to treat TREPA-associated diseases, e.g. tumours and metastases (by inhibiting Vascularisa ០ ន -TTATCCCTGACTCCCCCACC 1073 ACTAGCTCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGATCTCGACTCCCCCTG 1133 cagacceccagescarrererrererererereresesassassasses ----CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGA 1193 CACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCAAAGAGACTGGGC 1253 gecasgagrieceaaargraaggaggaaa-aacaagacaagcreereeraa nucleic acid encoding TREPA - useful for diagnosis and of autoimmune disease, tumours and inflammation. GCCAGAAGTTCCCAACTGTGAGGGGGAAGAGCTGGGGACAAGCTCCTCCTGGA-CTGTGGATTTTTAAAACAGATATTATTTTTTTATTATTATTGTGACAAAATGTGA ss; TNF; endothelium proliferative agent; TREPA; wound healing; tissue grafting; vascularisation; apoptosis; autoimmune; birth c related endothelium proliferative agent gene. 937 CACCCGACCACGTGTTTATTGACTTTGTGCAC-Claim 11; Page 123-4; 142pp; English Location/Qualifiers 1. .750 /product= "TREPA" ВÞ 892 ACTAGCTCCCAAAGCCCCTAC-AAV47613 standard; cDNA; 1236 97US-00798692. 98WO-US002859 (first entry) ๙ /\*tag= WPI; 1998-447255/38. P-PSDB; AAW29745. (ABBO ) ABBOTT 12-FEB-1998; 12-FEB-1997; Homo sapiens WO9835061-A2 10-FEB-1998; 27-OCT-1998 13-AUG-1998 Detecting treatment Wiley SR; 1080 1312 AAV47613; 696 AAV47613 l inflammatory diseases or inherited genetic disorders, by nto cells, and expressing, therapeutically effective amounts e.g. a virus comprising a gene encoding TRELL. It may also the preparation of prepare probes for screening etic DNAs for TRELL-encoding sequences and for antisense

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837 967 ---TTATCCTGACTCCCCACCCACT 936 541 612 661 732 721 792 780 847 907 891 132 CTGGGCAACGCTGTCTGCCCAGGAGCCTTCTCAGGAGGAGCTGACAGAGAGGAC 121 192 181 252 241 312 301 372 361 432 CGACCGCCAGATIGGGGAAITITACAGICAICAGGGCIGGGCTCTACIACTACTGTAC 421 492 481 552 601 acrececercieceaegierereceaerierieeceereceaecaaegieerecene 672 19 ccaggircacigaggggccciggircicccgcagrcgiccaggcrgccggcrcc AGTCCTGTCTCTCC - - TCAAAGGCAGCCAGAGCTTGTTCACATGTTTCCATTCC -<u>vaáracagtatricicaetetraterraciaagaagecedegecegericidaeere</u> TCAAGTTCACTGAGGGCCTTGCTCTCCCAGATTCCTTAAACTTTCCCTGGCTCC z da a consocreto en constante de la constanta -ACAGACGTATCCTTGCTCTTAACATCCCATCCCACCACAACTATCCACCTC CATCACCACACCTCCCTACCCCACCCCCACTCCTCCACCCCCTC-GCTGCTCCTT GGGCCTGGCCTGGCCTGCCTCCTCCTGCTGGTTTTG CCGACTAGTTCGCCCTCGAAGAGTGCACCTAAAGGCCCGGAAAACACGGGCCTCGA TATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACAAGCA GGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCCTCTG caacceccagarceggagriraragreacceggereggereracracrerac GGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAAC GGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGAT GCTGGCCCTGCGCTGCCTGGAAGAATTCTCAGCCACAGCAGCAAGCTCTCCTGGG Geredecerrecerredaddanirereadeceredededenereereded ACTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCAGGGTCTTCCCTT CCGCACCCTCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTACTTTGGA cescaceerecerradaceearereaageeraceeerrecerrectreceracerredga GAGCCTGGGCGCTGGCCTGCCTTGGCCTCCTGCTGGTCGTGGTCAGCCTG GGAGCCCCCTGAACTGAATCCCCAGACAGAGAAAGCCAGGATGTGGTACCTTTC GGACCCGTCGGAACTGAATCCCCAGACAGAAGAAAGACCAGGATCCTGCGCCTTTC ACAACTAGTCCGGCCTCGAAGAAGTGCTCCTAAAGGCCGGGAAGGCGCGGCCTCGC 3CTCCCAAAGCCCTAC------

1088 CACTICAGGCACTAAGAGGGGCTGGACCTGGCGCAGGAAGCCAAAGAGAGCGC 968 ACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGATCTCGACTCCCCCTG 1028 cagacccccasesariererrcacrerareresescaassarsesrcasaas ----CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGA GCCAGAAGTTCCCAACTGTGAGGGGGAAGAGCTGGGGACAAGCTCCTCCCTGGA--CCTGTGGATTTTGAAAGATACTATTTT 1108 1207 cérérégartritaaaacagarartarri 1235 CACCCGACCACGIGITIATIGACTITGIGCAC-1148 696 1024 937 1080 임 à pp ਨੋ 셤 ò 셤 à

Gaps

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Human TREPA (TNF related endothelium proliferative agent) cDNA. BP. AAD04350 standard; cDNA; 1236 (first entry) 04-JUL-2001 Human;

AAD04350

nn; tumour necrosis factor; TNF; angiogenesis; wound healing; related endothelium proliferative agent; tumour; metastasis; grafting; vulnerary; ss sapiens Ношо

Location/Qualifiers

/\*tag= a // human TREPA (TNF related endothelium proliferative agent) US6207642-B1 27-MAR-2001

98US-00105343

26-JUN-1998; 12-FEB-1997; 10-FEB-1998;

97US-00798692. (ABBO ) ABBOTT LAB Wiley SR; 

WPI; 2001-280760/29.

P-PSDB; AAE00891

Inducing angiogenesis in mammal at desired sites for promoting won healing, by administering soluble fragment of extracellular domaintumor necrosis factor related endothelium proliferative agent pro

Example 2; Col 73-74; 53pp; English.

The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molec designated as TREPA (TNF related endothelium proliferative agent) Soluble biologically active TREPA are used to treat TREPA-associal diseases, tumours or metastases. TREPA is used for inducing anglo in human for promoting wound healing and for vascularising grafte for successful grafting and to promote tissue grafts. The present sequence is a cDNA clone ID #690050 encoding human TREPA

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Sequence 1236 BP; 225 A; 416 C; 358 G; 237 T; 0 U; 0 Other;

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This invention describes isolated Tumor Necrosis Factor (TNF) fareceptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 TURNIA and I their active fragments. APO4 is useful for diagnosing prostate catestermining levels of APO4 in an individual. Prostate cancer can treated using APO4 selective binding agents linked to a theraper moiety. APO4 polypeptides are also useful for identifying select binding agents, useful in diagnosis/treament of disease by binding agents to the polypeptide/active fragment which is extracellular expressed on the cell surface. The binding as preferably perform vivo. APO4 polypeptides/ active fragments are also useful for section and antagonists by binding and observing the change activity. Effective pharmacological agents useful in diagnosis of treatment of disease are also identified using APO4 polypeptides fragments and APO4 signal transducer molecules that specifically with a cytoplasmic domain of APO4 and detecting a change in leve
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                                                                    Gaps
                                                                    68;
Length 1236;
                                                                    Indels
          DB 4;
                                                                        0; Mismatches 222;
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      Score 597.8; DB 4;
Pred. No. 2.5e-151;
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          51.2%;
75.2%;
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New Tumor Necrosis Factor family receptor polypeptides and ligamuseful for diagnosis and treatment of prostate cancer and develo or gestational abnormalities.
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                                    1088 CACTTCAGGCACTAAGAGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGG
                                                                                                                                                        eccadeagricccaaarerdagggggggaga-aacaagacaagcrccrcccrrgags
-----CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGG
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                                                                                                                                                                                                             CCTGTGGATTTTGAAAGATACTATTTTT
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/product= "TNRL3"
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(first entry)

26-SEP-2001

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                                                                                                                                                                                                                                                                                                                                                                       09
nethod is performed in vivo or in vitro. APO polypeptides as immunogens for preparing antibodies. APO4 is also prosis/treatment of developmental or gestational APO8 was transfected to human breast carcinoma cell line
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                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                Length 1030;
                                                                                                                                                            3P; 223 A; 317 C; 279 G; 211 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                Score 522.8; DB 2;
Pred. No. 4.8e-131;
                                                                                                                                                                                                                                                                     Mismatches 137;
                                                                                                                                                                                                                                                                   0;
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dard; DNA; 898 BP.

783 rrcc 837

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ocular neovascularisation; diabetic retinopathy; neovascular glaudretinoblastoma; retinopathy of prematurity; retrolental fibroplasi rubbosis; uveitis; macular degeneration; arthritis; rheumatism; decorneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic j preneoplastic condition; myocardial anglogenesis; wound granulatic scleroderma; vascular adhesion; telangiectasia; ischaemia; human; atherosclerotic plaque neovascularisation; coronary atherosclerosi peripheral atherosclerosis; pDC409-LZ-TWEAK; TWEAK receptor; TWEAK
                                                                                                                                                                                                                                                                                     /product= "Fusion protein comprising a growth horn
leader, a leucine zipper multimerisation domain, i
human TWEAK extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Card
                                                                   TWEAK extracellular domain; tumour necrosis factor; TNF; angiogene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of o
                                            Expression vector pDC409-LZ-TWEAK fusion protein-encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating anglogenesis in a mammal for treating diseases anglogenesis, e.g. solid tumors and vascular deficiencies peripheral tissue, by administering antagonist or agonist
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-1999; 99US-0172878P.
10-MAY-2000; 2000US-0203347P.
                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2000; 2000WO-US034755
                                                                                                                                                                                                                                                                                ď
                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-417975/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAU03499
                                                                                                                                                                                            fusion protein.
                                                                                                                                                                                                                                                                                                                                         WO200145730-A2
                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                28-JUN-2001
                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wiley SR;
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The sequence represents a DNA from the expression vector pDC409-L.
which encodes a fusion protein comprising a growth hormone leader
leucine Lipper multimerisation domain, and the extracellular doma
human TWEAK. The fusion protein was used in the isolation of human
receptor (TWEAKR)-expressing clones from a COS cell human cDNA li:
The TWEAK protein is a member of the tumour necrosis factor (TNF)
and induces angiogenesis. TWEAKR may therefore be used to screen
develop TWEAKR agonists and antagonists for the modulation of
angiogenesis, to be used in the treatment and diagnosis of human
complexity of an induces mediated by angiogenesis include ocular disorders
considered by ocular necvascularisation such as diabetic retin
neovascular glaucoma, retinoblastoma, retinopathy of prematurity,
corneal graft neovascularisation, and inflammatory diseases such
corneal graft neovascularisation, and inflammatory diseases such
malignant and metastatic conditions such as sarroomas and carcinom
mignant and metastatic conditions such as sarroomas and carcinom benign tumours and preneoplastic conditions, myocardial angiogene haemophilic joints, scleroderma, vascular adhesions, atherosclero plaque neovascularisation, telangiectasia, wound granulation, cor atherosclerosis, peripheral atherosclerosis and ischaemia

Example 1; Page 39-40; 46pp; English.

Sequence 898 BP; 187 A; 266 C; 267 G; 178 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTGTCAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TECGGATCCGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCTTCCTCACCTAC 849
                                                                                                       TGGGGAGCTGGGCAACGCTGTCTGCCCAGGAGCCTTCTCAGGAGGAGCTGACAGCA 115
                                                                                                                                                                                                              ACCGCCGGGGGCCCCCTGAACTGAATCCCCAGACGAAGGAAAGCCAGGATGTGGTA 175
                                                                                                                                                                                                                                                                                                                                                      TCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGG 429
                                                                                                                                                                                                                                                                                                                                                                                                                            GCCGAGCTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCAGGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCGCTACGACGCCAGATTGGGGAATTTACAGTCATCAGGGCTGGGCTCTACTAC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGGIGTGTGCTGCCCTGCCTGCAAGAATTCTCAGCCACAGCAGCAGCTCT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGTGTGCTGGCCTGCCTGCCTGGAGGATTCTCAGCCACTGCGGCCAGTTC 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396CCCCAGCTCCGCCTCTGCCAGGTGTCTGGGCTGTTGGCCCTGCGGGCCAGGGTCC 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITCGGAICCGCACCCICCCCTGGGCTCAICITAAGGCTGCCCCCTTCCTAACCTAC 655
                                                                                                                                                      TGGGGAGCCGGGCATCGCTGTCCCCCAGGAGCCTGCCCAGGAGGAGGTGGTGGCA 309
                                                                                                                                                                                                                                                  AGGACCAGGACCCGTCGGAACTGAATCCCCAGACAGAAGAAGAAGCCAGGATCCTGCG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36GCCCCAGCTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCAGGGTCT 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCAGGTGTGGACGGGACAGTGACTGGGTGGGAGGAAGCCAGAATCAACAGCTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTTGGAACAACTAGTCCGGCCTCGAAGAAGTGCTCCTAAAAGGCCGGAAGGCGGG
                                                       Gaps
                                                       0;
42.7%; Score 498.8; DB 4; Length 898; arity 87.0%; Pred. No. 1.4e-124; Onservative 0; Mismatches 82; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGACTCTTTCAAGTTCACTGAGGGCC 685
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il 7, 2004, 17:38:07 ; Search time 9.28291 Seconds
(without alignments)
1262.081 Million cell updates/sec LSLGLALACLGLLLVVVSL.....PWAHLKAAPFLTYFGLFQVH 225 141681 GenCore version 5.1.6 opyright (c) 1993 - 2004 Compugen Ltd. s satisfying chosen parameters: 681 segs, 52070155 residues .nimum Match 0% uximum Match 100% .sting first 45 summaries n search, using sw model SUM62 Op 10.0 , Gapext 0.5 jth: 0 jth: 2000000000 09-245-198A-2 vissProt\_42:\*

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## SUMMARIES

the number of results predicted by chance to have a than or equal to the score of the result being printed, at by analysis of the total score distribution.

Description	49	gallı	m tumor	097626 canis famil	r tum	homo	homod	homo	pan t	aotu	calli	043557 homo sapien	นานธ ก	P29965 homo sapien	macac		P48746 oryctolagus	P36940 rattus norv	Q9d777 mus musculu	Q9xt47 macropus eu		drosc	homod '	-	_	_	oryc	m	77 8	23678 caenor	6821 homo	097605 felis silve
DB ID	5 1 TN12 MOUSE	1 TNF5	Н			7				н	7	Н	ч	7	Н	Н	Н	٦		7	1	1 LVA_D	-	Н	-1		1 TNFB	٦		1 U104	MAPB_H	
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Q9qyu3 P42497	Q9y275 Q8thj0	Q8pxj0 Q06481	Q9xt48 095mg5	P41047	V28038 P18838	P49321
KCG2 RAT	T13B_HUMAN GATB_METAC	GATB_METMA APP2_HUMAN	TNFB MACEU	TNF6 MOUSE	NAHI BOVIN SMP ECOLI	NASP_HUMAN
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480	285 495	495	201	279	817 214	788
8.8	6.7	6.7	6.7	9.9	9.9	9.9
78.5	788	78	77.5	77	76.5	76.5
80 ג 44 ת	3 6 6	80 6	40	424	4 4 4 4	45

## ALIGNMENTS

10; AAC53517.1; -.

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Right Stransberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.I.

Altschul S.F., Zeeberg B., Buderow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Ward J., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Righteron M.J., Usdain T.B., Toshiyuki S., Carninci P., Frange C.

Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.I.

Richards S.H., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahasley R.W., Touchman M., Madan A., Rodrigues S., Sanche:

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raksley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rutterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16903(2002).
MEDLINE=98070415; PubMed=9405449; Chicheportiche Y., Bourdon P.R., Xu H., Hsu Y.-M., Scott H., Hession C., Garcia I., Browning J.L.; Hession a new secreted ligand in the tumor necrosis factor family weakly induces apoptosis."; J. Biol. Chem. 272:32401-32410(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBGINIT: Homotrimer (Potential)
-!- SUBGELIGIAR LOCATION: Type II membrane protein and secreted.
-!- IISSUB SPECIFICITY: Highly expressed in adult heart, pancrea skeletal muscle, brain, colon, small intestine, lung, ovary, prostate, spleen, lymph node, appendix and peripheral blood lymphocytes. Low expression in kidney, testis, liver, placen thymus and bone marrow. Also detected in fetal kidney, liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL ou the European Bioinformatics Institute. There are no restriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is i modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99185061; PubMed=10085077;
Lynch C.N., Wang Y.C., Lund J.K., Chen Y.-W., Leal J.A., Wiley S. TymbaK induces anajogenesis and proliferation of endothelial cell-10. Chem. 274:8459(1999).
-!- FUNCTION: Binds to FN14 and possibly also to TMRFSF12/APO3 induces of apoptosis in some cell types. Mediates NF-KappaB activation. May promote angiogenesis and the proliferation of endothelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of a ligand for the death-domain-containing recer
                                                                                                                                                                                                                                                                                                                                              Marsters S.A., Sheridan J.P., Pitti R.M., Brush J., Goddard A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by proteolytic processing.
-!-SIMILANITY: Belongs to the tumor necrosis factor family.
-!- CAUTION: Ref. 3 sequence differs from that shown due to a frameshift in position 125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lung and brain.
PTM: The soluble form derives from the membrane form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                      MEDLINE=98228355; PubMed=9560343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apos. ;
Curr. Biol. 8:525-528(1998).
                                                                                                                                                                                                                                                                                      rissum=Fetal kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissum=Toneil;
                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION
                        OT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation-Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial ires a license agreement (See http://www.isb-sib.ch/announce/ail to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 12, MEMBRANE FORM
MEMBER 12, SECRETED FORM (BY SIMILARITY)
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNDQTEESQDVVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPF
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
is factor ligand superfamily member 12 (INF-related weak poptosis) (TWEAK) (APO3 ligand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      etazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
theria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL)
90C412CC0480659B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jiogenesis; Apoptosis; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1162; DB 1; Length 225; Pred. No. 2.5e-95; 0; Mismatches 0; Indels 0;
                     processing (By similarity). Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALCOVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFOVH 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLCOVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFOVH 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLEAVAGE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                     9; BAB32249.1; -... (259; Thfef12. (2006.052; TNF_family. (2008.983; TNF_like. ); TNF; 1... (251; TNF; 1; FALSE_NEG (251; TNF; 1; FALSE_NEG (251; TNF_1; FALSE_NEG (251; TNF_1; FALSE_NEG (251; TNF_1; FALSE_NEG (251; TNF_2; 1... (
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EMBL; AF030099; AAC51923.1; -. EMBL; AF055872; AAC39724.1; -.

M N.A., AND N-TERMINUS OF SOLUBLE FORM liver, and Tonsil;

(Human)

100.0%; 24781 MW;

70 186 115

AA;

21

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Conservative

arity.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TÜMOR NECROSÍS FACTOR LIGAND SUPERFA
MEMBER 5, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFA
MEMBER 5, SOLUBLE FORM (BY SIMILARIT
CYTOPLASMIC (POTBNTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGAND SUPERFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 VQTIGTVLFCLYLHMKMDKMEBVLSLNEDYIFLRKVQKCQTGEDQKSTLLDCEKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VISIGIALACIGILLIVVVSLGSWATLSAQ----EPSQEELTAEDRREP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 ELNPOTEESQDVVPFLEQLVRPRRSAPKGRK----ARPRRAIAAHYEVHPRPGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GVDGTVSGWEETK-INSSSPLRYDRQIGEFTVIRAGLYYLYCOVHFDEGKA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 NTTVRVLKWMTTSYAPTSSLISYHE--GKLKVEKAGLYYIYSOVSFCTKAAASAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YLKLDLLVNGVLALRCLERFSATAASSPGPQLRLCQV----SGLLPLRPGSSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 DLOCKDRTASEELPKFEMHRGHEHPHLKSRNETSVAEEKROPIATHLA-----
-!- SUBUNIT: Homotrimer (By similarity).
-!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists
-:- SUBCELLULAR SOluble form (By similarity).
-!- PIM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 272;
                                                                                                             proteolytic processing (By similarity).
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8CD0338A924E044B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSF; F2395; IAM:
GO; GO:(0016021; C:integral to membrane; ISS.
GO; GO:(0016021; C:integral to membrane; ISS.
GO; GO:(00174; F:CD40 receptor binding; ISS.
GO; GO:(0016054; P:inflammatory response; ISS.
GO; GO:(000654; P:inflammatory response; ISS.
GO; GO:(0007159; P:inflammatory response; ISS.
GO; GO:(00168; P:platelet activation; ISS.
InterPro; IPR006052; TNF 5.
InterPro; IPR006052; TNF 1ike.
InterPro; IPR008083; TNF 1ike.
InterPro; IPR008083; TNF 1ike.
InterPro; IPR008083; TNF 1ike.
Ffam; PF00229; TNF; 1.
ProDom; PD00201; TNF; 1.
ProDom; PD002012; TNF 5, 1.
ProDom; PD002012; TNF 5, 1.
ProDom; PD002012; TNF 5, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.3%; Score 108.5; DB 22.5%; Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 WAHLKAAPFLTYFGLFQV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 STAVNVNPGNTYFGMFKL 272
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ243435; CAB95748.2; -.
HSSP; P29965; 1ALY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30832 MW;
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222
1229
146
251
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Best Local Similarity
Thes 58; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 1
251 2
272 AA;
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  SOLUTION DE LA PROPERTION DE LA PROPERTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vpresapkgrktrarralaahyevhpregodgagagvogtvsgweearinsseplr 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEMBER 12, MEMBRANE FORM.
WINDR, NEGROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 12, SECRETED FORM.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                            TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .., Young J.R., Burnside J.;
putative chicken CD40 ligand.";
R-2003) to the EMBL/GenBank/DDBJ databases.
Cytokine that binds to TNFRSF5. Mediates B-cell
cytokine that binds to TNFRSF5. Mediates B-cell
in the absence of co-stimulus as well as IgE
in in the presence of IL-4. Involved in immunoglobulin
tching (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                          .ogenesis; Apoptosis; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1020; DB 1; Length 249;
Pred. No. 9.4e-83;
9; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LINKED (GLCNAC. . .).
E660843361C28EBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                               ); C:integral to plasma membrane; TA; F:receptor binding; TAS.
); P:induction of apoptosis; TAS.
); P:signal transduction; TAS.
)0652; TNF family.
08983; TNF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLEAVAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
  7; AAH19047.1; ALT_FRAME..927; INFSF12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leghorn; TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                        7; TNF; 1.
251; TNF 1; FALSE NEG.
349; TNF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rel. 41, Created)
Rel. 43, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27216 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AA;
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)6; Q9JJK8; Q9JJK9; Q9R1Y0; (Rel. 40, Created) (Rel. 40, Last sequence update) (Rel. 42, Last annotation update) (Rel. 42, Last annotation update) is factor ligand superfamily member 11 (Receptor activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            novel ligand of the tumor necrosis factor receptor family ss c-Jun N-terminal kinase in T cells."; 172:25190-25194(1997).
                                                                                                                                                                               B ligand) (RANKL) (TNF-related activation-
E) (Osteoprotegerin ligand) (OPGL) (Osteoclast
(ODF) (Osteoclastogenesis-inhibitory factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8248; PubMed=9520411;
hima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
-I., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.
Higashio K., Udagawa N., Takahashi N., Suda T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   differentiation factor is a ligand for rin/osteoclastogenesis-inhibitory factor and is identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the TNF receptor and its ligand enhance T-cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Limms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J., Arron J., Robinson E., Orlinick J., Chao M., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                                                                                                                                                                        stazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
theria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erin ligand is a cytokine that regulates osteoclast ion and activation."; 176(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maraskovsky E., Billingsley W.L., Dougall W.C., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acad. Sci. U.S.A. 95:3597-3602(1998)
316 AA.
                                                                                                                                                                     actor kappa B ligand) (RANKL)
cine) (TRANCE) (Osteoprotegeri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4075; PubMed=10196481;
                                                                                                                                                                                                                                                                                                                OR TRANCE OR OPGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        c lymphoma;
2977; PubMed=9367155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0112; PubMed=9312132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7661; PubMed=9568710;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIN.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  marrow stroma;
                                                                                                                                                                                                                                                    factor)
                                                                                                                                                                                                                                                                                                                                              (Mouse)
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                                                                                                                                                                                                                                                                                                                ANKL
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characterization of the gene encoding mouse osteoclast

M N.A. (ISOFORMS 1; 2 AND 3)

ion factor."; -127(1999).

ashio K.;

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2.2-A resolution.",
J. Biol. Chem. 277:6611-6636(2002).
I. FUNCTION: Cytokine that binds to TNPRSFIIB/OPG and to
TNPRSFIIA/RANK. Obsteoclast differentiation and activation fa
Augments the ability of dendritic cells to stimulate naive T
proliferation. May be an important regulator of interactions
between T cells and dendritic cells and may play a role in t
regulation of the T cell-dependent immune response. May also
an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by protecolytic processing. The cleavage may be catalyzed by ADAM17. A further shorter soluble form was observed.

DISEASE: Deficiency in TWFSF11 results in failure to form lo alveolar mammary structures during pregnancy, resulting in of newborns. Trance-deficient mice show severe osteopetrosis no osteoclasts, marrow spaces, or tooth eruption, and exhibit profound growth retardation at several skeletal sites, inclute limbs, skull, and vertebrae and have marked chondrodysplwith thick, irregular growth plates and a relative increase simple invpertrophic chondrocytes.

SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                Lam J., Nelson C.A., Ross F.P., Teitelbaum S.L., Fremont D.H.; "Crystal structure of the TRANCE/RANKL cytokine reveals determin of receptor-ligand specificity."; J. Clin. Invest. 108:971-979(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrictic use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch
                                                                                                                                                                              MEDLINE=99240759; PubMed=10224132;
Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage H
Schloendorff J., Tempst P., Choi Y., Blobel C.P.,
Evidence for a role of a tumor necrosis factor-alpha
(TNF-alpha)-converting enzyme-like protease in shedding of TRANC
TNF family member involved in osteoclastogenesis and dendritic c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ito S., Wakabayashi K., Ubukata O., Hayashi S., Okada F., Hata T "Crystal structure of the extracellular domain of mouse RANK lig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NOD NOT IN NONLYMPHOLD TISSUES AND IS ABUNDANTLY EXPRESSED IN T BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN TRABECULAR BONE AND LUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: N-glycosylated.
-!- PTM: The soluble form of isoform 1 derives from the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (isoforms 1 and 2); Cytoplasmic (isoform 3).
MEDLINE=21150053; PubMed=11250921;
Ikeda T., Kasai M., Utsuyama M., Hirokawa K.;
"Determination of three isoforms of the receptor activator of n
factor-kappaB ligand and their differential expression in bone
                                                                                                                                                              SEQUENCE OF 139-147, PROCESSING, AND N-GLYCOSYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 137-316.
MEDLINE=21839021; Pubmed=11733492;
                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 158-316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=035235-2; Sequence=VSP_006449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lsoId=035235-3; Sequence=VSP_006448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=035235-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 274:13613-13618(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21464816; PubMed=11581298;
                                                                                                                Endocrinology 142:1419-1426(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypercalcemia of malignancy.
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EMBL; AF086711; AAD04375.1; -.
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                                                                                                  CANFA
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                                                                                 RESULT 5
TNF5_CANFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDTLIPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALACLGLLLVVVSLGSWATLSAQ-EPSQEELTAEDR------REPPELNPQT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GRKARPRR--SAPK------GRKARPRRAIA 84
                                                                                                                                                                                                                                                                                                                              SSEEMGSGPGVPHEGPLHPAPSAPAPAPPPA -> TP (in
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                                                                                                                                                                                                                                 MEMBER 11, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 11, SOLUBLE FORM.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                   3D-structure; Alternative splicing.
316 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                          ferentiation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.8%; Score 102.5; DB 1; Length 316; 24.3%; Pred. No. 0.096;
                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                Missing (in isoform 3)
                                                                                                                                                                                                                                                                                                                                                /FTId=VSP 006449.
G -> D (IN REF. 2).
MISSING (IN REF. 5).
                                                                                                                                                                                                                                                                                                                         FTId=VSP 006448.
                                                                                                                                                                                                                                                                                                                                         isoform 2).
/FTId=VSP C
                                                                                                                                                                                                                                                                           (POTENTIAL)
to license@isb-sib.ch)
                                                                                                                   7. P. organogenesis; IMP.
7. P. organogenesis; IMP.
7. P. organogenesis; IMP.
7. P. organogenesis; IMP.
7. P. organization; IMP.
7. Organization; IMP.
7. Organization; IMP.
7. Organization; IMP.
                                                                                                                                                                                                                                                                                         CLEAVAGE
                             251; TNF_1; FALSE_NEG. 049; TNF_2; 1.
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012; TNF subf; 1.
7; TNF; 1.
                AAC71061.1; -.
                         AAB86812.1;
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1143
1172
1182
1187
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1201
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TUMOR NECROSIS FACTOR LIGAND SUPERF
MEMBERS 5, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERF
MEMBER 5, SOLUBLE FORM (BY SIMILARI
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                    217 ANICFRHHETSGSVPTDYLOLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFY
165 AHLTINAASIPSGSH----KVTLSSWYHDRGWAKISNMT-----LSNGKLRVNQDGF
                                                                                             141 ---CQVHFDEGKAV---YLKLDLLV----NGVLALRCLEEFSATAASSPGPQLRL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                canis ramilialis (VOG).
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          097626,
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 5 (CD40 ligand).
TNFSF5 OR CD40LG OR CD40L
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GO; GO:0016021; C:integral to membrane; ISS.
GO; GO:0016174; F:CD40 receptor binding; ISS.
GO; GO:0005174; F:CD40 receptor binding; ISS.
GO; GO:000554; P:inflammatory response; ISS.
GO; GO:0007159; P:inflammatory response; ISS.
InterPro; IPR003563; TNF 5.
InterPro; IPR008563; TNF 1.
InterPro; IPR008565; TNF 1.
INTERPRO; PR001702; CD40LIGAND.
ProDom; PD000600; TNF 5; 1.
PROSITE; PS00207; TNF 1.
INTERPROSITE; PS00207; TNF 1.
INTERPROSITE; PS00209; TNF 2; 1.
INTERPR
                                                                                                                                                                                                                                                                                                                                                                                                        277 GGFFKLRAGBEISİQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                           189 SGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFOV
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23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) 47 260 EXTRACELLULAR (POTENTIAL). 11 112 CLEAVAGE (BY SIMILARITY). 77 217 POTENTIAL. 139 239 N-LINKED (GLCNAC) (POTENTIAL). 139 239 N-LINKED (GLCNAC) (POTENTIAL). 139 239 N-LINKED (GLCNAC) (POTENTIAL). 138	STANDARD; PRT; 318 AA.  9; (Rel. 41, Created) (Rel. 41, Last sequence update) (Stactor ligand superfamily member 11 (Receptor activator actor netor long to TRANCE) (Osteoprotegerin ligand) (OPGL) (ODF) (ODF) (ODF) (Steoclast (OD	1 N.A.  1 bone;  1945; PubMed=11092398;  J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,  Juence and functional characterization of the rat receptor activator of NF-kB ligand.";  C. Res. 15:2178-2186 (2000).	2371; PubMed=11804028; 2371; PubMed=11804028; Xim N., van Wesenbeeck L., MacKay C., Mason-Savas A., Popoff S.N., Lengner C., van-Hul W., Choi Y., x.; x. the rat osteopetroctic mutation toothless (tl) is not in (TRANCE, RANKL, ODF, OPGL) gene."; Biol. 45:853-859(2001).	cytokine that binds to TNFRSF11B/OPG and to A/RANK. Osteocalsst differentiation and activation factor. the ability of dendritic cells to stimulate naive T-cell ation. May be an important regulator of interactions T cells and dendritic cells and may play a role in the on of the T cell-dependent immune response. May also play tant role in enhanced bone-resorption in humoral Homotriner (By similarity).  LAR LOCATION: Type II membrane protein and secreted (By LV).  PECIFICITY: Highly expressed in thymus and bone tissues. soluble form derives from the membrane form by

뿦됮먑똣묽몀뮵뭠뭑뭑뭑뭙읭吕믕뚕쭕푶퍞뿄첉첉탿퍞됮썙첉꾶첉첉뀵줥뷺봍븀뭑윉얁얁얁얁얁얁얁얁얁

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(POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
CLEAVAGE (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
I -> M (IN REF. 2).
W, 4887A4D706AD098F CRC64;
                                                                                       NOT entry is copyright. It is produced through a collistic solution to Bioinformatics and the EMBL out a Bioinformatics Institute. There are no restriction profit institutions as long as its content is in this statement is not removed. Usage by and for this statement (see http://www.isb-sib.ch.mail to license@isb-sib.ch).
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larity 23.3%; Pred. No. 1.1;
Conservative 36; Mismatches 108; Indels 67;
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(Rel. 14, Created)
(Rel. 29, Last sequence update)
(Rel. 43, Last annotation update)
osphatase, placental-like precursor (EC 3.1.3.1) (Nag arm-cell alkaline phosphatase) (GCAP) (FLAP-like) (AL iPpL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR LIGAND SUPERFY MEMBER 11, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFY MEMBER 11, SOLUBLE FORM.
STORPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PRO-
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tic processing (By similarity). (Y: Belongs to the tumor necrosis factor family.
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R008983; TNF like.
R003636; TNF subf.
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2012; TNF subf; 1.
07; TNF; 1.
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140
199
264
317
18 AA;
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Query Match Best Local Similarity 28.6 Matches 44; Conservative STANDARD; 531 5 532 AA; RESULT 8 MINT HUMAN ID MINT HUMAN CONFLICT CONFLICT SEQUENCE DISULFID CONFLICT CONFLICT CONFLICT ACT SITE CARBOHYD CONFLICT CONFLICT CONFLICT CONFLICT PROPEP CHAIN SOLUTION STATEMENT OF THE STATEMENT OF STATE ð 셤 ò 셤 à Feinged B.A. Grouse L.H., Derge J.G.,
Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,
Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Jedin T.B., Tooshiyuki S., Carninci P., Prange C.,
Lellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Jorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
on E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
dan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Grimwood J., Schmutz J., Myers R.M.,
S.N., Krzywinski M.I., Skaleka U., Smallus D.E.,
Schimwood J., Schmutz J., Myers R.M.,
Schimwood J., Schmutz J., Myers R.M.,
Schimwood J., Schmutz J., Marra M.A., Shallus D.E.,
Schimwood J., Schmutz J., Marra M., Smallus D.E., AR LOCATION: Attached to the membrane by a GPI-anchor. SCIFICITY: TRACE AMOUNTS IN THE TESTIS AND THYMUS, STATED AMOUNTS IN GERM CELL TUMONS.
30US: In most mammals there are four different isozymes: placental-like, intestinal and tissue non-specific Nagao isozyme is encoded by a germ-cell alkaline ACTIVITY: An orthophosphoric monoester + H(2)0 = an azoa, Chordata, Craniata, Vertebrata, Euteleostomi, eria, Primates, Catarrhini, Hominidae, Homo. a Nagao-type, phosphatidylinositol-glycan anchored hatase in human choriocarcinomas."; initial analysis of more than 15,000 full-length cDNA sequences."; atanabe T., Li W.L., Soong B.-W., Chou J.Y.; the germ cell alkaline phosphatase gene in human a cells."; 1 H., Kan Y.W., Kam W.; sequence of a putative human placental alkaline s J.W., Sack T.L., Kim Y.S.;
ning of complementary DNAs encoding alkaline
human colon cancer cells."; ad. Sci. U.S.A. 99:16899-16903(2002). Sci. U.S.A. 85:3024-3028(1988). Res. 16:5694-5694(1988) 264:12611-12619(1989). 57; PubMed=12477932; 96; PubMed=2745460; 578; PubMed=3387245; 11; PubMed=2297757; PubMed=2162249; 32; PubMed=2834730; :3956-3962(1990). :1085-1091 (1990) phosphate. auss A.W.; arcinoma; anes T.; ke gene Juman) N.A. N.A. дë

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This SWISS-PROT entry is copyright. It is produced through a collébetween the Swiss Institute of Bioinformatics and the EMBL outs the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified annotate and in the statement is not removed. Usage by and for centities requires a license agreement (See http://www.isb-sib.ch/ē or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 KARDRKA----YTVLLYGNGPGYVLKDGARPDVTESESGSPEYROOSAVPLDGETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Indels 50; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 KARPRRAIAAHYEV---HPRPG---QDGAQAGVDGTVSGWEETKINSSSPLRYDRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 TVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGV------LALRCLEFFSA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 VAV------PARGPQAH----LVHGVQEQTFIAHVMAFAACLEPYTACD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALKALINE PHOSPHATASE, PLACENTAL-LIKE REMOVED IN MATURE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.

BY SIMILARITY.
PHOSPHOSERINE INTERMEDIATE.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (FOTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R GO; GO:0016020; C:membrane; NAS.
R GO; GO:0004035; F:alkaline phosphatase activity; NAS.
GO; GO:0016310; P:phosphorylation; NAS.
R InterPro; IPRO01922; Alk phosphise.
R PRINTS; PRO0113; Alk phosphise.
R PRINTS; PRO0113; AlkPHPHTASE.
R PRODON: PDO01668; Alk phosphise; 1.
R PROSITE; PS00123; AlkALINE PHOSPHATASE; 1.
R PROSITE; PS00123; AlkALINE PHOSPHATASE; 1.
R Hydrolase; Zinc; Magnesium; Phosphorylation; Transmembrane; M Multigene family; Glycoprotein; GPI-anchor; Signal.
I SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (liver/bone/kidney).
-!- SIMILARITY: Belongs to the alkaline phosphatase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.6%; Score 88; 'DB 1; Length 532;
28.6%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84AB5B28F13D6D82 CRC64;
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tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                 EMBL; J04948; AAA51700.1; --
EMBL; J03252; AAA98616.1; --
EMBL; X55279; CAA37374.1; --
EMBL; X52279; CAA37374.1; --
EMBL; X07247; CAA30232.1; ALT_SEQ.
PIR; S12076; S12076.
HSSP; P00634; IAJC.
Genew; HGNC:441; ALPEL2.
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438
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688
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shikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
It the coding sequences of unidentified human genes. XIII.
sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ostezka U., Astrahantseff K., Bourteele S., Dillinger K.,
Cudwig L., Wilda M., Hameister H., Knoechel W., Liptay S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ome proliferator-activated receptor delta, an integrator cional repression and nuclear receptor signaling."; Acad. Sci. U.S.A. 99:2613-2618(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schwabe J.W.R., structural motif reveals the essential transcriptional unction of Spen proteins and their role in developmental
           [Rel. 42, Created)
[Rel. 42, Last sequence update)
[Rel. 42, Last annotation update)
.ing protein (SWART/HDAC1 associated repressor protein).
                                                                                                                                                            AND INTERACTION WITH NCOR2; HDAC1; HDAC2; RBBP4; MBD3;
                                                                                                                                                                                                                                                                                                                                                                                                                  o, and Teratocarcinoma;

a T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
nagai K., Tugiya S., Komai F., Hara R., Takkuchi K.,
sekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
                                                                                        itazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
.heria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                     ss M., Xie W., Kao H.-Y., Ordentlich P., Tsai C.-C., 3 R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel component of the Notch/RBP-Jkappa signalling
                                                                                                                                                                                                                                         iducible cofactor that integrates nuclear receptor
                                                                                                                                                1 N.A., FUNCTION, SUBCELLULAR LOCATION, INDUCTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequencing project.";
IG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                             M-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                         IN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                        793-1595 FROM N.A., AND VARIANT PRO-1091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLOGRAPHY (1.8 ANGSTROMS) OF SPOC DOMAIN.
 .8; Q9NWH5; Q9UQ01; Q9Y556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH RBPSUH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1127; PubMed=11867749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7836; PubMed=12897056;
                                                                                                                                                                                     and Pituitary;
1190; PubMed=11331609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5063; PubMed=10231032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :002-3664 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oteins in vitro.";
3-70(1999).
                                                                                                                                                                                                                                                         nd activation.";
5:1140-1151(2001).
                                                                                                                                                                                                                                                                                                                                                    94-3664 FROM N.A.
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                                                                                (Human)
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REMEL; AF856524; AAR52750.1; -.

REMEL; AL034555; CAB65442.1; ALT_SEQ.
REMEL; AL034555; CAB65442.1; ALT_SEQ.
REMEL; AL03968; -. NOT ANNOTATED COS.
REMEL; AL450998; -. NOT ANNOTATED COS.
REMEL; AL450998; -. NOT ANNOTATED COS.
REMEL; AL609682; BA691405.1; ALT_INIT.
REMEL; AK002949; BA614124.1; ALT_INIT.
REMEL; AK002949; BA614124.1; ALT_INIT.
REMEL; AK002949; RAM4 rec_mot.
REMEL; AM00360; RRM; 4.
SMART; SM00360; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptors (By similarity).
--- DOMAIN: The SPOC domain, which mediates the interaction with NCOR2, is essential for the repressive activity.
---- SIMILARITY: Belongs to the Spen family.
---- SIMILARITY: Contains 1 RID (receptor interacting) domain.
---- SIMILARITY: Contains 4 RNA recognition motif (RRM) domains.
---- SIMILARITY: Contains 1 SPOC domain.
---- CAUTION: Ref. 2 sequences differ from that shown due to erron
FUNCTION: Essential corepressor protein, which probably regu-
different key pathways such as the Noch pathway. Negative
regulator of the Notch pathway via its inceraction with RBPSI
which prevents the association between NOTCH1 and RBPSUH, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL ou the Buropean Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is imposfied and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH MSX2 (BY SIMILARIT INTERACTION WITH RBPSUH (BY SIMILAR ARG-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene model prediction.
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Name=1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1LYYL----YCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miner C.M., Campbell R.D.; of the immunoglobulin superfamily and a V-ATPase G mongst the predicted products of novel genes close to the
                                                                                                                                                                                                                                                                                                                                                                                    AEDRREPPELNPQTEESQ-------DVVPFLEQLVRPRRSAPK----
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lel: 29, Created)
lel: 29, Last sequence update)
lel: 43, Last annotation update)
let (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor or ligand superfamily member 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on of two lymphotoxin beta isoforms expressed in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Neria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Ngam-Ek A., Lawton P., Demarinis J., Tizard R., salon C., O'Rbine-Creco B., Poley S.F., Ware C.F.; seta, a novel member of the TNF family that forms a omplex with lymphotoxin on the cell surface.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Renard N., Charlot C., Bienvenu J., Coiffier B.,
                                                                                                                                                                                                                                                                                               7.6%; Score 88; DB 1; Length 3664; 23.1%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                            62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the human MHC."; P-1997 to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                      402245 MW; 5228C58533E5B27B CRC64;
                                                                                                                                                                            N -> D (in dbsNP:848210).
/FTId=VAR_017121.
                                                                                                  A -> V (in dbSNP:848208).
/FTId=VAR 017119.
L -> P (in dbSNP:848209).
/FTId=VAR 017120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lines and non-Hodgkin's lymphomas.";
hys. Res. Commun. 238:273-276(1997).
                                                                                                                                                                                                         TIG=VAR 017121.
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                                                                                                                                                                                                                                                                                                                                            20; Mismatches
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                 ARG-RICH.
TYR-RICH.
PRO-RICH.
                                                                                PRO-RICH
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3482
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0 6 4 8 0 0
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첉퉑뎍잌탼톂탼꺴윉찞찞읏묫몷뿘믶씂줖콓춖눑튽륁줐짷짫첉첉맖맖콯찞짫첉랻맖늗և

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Rieder M.J. Livingston B.J. Daniels M.R., Montoya M.A., Chung M. Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M. Miyamoto K.E., Nguyen D.A., Poel C.L., Robertson P.D. Schackwitz W.S., Sherwood J.K., Wittak L.A., Nickerson D.A., Submitted (JAN-2003) to the EMEL/GenBank/DDBJ databases.

L. PUNCTION: VGrokime that binds to LIBR/TURRSP3. May play a specific in immune response regulation. Provides the membrane and for the attachment of the heterotrimeric complex to the cell surface. Isoform 2 is probably non-functional.

C. SUBUNIT: Heterotrimer of either two LTB and one LTA subunits (Less prevalent) one LTB and two LTB and one LTA subunits.

C. SUBGELLUIAR LOCATION: Type II membrane protein (Potential).

EVENT. SUBUNITY PRODUCTS:

EVENT. SUBUNITY PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a coll between the Swiss Institute of Bioinformatics and the EWBL out the European Bioinformatics Institute. There are no restriction was by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centities requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
Shilna S., Tamiya G., Oka A., Inoko H.;
Shilna S., Tamiya G., Oka A., Englina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
               SEQUENCE FROM N.A. (ISOFORM 1).

Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,

Rowen L., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,

Lasky S., Hood L.,

"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                               Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth B.J., Yi Q., Nickerson D.A., Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS GLU-70 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=006643-2; Sequence=VSP 006441, VSP 006442;
-!- TISSUE SPECIFICITY: Spleen and thymus.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                           Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0015070; F:toxin activity; NAS.
GO; GO:0007267; F:cell-cell signaling; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR006053; TNF abc.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF-like.
InterPro; IPR003836; TNF-like.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q06643-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, L11015, AAA36191.1, -...
EMBL, T4768, CAA75069.1, -...
EMBL, AF12976, AAD18089.1, -...
EMBL, AP000505, BAB63395.1, -...
EMBL, AY070219, AAL49955.1, -...
EMBL, AY070219, AA44955.1, -....
EMBL, AY070219, AAA9191.1, -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L11016; AAA99888.1; -. EMBL; U89922; AAC51769.1; -. EMBL; U79029; AAB37342.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew, HGNC:6711; LTB.
MIM; 600978; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A46066; A46066.
PIR; JC5645; JC5645.
HSSP; P01374; 1TNR.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CL) (CD154 protein).
TURSFS OR CD40LG OR CD40L
Eukaryota; Metazoa; (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-328(5001).
-!- FUNCTION: Cytokine that binds to TNFRSFS. Mediates B-cell proliferation in the absence of IL-4. Involved in immunoglobuliz class switching (By similarity).
-!- SUBGNUT: Homotrimer (By similarity).
-!- SUBGNUT: ACATION: Type II membrane protein. Also exists as extracellular soluble form (By similarity).
-!- PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collebetween the Swiss Institute of Bioinformatics and the EMBL outs the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centifies requires a license agreement (See http://www.isb-sib.ch/corsend an email to license@isb-sib.ch).
                                                                                                                                                                         105 TVSGWEE----TKINSSSPLRYDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDI
                                                                                                                                                                                                                    136 SVLOWAEKGYYTMSNNLVTLENGKOL---TVKROGLYYIYAQVTFCSNREASSQAPF
                                                                                                                                                                                                                                                             161 GVLALRCLEEF-----SATAASSPGPQLRLC-----OVSGLLPLRPGSSLRIRTLE
                                                                                                                                                                                                                                                                                         --LCLKPPNRFERILLRAANTHSSAKP----CGQQSIHLGGIFELQPGASVFVVVT
                    .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21383618; PubMed=11491535;
Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
Weiss W.R., Ansari A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteolytic processing (By similarity).
SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                             7.5%; Score 87; DB 1; Length 261;
5.9%; Pred. No. 1.8;
ve 21; Mismatches 55; Indels
                           (4) N-LINKED (GLCNAC. . .) (PC 29357 MW; 85E1588B507901B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G0:0016021; C:integral to membrane; ISS. G0; G0:0016021; C:integral to membrane; ISS. G0; G0:0005174; F:CD40 receptor binding; ISS. G0; G0:0006954; P:inflammatory response; ISS. G0; G0:0007159; P:inflammatory response; ISS. G0; G0:0030168; P:platelet activation; ISS. InterPro; IPR003263; TNF_5.
                    N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 AA.
  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF344844; AAK37603.1; -.
HSSP; P29965; 1ALY.
                                                                                                                                                                                                                                                                                                                                                    210 LKAAPFLTYFGLFQV 224
                                                                                                                                                                                                                                                                                                                                                                               : | | | ::
247 VSHGTGFTSFGLLKL 261
                                                                                                         25.9%;
                                                                                                           Best Local Similarity 25.99
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
218
240
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                                           261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALJA
                                                                                                                                                                                                                                                                                                           193
  DISULFID
                                           SEQUENCE
                                                                                      Query Match
                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SENGEO
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    1. 41, Last sequence update)
    1. 41, Last annotation update)
    factor ligand superfamily member 5 (CD40 ligand) (CD40-

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, SOLUBLE FORM (BY SIMILARITY). CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R LOCATION: Type II membrane protein. Also exists as an lar soluble form (By similarity). oluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, MEMBRANE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL)
                                                                                                                                                                                                                                             tus (Night monkey) (Douroucouli).
azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine that binds to TNFRSF5. Mediates B-cell ion in the absence of co-stimulus as well as IgE in the presence of IL-4. Involved in immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encing, and homology analysis of nonhuman primate and co-stimulatory molecules."; 53:315-328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                    í8; PubMed=11491535;
Bostik P., Mayne A.E., King C.L., Genain C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               processing (By similarity).
Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         usmembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:integral to membrane; ISS.
F:CD40 receptor binding; ISS.
P:B-cell proliferation; ISS.
P:helamatory response; ISS.
P:leukocyte cell adhesion; ISS.
P:platelet activation; ISS.
                                                                                      261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ching (By similarity).
omotrimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03263; TNF 5.
06052; TNF_family.
08983; TNF_like.
03636; TNF_subf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    00; TNF_5; 1.
                                                                                                                               41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; AAK37542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; CD40LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51; TNF 1; 1.
                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sari A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261
113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261
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43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNF; 1.
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SECONDARY SERVICE CONTRACTOR SECONDARY SECONDA

HVEM/TR2, stimulates proliferation of T cells and inhibits HT29 c rissum-Brain; 9 WEE----TKINSSSPLRYDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVN 160 WAEKGYYTMSNNLVTLENGKOL---TVKROGLYYIYAQVTFCSNRBASSQAPFIAS 192 LRCLEEF-----SATAASSPGPQLRLC----QVSGLLPLRPGSSLRIRTLPWAH 209 1 N.A. (ISOFORM 1).
(340; PubMed=9462508;
bner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
ben S., Murphy M., Bisenberg R.J., Cohen G.H., Spear P.G., , member of the TNF superfamily, and lymphotoxin alpha are erpesvirus entry mediator.";
-.30(1998). 251; TNF 1; 1.
049; TNF 2; 1.
nsmembrane; Glycoprotein; Signal-anchor.
1 261 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
13 261 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
14 261 MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
1 22 CYTOPLASWIC (POTENITAL)
23 43 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) Rel. 40, Created)
Rel. 40, Last sequence update)
Rel. 42, Last annotation update)
s factor ligand superfamily member 14 (Herpesvirus entry ad) (HVEM-L). 24; Gaps McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J., R., Spampanato J., Silverman C., Hensley P., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M., oung P.R.; tazoa; Chordata; Craniata; Vertebrata; Euteleostomi; .) (POTENTIAL). entry mediator ligand (HVEM-L), a novel ligand for 7.5%; Score 87; DB.1; Length 261; Catarrhini; Hominidae; Homo. 55; Indels EXTRACELLULAR (POTENTIAL). 240 N-LINKED (GLCNAC. . .) (PC 29360 MW; 10CA588D923754EB CRC64; 1 N.A. (ISOFORM 1), AND CHARACTERIZATION. CLEAVAGE (BY SIMILARITY) 240 AA. 25.9%; Pred. No. 1.8; iive 21; Mismatches POTENTIAL) POTENTIAL. 006052; TNF family. 008983; TNF\_like. 003636; TNF\_subf. ; TNF, 1. 6; Q8WVFB; Q96LD2; 600; TNF 5; 1. 012; TNF subf; 1. 7; TNF; 1. heria; Primates; 06; 02: CD40LIGAND. PFLTYFGLFQV 224 TGFTSFGLLKL 261 GHT OR HVEML. onservative 113 218 240 (Human) 1 AA; nd)

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TISSUE-BITAIN.

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TISSUE-BITAIN.

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TISSUE-BITAIN.

Trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Colling F.S., Wagner L.L., Shenmen C.W., Schuler G.L.

Altschul S.F., Zeeberg B., Buetow, K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,

Stapleton M.J., Usdin T.B., Doshiyuki S., Carninci P., Prange C.

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy E.

Brownstein M.J., Wckwan P.J., McKernan K.J., Malek J.A., Gunaratne P.F.

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Schnerct A., Schein J.E., Jones S.J.M., Marra M.A.;

Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

T. FUNCTION: Cytokine that binds to THRREFS/TORE. Binding to the

Gecy receptor ThrRsFeb modulates its effects. Activates NFKE

stimulates the proliferation of T cells, and inhibits growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isold=043557-1; Sequence=Displayed;

Name=2; Synonyms=LIGHT delta-TM;
Name=2; Synonyms=LIGHT delta-TM;
Name=2; Synonyms=LIGHT delta-TM;
Isold=043557-2; Sequence=USP 00645;

-:- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESED IN THE SPLEEN BUT
TISSUES SPECIFICITY: PREDOMINANTLY EXPRESED IN THE SPLEEN BUT
TISSUES AND IN HERRY, PLACENTA, LIVER, LUNG, APPENDIX, AND KI
AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OF
NONHEMATOPOIETIC TUMOR LINES.

-:- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.

-:- PTM: N-glycosylated.

-:- PTM: N-glycosylated.

-:- PTM: N-glycosylated.

-:- PTM: The soluble form of isoform I derives from the membrane
by proteolytic processing.

-:- SMILLARITY: Belongs to the tumor necrosis factor family.

-:- CAUTION: Ref. 4 sequence differs from that shown due to a
frameshift in position 178.
                                                                                                SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
MEDLIRE=21528948; PubMed=11673523;
Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.
"Genomic characterization of LIGHT reveals linkage to an immune
response locus on chromosome 19p13.3 and distinct isoforms genera
by alternate splicing or proteolysis.";
J. Immunol. 167:5122-5128(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collbetween the Swiss Institute of Bioinformatics and the EMBL out the Buropean Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (isoform 1); Cytoplasmic (isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
bwth.";
Biol. Chem. 273:27548-27556(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF036581; AAC39563.1; -.
EMBL; AF064090; AAC25169.1; -.
EMBL; AY028261; AAK26160.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Homotrimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Isold-p13808-5; Sequence=VSP 000459, VSP 000461;
TISSUE SPECIFICITY: Isoform a is widely expressed at similar levels in all tissues examined. Isoforms B1 and B2 are predominantly expressed in stomach although they are also deteat lower levels in other tissues. Isoform C1 is stomach-specifisoform C2 is expressed at slightly higher levels in lung and stomach than in other tissues.
SIMILARITY: Belongs to the anion exchanger family.
                                                             Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
"Cloning and characterization of a murine band 3-related cDNA from
kidney and from a lymphoid cell line.";
J. Biol. Chem. 263:17092-17099(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collibetween the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centifies requires a license agreement (See http://www.isb-sib.ch/cor send an email to license@isb-sib.ch).
                                                                                                                                                                       Lecanda J., Urtasun R., Medina J.F., ^{\prime}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY. MEDLINE=20462926; PubMed=11006093;
                                                                                                                                                                                                    exchanger gene.";
Biochem. Biophys. Res. Commun. 276:117-124(2000)
-!- FUNCTION: Plasma membrane anion exchange protein of wide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                distribution.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                           IsoId=P13808-2; Sequence=VSP_000458;
                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P13808-3; Sequence=VSP_000457;
                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P13808-4; Sequence=VSP_000460;
                                                                                                                                                                                                                                                                                                                            IsoId=P13808-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, A31789; A31789.
HSSP; P02730; IBTO.
MGD; MGI:109351; S1C4a2.
InterPro; IPR001717; Anion exchange.
InterPro; IPR003020; HCO3 cotranspt.
Pfam; PF00955; HCO3 cotransp; 1.
PRINTS; PR01231; HCO3 TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                              SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=89034212; PubMed=3182834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J04036; AAA65505.1; -.
   NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                733
733
790
822
                                                                                                                                                                                                                                                                                                                                            Name=B1;
                                                                                                                                                                                                                                                                                                                                                                           Name=B2
                                                                                                                                                                                                                                                                                                                 Name=A
                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
   118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIQERRS------SGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|:|||:
ELELLVS------QSSPCGRATSSSRVWWDSSFLGGVVHLEAGEEVVVRVIDER 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LACLGLLLVVVSLG----SWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVGLGLLLLLMGAGLAVQGWFLLQLHWRLGEMVT----RLP-----DGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RQI-----GKAVYL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSGLLPLRPGSSLRIRTLPWA
                                                                                                                                                                                                                                                                                             TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                         TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 14, SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               il. 43, Last annotation update)
protein 2 (Non-erythroid band 3-like protein) (B3RP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           azoa, Chordata, Craniata, Vertebrata, Buteleostomi, eria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87; Indels 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 86.5; DB 1; Length 240;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49D0BF67E1390B39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.

N-LINKED (GLCNAC. )

Missing (in isoform 2).

/FIId=VSP 006452.

L -> V (IN REF. 4).

E -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                                            MEMBER 14, MEMBRANE FORM
                                                                                                                                                                                                                                                               smembrane; Glycoprotein; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                     CLEAVAGE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Q9ES10, Q9ES11; Q9ES12; Q9ES13; el. 13, Created)
                                                                        P:induction of apoptosis; TAS.
P:signal transduction; TAS.
06053; TNF abc.
06052; TNF family.
08983; TNF like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                           F:receptor binding; TAS.
                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
AAH18058.1; ALT_FRAME.
                                                                                                                                                                                                                              1; FALSE NEG.
                                                                                                                                                                              34; TNECROSISFCT.
)12; TNF subf; 1.
); TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||| | 1
DGTRSYFGAFMV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-FLTYFGLFQV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26351 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.28;
                             930; TNFSF14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nservative
                                                                                                                                                                                                                                151; TNF 1
149; TNF 2
                                                                                                                                                                                                                                                                                             240
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el. 43, 1
                                                                                                                                                                    TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse).
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Braesch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A.,
                                                                                                                                             Cell 72:291-300(1993).
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          Matsuda
  12;
                                                                                                                                                                                                                                                                                                                                                                    PRRAIAAHYEVHPRPGQDGAQAGV------DGTVSGWEETKI---N 115
                                                                                                                                                                                                                                                                                                                                                                                                                          TIEEGEEDEEEASEAEGFRAPPQ-QPSPATTPSAVQFFLQEDEGAERKPERTSPSP 173
                                                                                                                                                                                                                                                                                                                                                                                                             LRYDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYL---KLDLL------VNGVL-- 163
                                                                                                                                                                                                                                                                                                                            TLSAQEPSQEELT-AEDRREPPELNPQTEESQDVVPFLEQ-----LVRPRRSAPKG 74
                                                                                                                                                                                                                     ERTSPSEPPTQTPHQEAAPRASKGAQTG -> MPAFQEWKSG
GLREEAVFGAHGCSVCR (in isoform C2).
FTTd=vSP 000461.
A -> G (IN REF. 2).
W; 1A0782C0071782EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 25, Last sequence update)
(Rel. 43, Last annotation update)
a factor ligand superfamily member 5 (CD40 ligand) (CD40-
ed activation protein) (TRAP) (T cell antigen Gp39)
                                                                                                                 S-palmitoyl cysteine (By similarity).
MSSAPRRPASGADSLHT -> MDFLLRPQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                         P-----HOEAAPRASK-GAQTGTLVBEMVAVASATAGGDDGGAAGRPLTKAQPGH
                                                                                                                                                        MSSAPRRPASGADSLHT -> MTQ (in isoform B1).
                                                                                                                                                                                                                                                                                                        51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stazoa, Chordata, Craniata, Vertebrata, Euteleostomi, theria, Primates, Catarrhini, Hominidae, Homo.
                                                                                            (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                         POLY-SER.
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                  7.4%; Score 86.5; DB 1; Length 1237; 27.9%; Pred. No. 13; ive 19; Mismatches 77; Indels 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6854; PubMed=1280226;
Lhaeuter U., Magee H.W., Senger G., Kroczek R.A.;
FRAP, a ligand for CD40 on human T cells.";
nol. 22:3191-3194(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9181; PubMed=1385114;
D., Grosmaire L.S., Kullas C.D., Chalupny J.N.,
                                                                                                                                                                    /FTId=VSP 000458.
Missing (in isoform C2).
                                                                                                                                                                                         /FTId=VSP 000459.
Missing (in isoform C1).
                                                                                                                                                 FTId=VSP 000457
                                                                                                                                                                                                              FTIG=VSP 000460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 AA.
                                                                                             N-LINKED (
                                            POTENTIAL.
                                                      PRO-RICH.
HIS-RICH.
                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEEFSATAA---SSPGPQLR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAKGSTQAAREGREPGPIPR 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10LG OR CD40L OR TRAP.
                                                                                                                                                                                                                                                                 136813 MW;
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                                                                                                                                                                                                                                                                                                          onservative
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    950
1006
1053
1132
1195
316
                                                                                                                 1169
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Aruffo A.;
"The human T cell antigen gp39, a member of the TNF gene family,
ligand for the CD40 receptor: expression of a soluble form of gp3
with B cell co-stimulatory activity.";
EMBO J. 11:4313-4321(1992).
                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANTS HIGM1 128-ARG-GLY-129 AND PRO-23 MEDLINE=93145330; PubMed=7678782; Aruffo A., Farrington M., Hollenbaugh D., Li X., Milatovich A., Anofyama S., Bajorath J., Grosmaire L.S., Stenkamp R., Neubauer M. Roberts R.L., Noelle R.J., Ledbetter J.A., Francke U., Ochs H.D.; "The CD40 ligand, gp39, is defective in activated T cells from patients with X-linked hyper-IgM syndrome.";
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Macduff B.M., Sato T.A., Maliszewski C.R., Fanslow W.C.;
"Recombinant human CD40 ligand stimulates B cell proliferation an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "2-A crystal structure of an extracellular fragment of human CD4(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98266353; PubMed=9605317; Singh J., Garber E., van Vlijmen H., Karpsusas M., Hsu Y.-M., Zheng Z., Naismith J.H., Thomas D.; "The role of polar interactions in the molecular recognition of with its receptor CD40."; Protein Sci. 7:1124-1135(1998).
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Karpsusas M., Hsu Y.-M., Wang J.-H., Thompson J., Lederman S.,
Chess L., Thomas D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Defective expression of T-cell CD40 ligand causes X-linked immunodeficiency with hyper-IgM."; Nature 361:539-541(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Shimadzu M., Terasaki H., Ninomiya R., Shimizu S., Nunoi H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT HIGMI GLU-123.
MEDLINE-93156840; PubMed-8094231;
Disanto J.P., Bonnefoy J.Y., Gauchat J.F.M., Fischer A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93156839; PubMed=7679206;
Korthaeuer U., Graf D., Mages H.W., Briere F., Padayache
Malcolm S., Ugazio A.G., Notarangelo L.D., Levinsky R.J.
Kroczek R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D-STRUCTURE MODELING OF COMPLEX WITH CD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 113-117, AND PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inside microsomes.";
J. Biol. Chem. 271:5965-5967(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS HIGM1 ARG-36 AND GLY-140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93094757; PubMed=1281209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin E secretion.";
J. Exp. Med. 176:1543-1550(1992).
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-543 (1993).

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entities requires a license agreement (See http://www.isb-sib.ch/\epsilon or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 TVSGWEE----TKINSSSPLRYDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 SVLQWAEKGYYTMSNNLVTLENGKQL---TVKRQGLYYIYAQVTFCSNREASSQAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 GVLALRCLEEF-----SATAASSPGPQLRLC-----QVSGLLPLRPGSSLRIRTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 --LCLKSPGRFERILLRAANTHSSARP----CGQQSIHLGGVFELQPGASVFVNVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.4%; Score 86; DB 1; Length 261;
5.9%; Pred. No. 2.2;
ve 21; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM: 308230; ...

GG, GG:0005887; C:integral to plasma membrane; TAS. GG, GG:0005814; F:CD40 receptor binding; IPI. GG; GG:0005174; F:CD40 receptor binding; IPI. GG; GG:0006916; P:anti-apptosis; IDA. GG; GG:0006916; P:intlammatory response; IDA. GG; GG:00045190; P:intlammatory response; IDA. GG; GG:00045190; P:intlammatory response; IDA. GG; GG:00045190; P:intlammatory response; IDA. GG; GG:000159; P:intlammatory response; IDA. GG; GG:0001159; P:intlammatory response; IDA. GG; GG:0007159; P:intlammatory response; IDA. GG; GG:0007159; P:intlatelet activation; IDA. GG; GG:0007159; P:intlatelet activation; ISS. InterPro; IPR003263; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: April 7, 2004, 17:45:17 Job time: 10.2829 secs
                                                                                                                                                                              D31797; BAA06599.1; -.
D31793; BAA06599.1; JOINED.
D31794; BAA06599.1; JOINED.
D31795; BAA06599.1; JOINED.
D31796; BAA06599.1; JOINED.
                                                                                                       Z15017; CAA78737.1; -. X67878; CAA48077.1; -. L07414; AAA35662.1; -.
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                                                                               EMBL; X68550; CAA48554.1; -.
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Best Local Similarity 25.99
Matches 35; Conservative
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PDB; IALY; 17-SEP-97.
PDB; I19R; 22-MAY-02.
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cfects in TNFSFS are the cause of X-linked
ciency with hyper-igm type 1 (HIGM1) [MIN:308230]. HIGM1
moglobulin isotype switch defect characterized by
concentrations of serum igm and decreased amounts of all
ypes. Affected males present at an early age (usually
first year of life) recurrent bacterial and
ticl infections, including pneumocystis carinii pneumonia
tich infections, including pneumocystis carinii pneumonia
tich infection. Despite
on treatment with intravenous immunoglobulin, the
cgnosis is rather poor, with a death rate of about 10%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R LOCATION: Type II membrane protein. Also exists as an lar soluble form.
CIFICITY: Specifically expressed on activated CD4+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J., Allen R.C., Larche M., Greene J.M., Shigeoka A.O., rauf D.C., Belmont J.W., Conley M.E., and conformation polymorphism study of CD40 ligand. tion analysis and carrier detection for X-linked hyper
                             utations in X-linked immunodeficiency with hyper-IgM.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ion of nine novel mutations in the CD40 ligand gene in X-linked hyper IgM syndrome of various ancestry."; net. 56:898-906(1995).
                                                                                                                                                     mitage R.J., Conley M.E., Rosenblatt H., Jenkins N.A., Bedell M.A., Edelhoff S., Disteche C.M., Franslow W.C., Belmont J.W., Spriggs M.K.; ene defects responsible for X-linked hyper-IgM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            himadzu M., Toru H., Seyama K., Nunoi H., Neubauer M.,
                                                                                                                                                                                                                                                                                                                                      ALA-126; ARG-140 AND GLU-144.

38; PubMed=7717401;

1a A., Strina D., Sacco M.G., Morali F., Brugnoni D., ntuano E., Fasth A., Andersson B., Zegers B.J.M., zanick I., Levy J., Zan-Bar I., Porat Y., Airo P., zzoni P., Notarangelo L.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :624-627(1997).
Mediates B-cell proliferation in the absence of co-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the CD40 ligand gene in 13 Japanese patients with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s well as IgE production in the presence of IL-4. n immunoglobulin class switching.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO-155 AND VAL-227, AND VARIANT ARG-219.
                                                                                                          PRO-155; ASP-211 AND VAL-227.
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                                                                                                                                70; PubMed=7679801;
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:624-627(1997)
                                                                                                                                                                                                                                                                                              0-993(1993).
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DB 1; Length 261;

Of entry is copyright. It is produced through a collaboration wies Institute of Bioinformatics and the EMBL outstation isoinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way s its content is in no way Usage by and for commercial his statement is not removed.

Belongs to the tumor necrosis factor family

omotrime

H.D.;

NAME=CD40Lbase;

/www.expasy.org/cd40lbase/"

/ftp.expasy.org/databases/cd4olbase". NAME=PROW; NOTE=CD guide CD154 entry; //www.ncbi.nlm.nih.gov/prow/cd/cd154.htm".

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17   88   7.6   352   12   089341   089341   hendric is     18   88   7.6   353   12   Q66760   Q16727   Q66760   Q16727   Q06760   Q16727   Q06760   Q16727   Q07677   Q076	ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  BERKS;  1-MAR-2003 (TrEMBLrel. 23, Last sequence update)  1-MAR-2003 (TrEMBLrel. 23, Last sequence update)  1-MAR-2003 (TrEMBLrel. 25, Last annotation update)  1-OCT-2003 (TrEMBLrel. 25, Last annotation update)  us musculus (Mouse).  ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost ammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, CBL TaxID=10090;  11  EDLINE=22354683; PubMed=12466851;  De FANTOM CONSOCTIUM,  Ne FANTOM CONSOCTIUM,  Ne FANTOM CONSOCTIUM,  Analysis of the mouse transcriptome based on functional annotation of the mo	Qy 1 VISIGIALACIGLILVVVSLGSWATISA-QEPSQEELTAEDRREPPELNPQTEESQD'
Compugen Ltd.  Compugen Ltd.  Search time 31.3851 Seconds (without alignments) 2261.954 Million cell updates/secPWAHLKAAPFLTYFGLFQVH 225PWAHLKAAPFLTYFGLFQVH 225	cted by chance to have a score distribution.  Description  Description  OBBASE and musculu (281247 homo sapien (281247 homo sapien (281242 drosophila (28126 prosophila (28126	Q9vfd3 drosophila Q90wr9 gallus gall Q9v762 drosophila
GenCore version 5.1.6 yright (c) 1993 - 2004 Compugen I search, using sw model 7, 2004, 17:41:27; Search time 2261.954 Mil) -245-198A-2 IGLALACLGLLLVVVSLPWAHLKY JM62 10.0, Gapext 0.5 11.0 11. 2000000000 11. 2000000000 11. 2000000000 11. 20000000000 11. 20000000000 11. 20000000000 11. 20000000000 11. 20000000000 12. 20000000000 13. 20000000000 14. A S Summaries	cchea:* acteria:* and::* and::* anman:* anman:* bose::*  1363 287 224	

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GLALACLGLLLVVVSLGSWATLSAQQEPSQEELTAEDRREPPELNPQTEESQDVVP
                                                       LVRPRRSAPKGRKARPRRALAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSP
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leria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        usion protein.";
1-5720(2002).
; AAL90443.1; -.;
; C:membrane; IEA.
; F:tumor necrosis factor receptor binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B., Medema J.P., Lopez-Fraga M., Lozano J.C.,
M., Picard A., Martinez-A C., Garcia-Sanz J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 330;
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|RLCQTE-LQSLRREVSRLQRSGGPSQKQGERPWQSL 243
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Last sequence update)
Last annotation update)
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06052; TNF family.
08983; TNF like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324; PubMed=12411489;
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TrEMBLrel. 23, I
TrEMBLrel. 25, L
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51; TNF_1; 1.
49; TNF_2; 2.
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STRAIN-y, Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E. George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M. Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
TNF superfamily ligand, Eiger (Tumor necrosis factor family member
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 LSSŘRRHQGSM-GYHGDMYIGNDNERNSYQG-HFQTRDGVLTVTNTGLYYVYAQIC)
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SEQUENCE FROM N.A.
MEDLINE=22060500; PubMed=12065414;
Igaki T., Kanda H., Yammamoto-Goto Y., Kanuka H., Kuranaga E.,
Algaki T., Miura M.;
"Eiger, a TNF superfamily ligand that triggers the Drosophila JNK
pathway.";
EMBO J. 21:3009-3018(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                          EMBL; BT001889; ANTT1595.1;
FlyBase; PBGD0064801; BCDNA:RH51659.
GO; GO:0016209; C:membrane; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
InterPro; IPR006955; P:immune response; IEA.
InterPro; IPR008981; TNF family.
SMART; SM00207; TNF] 1.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota, Neoptera, Endopterygota, Diptera; Brachycera; Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 409;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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PROSITE; PS50049; TNF 2; 1.
SEQUENCE 409 AA; 46401 MW; FC2E9BD9E012D257 CRC64;
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Matches 50; Conserv
                                                                                                                                SEQUENCE FROM N.A.
                                                                                   NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                               ELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRSAPKGRKARPRRAIAAHYE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDLLVNGVLA-----LRCLEBFSATAASSPGPQLRLCQVSGLLPLRPGSSLR
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rokstein P., Hong L., Agbayani A., Carlson J., ez C., Dorsett V., Dresnek D., Farfan D., Frise E., alez M., Guarin H., Kronmiller B., Li P., Liao G., gall C.J., Nunco J., Pacleb J., Paragas V., Park S., nenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                          37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F:tumor necrosis factor receptor binding; IEA.
P:immune response; IEA.
16052; TNF_family.
18983; TNF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nogaster (Fruit fly).
zoa; Arthropoda; Hexapoda; Insecta; Pterygota;
zoa; Diptera; Brachycera; Muscomorpha;
osophilidae; Drosophila.
                                                                                                                                   F:tumor necrosis factor receptor binding; IEA.
                                                                                                                                                                                                                                                                                                                  DB 5; Length 409;
            .la tumor necrosis factor family member.";
1999) to the EMBL/GenBank/DDBJ databases.
BAC00950.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002) to the EMBL/GenBank/DDBJ databases.
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9; TNF 2; 1.
AA; 29780 MW; 13B6D5A04EC9122C CRC64;
                                                                                                                                                                                                                                                                           46331 MW; 8306AECCE14397B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                                                                                                                  Score 110.5; DB Pred. No. 0.039;
                                                                                                                                                                                                                                                                                                                                                          32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 AA
                                                                                                                                                      P:immune response, IEA. 5052; TNF family. 3983; TNF_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PWAHLKAAPFLTYFGLFQV 224
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C:membrane; IEA.
                                                                                               33483; eiger.
C:membrane; IEA.
                                                                           AA015310.1; -.
                                                                                                                                                                                                                                                                                                                  9.5%;
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9; TNF 2; 1.
AA; 46331 MW
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25,
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Sution Betwelery;

Media W.D., Celniker S.E., Holf R.A., Fvans C.A., Gocayne J.D.,

Adams W.D., Celniker S.E., Holf R.A., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

B. Gocoge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chem L.X.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfennkoch C., Baldwin D.

Ballew R.M., Basu A., Barwal B.P., Brandari D., Bolshakov S.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Bartis K.C., Busam D.A., Pauller H., Cadieu E., Center A., Chandra B. Cherry J.M., Cawley S., Daulter H., Cadieu E., Center A., Chandra B. Cherry J.M., Cawley S., Daulke C., Davenport L.B., Davies P.,

Borkova D., Bocchan M.R., Bouck J., Baysaktaroglu L., Bossley E.M.,

Bartis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra B., Cherry J.M., Cawley S., Daulke C., Davenport L.B., Davies P.,

Borkova D., Bocchan M.R., Bouck J., Baysaktaroglu L., Davies P.,

Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Bourbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Perritera S., Pleischmann F.R. Davies P., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.,

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Morkulov G., Milshina B., Murphy L., Muzny D.M., Nelson D.L.,

Merkulov G., Milshina B., Murphy L., Muzny D.M., Nelson D.L.,

Rako P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,

Lasko P., Lei Y., Mixon K.A., Nixon K., Nussern D.S., Pacelle J. F., Shen H.,

Ranger E., Spradling A.C., Stapleton M., Stupskin M., Shush M.,

Spier E., Spradling A.C., Stapleton M., Stupskin M., Shush M.,

Spier E., Spradling A.C., Stapleton M., Stupskin M., Shush M.,

Wang Z.-Y., Wassarman D.A., Worley K.C., Wun W., Stupskin M., Shush M., Williams S.
                                                                                                                                                                                                                        186 NSHD-----QNGFIVFQGDTPFLQCLN----TVPTNMPHKVHTCHTSGLIHLERN
                                                                                                                                                                                        87 YEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRAGLYYLYCQVH
                                                                                                                                                                                                                                                                                     147 EGKAVYLKLDLLVNGVLA-----LRCLEEFSATAASSPGPQLRLCQVSGLLPLRPG
                                                                                          29 QEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRS--APKGRKARPRRAIA
                                                                                                                                       77 OEKSSNEATSKESPAPLHHRRRMHSRH-----RHLLVRKGESLLSARSEDSRP----A
                                                 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
  Length 261;
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                 91;
       DB 5;
9.3%; Score 107.5; DB
13.1%; Pred. No. 0.042;
ve 34; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 AA.
                                                                                                                                                                                                                                                                                                                                                                                200 LRIRTL---PWAHLKAAPFLTYFGLFQV 224
                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
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                                                 Conservative
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                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Berkeley;
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EIGER OR CG12919
                               Best Local Sim
Matches 48;
       Query Match
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNĖATSKESPAPLHHRRRMHSRH-----RHLLVRKGESLLSARSEDSRP----AAH 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SŘRRHQĠŚM-ĠYHĠDMYIGNDNERNSYQG-HFQTRDĠVLTVTNTGLYYVYAQICYN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYLKLDLLVNGVLA-----LRCLEEFSATAASSPGPQLRLCQVSGLLPLRPGSS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRS--APKGRKARPRRAIAAH 86
hong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., yers E.W., Rubin G.M., Venter J.C.; equence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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iger, the Drosophila Homolog of the TNF Superfamily.";
:1263-1268(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; PubMed=12894227; aaty W.S., Chen P., Tomar R.S., Eby M.T., Chapo J. re N., Zachariah S., Sinha S.K., Abrams J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35;
                                                                                                                     1; AAF58848.1; -. 0033483; eiger. 0033483; eiger. 0; C:membrane; IEA. 4; F:tumor necrosis factor receptor binding; IEA. 066052; TNF family. 008983; TNF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor, Wengen, comprise a TNF-like system in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.3%; Score 107.5; DB 5; Length 325; 3.1%; Pred. No. 0.056; ve 34; Mismatches 91; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anogaster (Fruit fly).
azoa, Arthropoda; Hexapoda; Insecta; Pterygota;
pterygota; Diptera; Brachycera; Muscomorpha;
rosophilidae; Drosophila.
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F:tumor necrosis factor receptor binding; IEA.
P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                             36862 MW; 6E5CCB69694F1A3A CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | 
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TrEMBLrel. 22, L
TremBLrel. 25, L
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049; INF 2; 1.
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                                                                                                                                                                                                                                                                                                                                           7; TNF; 1
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Holmes !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 YEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRAGLYYLYCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 EGKAVYLKLDLLVNGVLA-----LRCLEEFSATAASSPGPQLRLCQVSGLLPLR
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Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AFVCLITIAPATAL----YAAADPQVEAL----RQELIELKRRYEAQQQALMVLEC
                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                231 OEKSSNEATSKESPAPLHHRRRMHSRH-----RHLLVRKGESLLSARSEDSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                       9.3%; Score 107.5; DB 5; Length 415; 23.1%; Pred. No. 0.077; Live 34; Mismatches 91; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).

EMBL; AE016784; AAN68461.1; -
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8.9%; Score 103; DB 16; Length 42
Best Local Similarity 29.1%; Pred. No. 0.22;
Matches 50; Conservative 17; Mismatches 65; Indels
                                                                                                                                                              46918 MW; E087A26DE222D2BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome.
SEQUENCE 426 AA; 46020 MW; FEDC7E266C982633 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
conserved hypothetical protein.
                                                                                                                                                                                                                                                 Best Local Similarity 23.1%; Pred. No. 0.077
Matches 48; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 IHLKDIHNDRNAVLREGNNRSYFGIFKV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 LRIRIL---PWAHLKAAPFLTYFGLFOV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
InterPro; IPR006052; TNF family.
InterPro; IPR00893; TNF like.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 2; 1.
PROSITE; PS50049; TNF 2; 1.
SRQUENCE 415 AA; 46918 MW; E(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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MEDLINE=21173698; PubMed=11259647;

MISTIME ATCC 19089 / CB15;

A. Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.

Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

POTOCKA I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely in Botocka T., Tran K., Ohta N. Sheptens C., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.

Complete genome sequence of Caulobacter crescentus.";

"Complete genome sequence of Caulobacter crescentus.";

II. Proc. Natl. Acad. Sci. U.S. A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LSLGLALACLGLLLVVVSLGSWATLS-AQEPSQEELTAEDRREPPE--LNPQTEESQI
                                                                                                                                                                                                                                                                                                                                                        10 LATGVÁLA-----GPLSSWAQSSPAĞGNPIDTLPRVDTSRPPEQKIHVQVQRPN
                                                                                                                                                                                                                                                                                                                                                                                                                        59 PFLEQL----VRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 --NSSSPLRYDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 YADRGYPL----SFAFVPAQTF-----EGGVVRI---TVVEGYVARMRIË
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LSLGLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 LRLGLAVFAAGVAATVIVQAAWRSLASSKIQTQAATAPLVIDKPRF---TGVLKDGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 EQLVRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGV----DGTVSGWEETKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 ATAASSPGP---QLRLC-------QVSGLLPLRPGSSLRIRTLP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 ITAERAERDAKDONIVRLTAPLLVRGYGEPNPSOATAKSGVYREAENTLLLTDEVKI
                                                                                                                                                                                                                            69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GKPGPLEARLRAISKHMMDERPLRRETFERVTGVLALQPGVQITATVQP
                                                                                                                                                                   DB 16; Length 557;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein, Complete proteome. SEQUENCE 210 AA; 22344 MW; 8B99830ADFBF7F45C CRC64;
                                                                                                    60786 MW; 8B974C147D710649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JTN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                            77;
EMBL, AL646082; CAD18246.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
Plasmid; Complete proteome.
SEQUENCE 557 AA; 60786 MW; 8B974C147D710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.8%; Score 90.5; DE 26.2%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 AA.
                                                                                                                                                             8.0%; Score 93.5; D. 26.6%; Pred. No. 2.5; iive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein CC1168
                                                                                                                                                                                                  Best Local Similarity 26.6%
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 SPLRYD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 EGFDFD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SPG-KLRWSSP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCSTP------PDLPHSD----VVSGWSEDIYREGHLVTYACQSG- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQ----LVRPRRS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genin S., Artiguenave F., Gouzy J., Mangenot S., ault A., Brottier P., Camus J.C., Cattolico L., oisne N., Claudel-Renard C., Cunnac S., Demange N., bault P., Whalen A., Robert C., Saurin W., Schiex T., Baucher C.A.;
Soucher C.A.;
Soucher C.A.;
Soucher C.A.;
Soucher C.A.;
          RQIGEF----TVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLAL 165
                                                                         ----LTLNGFLAL 153
                                                                                                                                                                                                                                                                                                                                                                                                                        că (Japanese lamprey) (Entosphenus japonicus).
zoa; Chordata; Craniata; Vertebrata; Hyperoartia;
mes; Petromyzontidae; Lethenteron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     obacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ing of C4bp/Cremp-like protein."; 2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAC77070.1; -.
A: 76964 MW; 124D0D555909DC26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBLrel. 20, Last sequence update)
EMBLrel. 24, Last annotation update)
Lion/secretion signal peptide protein.
                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acearum (Pseudomonas solanacearum)
                                                            EASGFFGGGKFSFETGVTY----THYDTRA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.4%; Score 98; DB 1:
ity 25.5%; Pred. No. 1.2;
servative 17; Mismatches
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                                                                                                                                                                                                                                      684 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGLLPLRPGS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGRPENPAN 195
                                                                                                                                                                                                                                                                                               EMBLrel. 25, CEMBLrel. 25, IEMBLrel. 25, I
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Salis Salis

ga G

RELIMINARY;

5692 / PAOL;

eruginosa.

pathogen.";

9-964 (2000)

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., I. P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Scheret S.E., I. P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N. Satton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.I. R. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin I. R.A. Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M. Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., R. Benos P.W., Buller H., Cadieu E., Center A., Chandra R. Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra R. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., R. Abdson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn R. Durbin K.J., Evangelista C.C., Ferriac C., Ferriac S., Fleischmann R. Posler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K., R. Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                             STRAIL-WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-22608306; PubMed=12692562;
Ikeda H., Ishikawa J., Hannoto A., Shinose M., Kikuchi H., Shibe Sakaki Y., Hattori M., Comura S., Shinose M., Kikuchi H., Shibe microorganism Streptomyces avermitilis.";
Microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL; AP005045; BAC73838.1;
EMBL; AP005045; DAC73838.1;
Pitcerpro, IPR077561; DUF552.
Pfam; PF04472; DUF552.
Pfam; PF04472; DUF552.
Hypothetical protein; Complete proteome.
SEQUENCE 213 AA; 23926 MW; 826FD2DD2D910030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 EPSQEELTAEDRR--EPPE----LINPQTEES-----QDVVPFLEQL---V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 EPELDPEPERDRRRHEPPHQSHQALHPQRDESVRVVQPPMQRDPVPHSASLPAESV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 SAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYD--
Kikuchi H., Shiba T., Sakaki Y., Hattori M., "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG31304 protein.
CG31304 OR CG6960 OR CG18442.
Drosophia melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endoprerygota, Diptera, Brachycera, Muscomorpha, Phylaroida, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.7%; Score 90; DB 16; Length 213; Best Local Similarity 27.7%; Pred. No. 1.6; Matches 41; Conservative 14; Mismatches 45; Indels 4
                                                                                               Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 EFTVIRAGLYYLYCQVHFDEGKAVYLKL 155
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                                                                                                                                         SEQUENCE FROM N.A.
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                                                                           metabolites.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APLGSARKPDEA------PVESLDQLRDEPLQLAWEKPR-----RQWPRR 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3APKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .VI---RAGLYYLYCQVHFDE--------GKAVYLKLDL--LVNGV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LILLALGGLAAQYIAYHFDELARQDAYRPWFAQLCPEIGCTLPSKVDVBQIRSSN 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----EQLV 65
                                                                                                                                                                                                                                                                                                                                                                                                           337; PubMed=10984043; Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Prinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., oulter S.N., Folger K. Kas A., Larbig K., Lim R.M., pencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., ier M.H., Hancock R.B.W., Lory S., Olson M.V.; ome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPEFSGALVVDAIIXNRASFSQPFPLLELRFADLNGHLIANRRFKPGEYL 381
                                                                                                                                                                                                                                                                         teobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.8%; Score 90.5; DB 16; Length 421; 2.6%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEELTAEDR------REPPELNPQTEESODVVPFL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; Complete proteome.
1 AA; 46442 MW; 68C5C17099953C3E CRC64;
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                                                                                                                                                   TrEMBLrel. 16, Last sequence update)
TrEMBLrel. 24, Last annotation update)
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'rEMBLrel. 24, Last sequence update)
'rEMBLrel. 25, Last annotation update)
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                                                                                     421 AA.
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                                                                                                                          TrEMBLrel. 16, Created)
                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                eae; Pseudomonas.
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03, PubMed=11572948;
a H., Ishikawa J., Hanamoto A., Takahashi C.,
kahashi Y., Horikawa H., Nakazawa H., Osonoe T.,

vermitilis.

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ELIMINARY;

PRT; 1363 AA.

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48;

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TNF-related apoptosis inducing ligand.

Gallus adilus (Chicken).

Bukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;

Archosauria, Aves, Neognathae, Galliformes; Phasianidae, Phasianin
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                                                                                                                                                                                                                29 QEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRSAPKGRKARPRR--AII
                                                                                                                                                      1040 EQPGQEEL----QPPPRTPTTEQ-----LSPPPARPPKSAELLQRYSPKKQVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 AAHYEVHPR-PGQDGAQAGVDG-----TVSGWEETKINSS-SPLRYDRQIGEFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 SAHLIFRPQNPAQDGSSRRFGNLSQSCRHAITRWEDSTIHSHLQNITY--RDGRLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 GLYYLYCQVHFD-------EGKAVYLKLDLLVNGVLALRCLEEFS
                                                                                                                                                                                                                                                                                                1148 SSSPGSAPPAHYSPPIPATVRLPHINQANGTLPLLPKKPQQLHGEKLFIKNG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Bridgham J.T., Johnson A.L.;
"TNF-related apoptosis inducing ligand (TRAIL) expression in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 ASSPGPQ--LRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQV 224
                                                                                     95;
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                                                                                                                                                                                          -----PGQDGAQAGVDGTVSGWEETKI------
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0016164; F:tumor necrosis factor receptor binding; IEA.

GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

INTERPROSED: P:mmune response; IEA.

INTERPROSED: TNF family.

INTERPROSED: TNF family.

INTERPROSED: TNF family.

INTERPROSED: TNF 1.

PERMITS: PRO0229; TNF: 1.

PRODOM; PRO0201; TNF: 1.

SMART; SM00207; TNF: 1.
                                                                                                                                                                                                                                                                                                                                                                   1200 HLIDGEALLAKTDVAMSGLLIKLDQVAAQC----SVAQAAGGGTSI 1241
                                                  Length 1363;
                                                                                                                                                                                                                                                                                                                                    144 HFDEGKAVYLKLDLLVNGVL-----ALRCLEEFSATAASSPGPQL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%; Score 89; DB 13; Length 287;
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65; Indels
PROSITE; PS50020; WW DOMAIN 2; 1. SEQUENCE 1363 AA; 148691 WW; 876292CEC51FBE8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovary.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYOS7941; AAL23702.1; -.
HSSP; 035235; 11QA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 287 AA; 32092 MW; DB06E1C95087B108 CRC64;
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Last annotation update)
                                                                                     55;
                                                    DB 5;
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24; Mismatches
                                                               21.7%; Pred NO. 2., mative 27; Mismatches
                                                  Score 89.5;
Pred. No. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TEMBLrel. 19, Created)
01-DEC-2001 (TEMBLrel. 19, Last seq
01-OCT-2003 (TEMBLrel. 25, Last ann
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                                                                                                                                                                                                                                                               116 SSS----PLRYDRQI-
                                                      Query Match 7.7%
Best Local Similarity 21.7%
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50049; TNF
                                                                                                                                                                                              87 YEVHPR----
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AAE01992	AAE26102	ADB16986	Ö	ADC78266	AAB62340	ABU39962	AAW83017		AAW59654	AAY17874	AAY91024	AAY84418	AAY84419	AAU78289	ABR42071	ABB99477	ABU08463	ABR55560	AAB62339	
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56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

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## ALIGNMENTS

RESULT 1

TRBLL; tumour necrosis factor related ligand; tnf; treatment; cand autoimmune disease; immune system; stimulation; suppression; graft rejection. Mus musculus tumour necrosis factor related ligand (TRELL). AAW47524 standard; protein; 225 AA. (first entry) 21-JUL-1998 AAW47524; AAW47524

1. .21 /note= "hydrophobic, transmembrane domain" Location/Qualifiers Mus musculus. Key Domain 

97WO-US013945. WO9805783-A1. 07-AUG-1997; 12-FEB-1998.

6) 4)

(BIOJ ) BIOGEN INC. (UYGE-) UNIV GENEVA FACULTY MEDICINE. 96US-0023541P. 96US-0028515P. 97US-0040820P. 07-AUG-1996; 18-OCT-1996; 18-MAR-1997;

Chicheportiche Y, Browning JL; WPI; 1998-145619/13. N-PSDB; AAV18599. Tumour necrosis factor related ligand - useful for, e.g. treating auto-immune disease and immune responses to tissue grafts.

Claim 12; Page 48-50; 69pp; English.

The sequence is that of mouse tumour necrosis factor related liga. (TRELL). TRELL or active fragments can be included with a carrier pharmaceutical compositions to treat cancer, autoimmune diseases immune responses to tissue grafts, or to stimulate or suppress th system. It is useful to screen for TRELL receptors, by labelling

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bel and screening compositions for binding. Agents ith TRELL-receptor binding can also be screened for, can istered, optionally with interferon- gamma, to induce cell t, suppress or alter immune responses (especially involving reinoma cells) involving a signal pathway between TRELL and It's coding sequence can be used in gene therapy for TRELL-ders in mammals (especially humans), e.g. tumours, d inflammatory diseases or inherited genetic disorders, by nto cells, and expressing, therapeutically effective amounts e.g. a virus comprising a gene encoding TRELL. It may also the preparation of prepare probes for screening etic DNAs for TRELL-encoding sequences and for antisense

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VRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPL 120 VRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPL 120 OLGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPG 180 OIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPG 180 GLALACLGILLUVUVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPF 60 GLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPF Gaps .. 0 100.0%; Score 1162; DB 2; Length 225; 100.0%; Pred. No. 3.1e-112; LCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225 Indels 0; Mismatches onservative

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dard; protein; 225 AA

(first entry)

guence of a soluble recombinant murine TWEAK protein.

agent, autoimmune disease, organ transplant rejection, ost disease, GVHD; lymphoid cell malignancy; shock; tumour. immunological disorder; immune response; inflammation; i; imm ig age Host

2000WO-US001044.

99US-011616BP.

5036/41.

d treating immune responses using modulators, especially I TWEAK, TWEAK receptors and TWEAK ligands, useful for inflammation and graft versus host disease. . 얼

Fig 1; 45pp; English

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The present sequence represents a TWEAK protein. The specificatic describes a method for preventing or treating an immunological di and/or inhibiting an immune response in an animal. The method com administering a TWEAK blocking agent. The method may be used for preventing and treating immune disorders associated with inapprof expression and/or activity of TWEAK. These disorders include autodiseases, acute and chronic inflammation, organ transplant reject Graft-versus-Host disease (GVHD). Iymphoid cell malignancies, segother forms of shock, loss of immune responsiveness (as seen in Fimmunodeficiency virus (HIV) infections) and failure of the immun
                                                                                                                                                                                                                                                                                                                                                                                            o
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VLSLGLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VLSIGLALACIGLLIVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LEQLVRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEQLVRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 RYDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RYDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEFFSATA
                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                            Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 POLRICOVSGLIPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFOVH 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 POLRLCOVSGLIPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFOVH 225
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1162; DB 3;
100.0%; Pred. No. 3.1e-112;
                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     100.08;
                                                                                                                                                                                                                                                 response to tumour growth
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                 Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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RESULT 3

ADC97712 standard; protein; 249 AA.

ADC97712;

15-JAN-2004 (first entry)

Murine FL-TWEAK.

Murine, FL-TWEAK, TNF relatedness and weak ability to induce cel.
TNF, Tumour Necrosis Factor; TWEAK, fibrosis; cardiac disease;
lung disease, idney disease; kidney disease; skin disease;
skeletal muscle disease, adipose tissue disease;
gastrointestinal tract disease; pancreatic disease;
bone disease, commective tissue disease;
commective tissue disease; cartilage disease;
dermatological; gastrointestinal; osteopathic. 

Mus sp.

WO2003086311-A2.

09-APR-2003; 2003WO-US011350.

09-APR-2002; 2002US-0371611P

(BIOJ ) BIOGEN INC.

Hahm K; Zheng T, Burkly L, Jakubowski A,

WPI; 2003-845256/78. N-PSDB; ADC97713.

Treating a TWEAK-related condition, e.g. liver, gastrointestinal bone, pancreatic, cartilage or neural tissue condition in a subj

nistering to the subject a TWEAK agonist or antagonist.

ID NO 1; 120pp; English.

tract disease, pancreatic disease, reproductive organ disease, cartilage disease, bone disease, connective cellular death, and a pathological condition of a tissue quence is murine transmembrane FL-TWEAK (TNF relatedness ty to induce cell death, where TNF is Tumour Necrosis is a member of the TNF family. TWEAK agonists or e useful for treating a TWEAK-related condition, e.g. iac disease; lung disease; kidney disease; skeletal muscle disease; adipose tissue disease; WEAK receptor

Gaps 0; Length 249; Indels 100.0%; Score 1162; DB 7; 100.0%; Pred. No. 3.6e-112; · 0 Mismatches . 0 nservative rity

9 84 LALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPF LALACIGLLIVVVSLGSWATLSAQEPSQEBLTAEDRREPPELNPQTEESQDVVPF

120 RPRRSAÞKGRKARPRRAIAAHYEVHPRÞGQDGAQAGVDGTVSGWETKINSSSPL 144 RPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPL

IGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPG 180 

COVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225

iard; protein; 211 AA

first entry)

otein.

.s factor receptor; signal transducer molecule; TNF; APO4; abnormality; gestational abnormalitity; prostate cancer; O9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease; nmain; immunogen; antibody preparation; breast carcinoma;

98WO-US018393

97US-00924634

ASHINGTON

rosis Factor family receptor polypeptides and ligands - agnosis and treatment of prostate cancer and developmental

This invention describes isolated Tumor Necrosis Factor (TNF) fami receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNF their active fragments. APO4 is useful for diagnosing prostate can determining levels of APO4 in an individual. Prostate cancer can care treated using APO4 selective binding agents linked to a therapeut: moiety. APO4 polypeptides are also useful for identifying selective binding agents to the polypeptide/active fragment which is extracellular, agents to the polypeptide/active fragment which is extracellular, expressed on the cell surface. The binding is preferably performed vivo. APO4 polypeptides/active fragments are also useful for sort for agonists and antagonists by binding and observing the changer activity. Effective pharmacological agents useful in diagnosis or reatment of disease are also identified using a PO04 polypeptides/i fragments and APO4 signal transducer molecules that specifically with a cytoplasmic domain of APO4 and detecting a change in level activity. The method is performed in vivo or in vitro. APO polyper are all useful as immunogens for preparing antibodies. APO4 is all and a phormalities. APO4 was transfected to human breast carcinoma cell. Claim 40; Fig 13B; 156pp; English. gestational abnormalities. MCF-7, and induced apoptosis 

Sequence 211 AA;

ö . 0 Length 211; Indels 93.7%; Score 1089; DB 2; 99.5%; Pred. No. 1.1e-104; cive 0; Mismatches 1; Conservative Local Similarity 210; Query Match Best Loca Matches

15 LVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRS 1 LVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRS

> 엄 à

61 RKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFT 75 RKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFT 셤

GLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSG 121 GLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEBFSATAASSPGPQLRLCQVSG 135 à q

RPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225 181 RPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 211 195 ò a

RESULT 5

AAW29745 standard; protein; 249 AA. AAW29745; AAW29745

(first entry) 27-OCT-1998

INF related endothelium proliferative agent protein.

TNF; endothelium proliferative agent; TREPA; wound healing; cance tissue grafting; vascularisation; apoptosis; autoimmune; birth co Homo sapiens. WO9835061-A2 13-AUG-1998. 

98WO-US002859 12-FEB-1998; 97US-00798692. 12-FEB-1997; 10-FEB-1998;

191/17.

255/38.

leic acid encoding TREPA - useful for diagnosis and autoimmune disease, tumours and inflammation.

e 123-4; 142pp; English.

ed endothelium proliferative agent (TREPA), or its agonists, are used to treat a deficit of TREPA, e.g. to healing or tissue grafting, by promoting vascularisation, e apoptosis for treating cancer and eliminating autoreactive adjuptions for treating defined and eliminating decoration adjunct to cancer chemotherapy or antiviral treatment.

s can also be used to target cytotoxic agents or for atton of the corresponding receptor, the nucleic acid for used to transform tumour cells to render them more.

TREPA and to screen for TREPA mimics. Ribozymes, antisense is or peptides, are used to treat TREPA-associated .

tumours and metastases (by inhibiting vascularisation), or a wide range of autoimmune conditions, conditions ornal stimulation of epithelial cells (e.g. or birth control (inhibiting ovulation and placental other angiogenic conditions (e.g. ulcers)

Gaps . 0 Length 249; 16; Indels 87.8%; Score 1020; DB 2; 88.8%; Pred. No. 2.1e-97; iive 9; Mismatches 16; onservative

; 0

LALACLGLILVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFL 61

RPRRSAPKGRKARPRRALAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLR 121 RPRESAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR 145 IGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGP 181

JGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGP

걸

CQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225

dard; protein; 249 AA

(first entry)

necrosis factor Apo-3 ligand protein sequence.

: necrosis factor; Apo-3 ligand; lymphotoxin; apoptosis; sendent transcription; JNK/SAPK-dependent response; cancer.

98WO-US021407.

97US-0062037P

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The present sequence represents a human tumour necrosis factor (T lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has sytostatic activity. Apo-3 ligand can be used to induce apoptosis mammalian cancer cells, to induce NF-kappaB-dependent transcriptito induce JNK/SAPK-dependent responses in mammalian cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 IGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDF
                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LSLGLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 EQLVRPRRSAPKGRKARPRRALAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 YNROIGEFIVTRAGLYYLYCQVHFDEGKAVYLKUDLLVDGVLALRCLEEFSATAAS
                                                                                                                                                                                                                                                                                                                                                                    / Match B7.8%; Score 1020; DB 2; Length 249; Local Similarity 88.8%; Pred. No. 2.1e-97; les 199; Conservative 9; Mismatches 16; Indels
                                                                                                                                                     New human Apo3- ligand (a tumor necrosis factor) homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 QLRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225
                                                                   Я,
                                                                   Pitti
                                                                                                                                                                                           Claim 1; Fig 1; 74pp; English.
97US-0069862P
                                                                     Marsters SA,
                                 (GETH ) GENENTECH INC
                                                                                                       WPI; 1999-287982/24.
                                                                                                                       N-PSDB; AAX56000
                                                                                                                                                                                                                                                                                                                                           Sequence 249 AA;
                                                                     Ashkenazi AJ,
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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AAY95338 standard; protein; 249 AA AAY95338

205

AAY95338;

25-SEP-2000 (first entry)

Human PRO207 antitumour protein.

PRO207; human; antitumour; tumour; therapy; cytostatic; breast caovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; central nervous system cancer; melanoma; leukaemia; neoplasm

Homo sapiens

24. .35 /note= "prokaryotic membrane lipoprotein lipid" 27. .33 /note= "N-myristoylation" 'note= "N-myristoylation" 1. .40
/label= Signal\_peptide
10. .14
/note= "amidation" Location/Qualifiers 35 Modified-site Modified-site Modified-site Modified-site Peptide Peptide 

"N-myristoylation" 36. .42 /note= "N-41. .249 Protein

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"Asn is N-glycosylated"
                    "N-myristoylation"
                                                            "N-myristoylation"
                                                                                  "N-myristoylation"
                                                                                                       "N-myristoylation"
                                                                                                                             'note= "N-myristoylation"
                                        "amidation"
label= PRO207
                                                                                                                   .134
                                                                        .127
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                                                  .124
                                                                                              . 131
                               .101
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                                                               note=
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99WO-US028565

99US-0145698P. 99WO-US021090. 99WO-US021547. 99WO-US005028. 99US-0130232P. 99US-0144758P. 98US-0113296P 99US-0131445P. 99US-0134287P

Marsters SA; Gurney AL, Godowski PJ, Goddard A, Gogotti RM,

68/38.

.ion to inhibit neoplastic cell growth or for treating tumor rises polypeptides PRO179, PRO207, PRO320, PRO219, PRO221, PRO301, PRO526, PRO362, PRO366, PRO509 or PRO866.

4; 172pp; English.

iguence is that of human antitumour protein PRO207, as foetal kidney cDNA clone (see AAA9717). PRO207 shows quence identity to tumour necrosis factor family members, nan lymphotoxin-beta (23.4%) and human CD40 ligand (19.8%). 216. A claimed method for inhibiting the growth of a tumour sexposing the tumor cell to PRO139, PRO320, Lair agonists or chimeric polypeptides incorporating our is especially a cancer selected from breast, ovarian, tal, uterine, prostate, lung, bladder and central nervous melanoma and leukaemia. Methods for the recombinant the antitumour proteins are also provided

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Gaps
                            .
0
Score 1020; DB 3; Length 249;
Pred. No. 2.1e-97;
9; Mismatches 16; Indels (
    87.8%;
              88.88;
                            nservative
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2 LSLGLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDV 26 LGLGLALACLGLILAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDP 62 EQLVRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSS 86 NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSS 122 YDRQIGEFTVIRAGLYYLXCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAAS. |-|||||| | ||||||||||||||||||||||||

· 0

Length 249; 16; Indels

Score 1020; DB 3; Pred. No. 2.1e-97; 9; Mismatches

87.8%; 88.8%;

Query Match 87.8 Best Local Similarity 88.8 Matches 199; Conservative

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response to tumour growth

Sequence 249 AA;

ALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFL 61 ALACIGLILAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL

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REPRESAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR 145 PPRESAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLR 121

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describes an equivalent or preventing or treating an immunological distandor inhibiting an immune response in an animal. The method compadministering a TWEAK blocking agent. The method may be used for preventing and treating immune disorders associated with inapproper expression and/or activity of TWEAK. These disorders include autodiseases, acute and chronic inflammation, organ transplant reject disease. Secular Loss of immune responsiveness (as seen in himmunodeficiency virus (HIV) infections) and failure of the immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preventing and treating immune responses using modulators, especii antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, useful for treating e.g. inflammation and graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                  TWEAK protein; immunological disorder; immune response; inflammat:
TWEAK blocking agent; autoimmune disease; organ transplant reject:
Graft-versus-Host disease; GVHD; lymphoid cell malignancy; ghock;
122 YDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAAS:
                                146 YNROIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence represents a TWEAK protein. The specification
                                                                                                                                                                                                                                                                                                                Amino acid sequence of a soluble recombinant human TWEAK protein.
                                                                                                206 QIRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 249
                                                                         182 QLRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225
                                                                                                                                                                                                      AAB07526 standard; protein; 249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 1, 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-2000; 2000WO-US001044.
                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-476036/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200042073-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-1999;
                                                                                                                                                                                                                                                                               20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rennert P;
                                                                                                                                                                                                                                          AAB07526;
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polypeptides and the polymuclectide sequences encoding them. The polypeptides, agonists, antagonists or anti-PRO antibodies are us treating benign or malignant tumours (e.g. renal, kidney, bladder breast, etc), leuksemisas and lymphoid malignancies, other disorders neuronal, glial, astrocytal, hypothalamic, glandular, macrophs stromal and blastococalic disorders, infilamatory, immune and angi disorders. The polymuclectide sequences are also useful in gene that AAU86162 represent the human PRO polypeptides of the inv Human, PRO, benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic discinflammatory disorder; immune disorder; angiogenic disorder; cytc 146 YNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEBFSATAAS The present invention relates to the isolation of novel human PRC Thirty five nucleic acids encoding PRO polypeptides, useful for benign or malignant tumors, leukemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders. Hillan KJ; Stone DM; QLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 249 QLRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH Gurney AL, Smith V, d A, Godowski PJ, Pitti RM, Roy MA, AAU86129 standard; protein; 249 AA. Claim 61; Fig 4; 302pp; English. 990S-0144758P. 990S-0145698P. 990S-0146222P. 990S-0149395P. 990S-0151689P. 99WO-US005028. 99US-0123972P. 99US-0133459P. 99WO-US012252. 2000WO-US003565 99US-0140650P 99WO-US020111 99WO-US021090 99WO-US028313 99WO-US028301 99WO-US028634 2000WO-US000219 (first entry) Goddard A, Human PRO207 polypeptide. Pan J, P Wood WI; (GETH ) GENENTECH INC. WPI; 2002-205567/26. N-PSDB; ABK40255 neuroprotective WO200153486-A1. Ashkenazi AJ, Marsters SA, F Watanabe CK, W 11-FEB-2000; 02-JUN-1999; 22-JUN-1999; 22-JUN-1999; Homo sapiens 05-JAN-2000; 15-JUL-2002 20-JUL-1999; 26-JUL-1999; 26-JUL-2001 11-MAR-1999 28-JUL-1999 17-AUG-1999 31-AUG-1999 01-SEP-1999 30-NOV-1999 01-DEC-1999 01-DEC-1999 AAU86129; 182 AAU86129 à 셤 ô members of tumour necrosis factor (TNF) family molecules, TREPA (TNF related endothellum proliferative agent). gically active TREPA are used to treat TREPA-associated ours or metastases. TREPA is used for inducing angiogenesis promoting wound healing and for vascularising grafted tissue is clone ID #690050 human TREPA. 121 RPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR 145 IGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGP 205 !IGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGP 181 61 necrosis factor; TNF; angiogenesis; wound healing; TREPA; ndothelium proliferative agent; tumour; metastasis; ogenesis in mammal at desired sites for promoting wound dministering soluble fragment of extracellular domain of s factor related endothelium proliferative agent protein. RPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLR ILALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFL 0; Gaps Length 249; TNF related endothelium proliferative agent). CQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 249 16; Indels COVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFOVH Score 1020; DB 4; Pred. No. 2.1e-97; 9; Mismatches 16; /label= Extracellular domain Location/Qualifiers dard; protein; 249 AA. 75-76; 53pp; English 87.8%; 88.8%; 98US-00105343. 97US-00798692 98US-00021706 (first entry) onservative 760/29.

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6:25:12 2004

.; 0 145 181 205 121 19 82 ALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFL PRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLR PRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR GEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGP GEFIVTRAGLYYLYCOVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGP Gaps .; 0 Length 249; QVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225 OVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFOVH 249 16; Indels Score 1020; DB 5; Pred. No. 2.1e-97; 9; Mismatches 87.8%; 88.8%; nservative rity

lard; protein; 249 AA

first entry)

otein.

necrosis factor; ligand; cytostatic; r; osteopathic tumour

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002WO~US023782.

001US-0307838P.

GENOME SCI INC.

osen CA;

ស់អ្នកទាក់ទីក្នុកទាក់ទីទីសមាល់ទីសមាប់មកទីលំទីកមាកមាល់ទីក្រុកប្រជាជាទីក្រុកក្រុកក្នុកក្នុកក្នុកក្នុក ក្រុម

59/40.

complex having a first polypeptide member of the r (TNF) ligand family, and a second different member, useful for treating cancer, osteoporosis or an factor family, imeric

ge 368-369; 388pp; English.

quence is the protein sequence for human TWEAK protein. The test to compositions comprising heterotrimeric complexes of sector (TNF) ligand family members, and their use in the vention and treatment of disease. In one embodiment, the complex comprises full-length or extracellular portions of length or extracellular portions of other TNF ligand, preferably VEGI or VEGI-SV. The heterotrimeric complexes on are useful for treating an autoimmune disease, cancer or and particularly for inhibiting cancer cell proliferation, or inducing apoptosis of T cells

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                                                                                                 26 LGIGLALACLGLILAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDP?
                                                                                                                                                                                                                                                  2 LSLGLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDV
                                                                                                                                                     62 EQLVRPRRSAPKGRKARPRRALAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSS
                                                                                                                                                                                           86 NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSS
                                                                                                                                                                                                                              YDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAAS:
                                       ٠,
Length 249;
                                                                                                                                                                                                                                                                                                                              206 OLRICOVSGILALRPGSSLRIRTLPWAHLKAAPFLIYFGLFQVH 249
                                                                                                                                                                                                                                                                                                        182 QLRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225
                                     Indels
                                     16;
87.8%; Score 1020; DB 6; 88.8%; Pred. No. 2.1e-97;
               Pred. No. 2.1e
9; Mismatches
                 Best Local Similarity 88.8
Matches 199; Conservative
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   Query Match
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Human TNF ligand family member #12. ADC35206 standard; protein; 249 AA. (first entry) 18-DEC-2003 ADC35206; 

RESULT 12

ADC35206

human; tumour necrosis factor; TNF ligand; endokine alpha; excessive bone resorption disorder; osteoporosis; Paget's disease, arterial calcification.

Homo sapiens.

US2003100074-A1.

29-MAY-2003.

15-AUG-2002; 2002US-00218547.

16-AUG-2001; 2001US-0312542P.

YU G. NI J. (XDGG/)

(ROSE/) ROSEN C A. (NARD/) NARDELLI B.

Nardelli B; Yu G, Ni J, Rosen CA,

WPI; 2003-696072/66. N-PSDB; ADC35205.

New Endokine alpha gene useful for preparing a composition for tredisease associated with excessive or insufficient bone resorption osteoporosis, Paget's disease or arterial calcification.

Disclosure; SEQ ID NO 24; 145pp; English.

tumour necrosis factor family ligand. A composition comprising the isolated antibody or its fragment is used for treating an individuced of decreased level of endokine alpha activity. The endokine polypeptide present in a heterotrimeric complex is used for treatindividual having a disorder associated with excessive bone resort individual having a disorder associated with insufficient bone recomprises administering an endokine alpha antagonist, which is the antibody that binds specifically to endokine alpha polypeptide. It The invention relates to an isolated nucleic acid molecule encodi

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Claim 40; Fig 13A; 156pp; English.
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88.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 88.8
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human TNRL3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-205191/17.
N-PSDB; AAX23424.
                                                                                                                                                Sequence 284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 il or active fragments can be included with a carrier in all compositions to treat cancer, autoimmune diseases or uses to tissue graffs, or to stimulate or suppress the immune a useful to exceen for TRELL receptors, by labelling with a useful and screening compositions for binding. Agents with TRELL-receptor binding can also be screened for, can istered, optionally with interferon- gamma, to induce cell
                                                                                                                                                                           121
                                                                                                                                                                                                    145
                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sis factor related ligand - useful for, e.g. treating cancer, lisease and immune responses to tissue grafts.
                                                                                                                     61
                                                                                                                                                85
ince represents the amino acid sequence of a tumour necrosis
                                                                                                                                                                                         !LALACLGLLIAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL
                                                                                                                     SLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFL
                                                                                                                                                                          TRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLR
                                                                                                                                                                                                                             JIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : necrosis factor related ligand; tnf; treatment; cancer; sease; immune system; stimulation; suppression;
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is that of human tumour necrosis factor related ligand
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o
                                                              Score 1020; DB 7; Length 249;
Pred. No. 2.1e-97;
9; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour necrosis factor related ligand (TRELL).
                                                                                                                                                                                                                                                                                                      CQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENEVA FACULTY MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Je 50-51; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                               dard; protein; 284 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ne Y, Browning JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US013945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0023541P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0028515P.
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                                                                            88.88;
                                                                                            onservative
            ligand
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춵첉뮵뚔냋뚔튽뚔뮵뚔캶찞퀂첉뺭뚔찞첉딦츚눑뮻뼚녪렖뚔찞첉뚔딦뒃쑴맭뚔딦탒쳞쮩쪞읭끙읭믱믱믱믱

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death or treat, suppress or alter immune responses (especially in human adenocarcinoma cells) involving a signal pathway between This receptor. It's coding sequence can be used in gene therapy for related disorders in mammals (especially humans), e.g. tumours, autoimmune and inflammatory diseases or inherited genetic disord introducing into cells, and expressing, therapeutically effective a vector, e.g. a virus comprising a gene encoding TRELL. It makes of use in the preparation of prepare probes for screening that attal/synthetic DNAs for TRELL-encoding sequences and for anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour necrosis factor receptor; signal transducer molecule; TNF developmental abnormality; gestational abnormality; prostate c. APO6; APO6; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; cytoplasmic domain; immunogen; antibody preparation; breast carc:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Tumor Necrosis Factor family receptor polypeptides and ligand useful for diagnosis and treatment of prostate cancer and develoy or gestational abnormalities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LSLGLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 EQLVRPRRSAPKGRKARPRRAIAAHYEVHPRPGODGAQAGVDGTVSGWEGTKINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 OLRICOVSGILALRPGSSIRIRTLPWAHLKAAPFITYFGIFOVH 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1020; DB 2;
Pred. No. 2.6e-97;
9; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW93590 standard; protein; 208 AA.
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eptides: ADO4, ADO6, ADO8 and ADO9 or their active isolated TNR related ligands 1 and 3 (TNRL1 and TNRL3) or ragments. ADO4 is useful for diagnosing prostate cancer by vels of ADO4 in an individual. Prostate cancer can also be APO4 selective binding agents linked to a therapeutic olypeptides are also useful for identifying selective. Useful in diagnosis/reatment of disease by binding of polypeptides/active fragment which is extracellular, or he cell surface. The binding is preferably performed in ypoptides/ active fragments are also useful for screening an antagonists by binding and observing the changer in APO4 cive pharmacological agents useful in diagnosis or isease are also identified using APO4 polypeptides/active APO4 signal transducer molecules that specifically interact smic domain of APO4 and detecting a change in level of APO4 method is performed in vivo or in vitro. APO polypeptides as immunogens for preparing antibodies. APO4 is also gnosis/treatment of developmental or gestational describes isolated Tumor Necrosis Factor (TNF) family uced apoptosis

Gaps ; Score 951; DB 2; Length 208; Pred. No. 2.5e-90; 8; Mismatches 15; Indels 81.8%; 88.9%; nservative

09 WATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRSAPKGRKA 77 

IAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRAGLY

137

120 197 VHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSGLLPLRPG LAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYYRQIGEFIVTRAGLY

RILPWAHLKAAPFLIYFGLFQVH 225 RTLPWAHLKAAPFLTÝFGLFOVH 208

ard; protein; 273 AA.

0; Gē

Length 273; 14; Indels 19 SLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRSAPKGF 67 SLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGI

81.8%; Score 951; DB 4; 88.9%; Pred. No. 3.6e-90; iive 9; Mismatches 14;

Matches 184; Conservative

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Similarity

Query Match Best Local S

Sequence 273 AA;

79 PRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRAC

first entry)

lular domain-containing fusion protein.

lular domain; tumour necrosis factor; TNF; angiogenesis; ularisation; diabetic retinopathy; neovascular glaucoma; r. tetinopathy of prematurity; retrolental fibroplasia; tis; macular degeneration; arthritis; rheumatism; neovascularisation; psoriasis; metastatic condition; ur; sarcoma; carcinoma; benign tumour; haemophilic joint; condition; myocardial angiogenesis; wound granulation; ascular adhesion; telangiectasia; ischaemia; human; c plaque neovascularisation; coronary atherosclerosis; erosclerosis; pDC409-LZ-TWEAK; TWEAK receptor; TWEAKR;

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The sequence represents a fusion protein encoded by the expression vector pDC409-LZ-TWEAK. The fusion protein comprises a growth horm leader, a leucine zipper multimerisation domain, and the extracell domain of human TWEAK. The fusion protein was used in the isolatic human TWEAK receptor (TWEAKR)-expressing clones from a COS cell human TWEAK receptor (TWEAKR)-expressing clones from a COS cell human TWEAK receptor (TWEAKR) expressing clones from a COS cell human TWEAK receptor (TWEAKR) gonists a member of the tumour necrosis (TWF) family and induces angiogenesis. TWEAKR may therefore be use screen for and develop TWEAKR agonists and antegonists for the moc of angiogenesis, to be used in the treatment and diagnosis of human disorderised by ocular neovascularisation such as diabetic retinct neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, rubeosis, uveitis, macular degeneration a rethritis, rheumatism and psoriasis. Other treatable diseases inclemalignant and metastatic conditions such as sarcomas and carcinomed the service of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating angiogenesis in a mammal for treating diseases mediated angiogenesis, e.g. solid tumors and vascular deficiencies of cardiperipheral tissue, by administering antagonist or agonist of TWEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     benign tumours and preneoplastic conditions, myocardial angiogenes haemophilic joints, scleroderma, vascular adhesions, atherosclerot plaque neovascularisation, telangiectasia, wound granulation, corratherosclerosis, peripheral atherosclerosis and ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 41; 46pp; English.
                                  19-DEC-2000; 2000WO-US034755.
                                                                                                    20-DEC-1999; 99US-0172878P.
10-MAY-2000; 2000US-0203347P.
                                                                                                                                                                                                                (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-417975/44.
                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS03964.
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LYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSGLLPLF SLRIRTLPWAHLKAAPFLTYFGLFQVH 225 SLRIRTLPWAHLKAAPFLTYFGLFQVH 273 7, 2004, 17:44:45 Search completed: April Job time : 48.0884 secs 199 247 139 셤 à à

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743.4 54.1 777 12 BI819200 BI819200 725.4 52.8 1071 12 BM921213 BM92121: 701.4 51.1 731 12 BI871711 B1871711	677.4 49.3 728 12 BI870393 BI870393 660.4 49.1 697 14 CF126932 CF126932	11 656.6 47.8 666 14 CP126539 CF126539 C C 12 584.4 42.6 609 12 B1966060 B1966060 i 13 581.4 42.3 1027 28 AF163779 AF16379 AF163	15 562 40.9 940 13 BQ884231 BQ884233 16 560.6 40.8 2237 11 AK044387 AK044387 17 545 39.7 545 14 CB141389 CB141389	544.4 39.7 575 14 CA413067 CA413067 538.8 39.2 569 14 CB529199 CB529199	20 535.6 39.0 569 13 BU631264 BU631264 21 534.6 38.9 569 12 BM971606 BM971606	531.6 35.7 910 12 BG110063 BG11006 516.8 37.6 531 12 BB24443 BIS24443 BIS244443	457.1.2 30.0 024 14 02938034 0593800000000000000000000000000000000000	27 458.2 33.4 1033 11 AK020909 AK020901 28 454.4 33.1 561 10 AK032337 AW763237 29 44.4 32.1 561 10 AK032337 AW763237	442.8 32.3 531 13 DUD 4188 DUD 74188	431.6 31.4 538 10 BF821434 . BF821434 404 29.4 436 28 AQ890280 AQ89028C	399.4 29.1 785 12 BI762908 BI762908 399.2 29.1 665 13 BY742288 BY742288	37 399 29.1 892 14 CB204861 CB204861 38 394.6 28.7 543 29 CG565104 CG565104	394 28.7 413 9 AI422796 AI422796 389.2 28.3 698 12 BI906850 BI906850	381 27.7 1064 14 CF994566 CF994566 379.6 27.6 692 13 BY748962 BY748962	374.2 27.3 416 9 AI291866 372.8 27.2 1319 14 CF594233 CF594233	5 372.6 27.1 584 10 AW917574 AW917574	ALIGNMENTS		776 bp m 2NbHBst Homo	ACCESSION EXOBOLISTS ; ITANELLS '42', MKNA BEQUENCE. VERSION EXOBOLIS 1 GT:27821952	S	Euk Mam			NAZP Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Fild 580, D-69120 Heidelberg, Germany RZPD, IMAGD998E15243.	RZPDIB: 1.M.A.G.E. cDNA Clone Collection; Human UnigeneSet - RZPDI (RZPDIB NO.972) http://www.rznd.do.CloneCasde/col	hin/showlib.pl.cg/jresponse7libNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	ic search, using sw model	ril 7, 2004, 17:30:19 ; Search time 3328.48 Seconds (without alignments) 12318.149 Million cell updates/sec		augicaligitagaciligagadaaaaggitgaraaatgg 1373 gwmrmv wmg	ENTITY NUC pop 10.0 , Gapext 1.0	513289 segs, 14931090276 residues	is satisfying chosen parameters: 55026578	3th: 0 3th: 200000000	inimum Match 0% aximum Match 100% isting first 45 summaries	1	em_escha:* em_eschum:* em_eschim:*	em estrau:	em estoy: * em estoy: *	htc:	gb_est1:* : gb_est2:* : gb_est2:*	: 95_ect.: : gb_ect.: : gh_ect	: gb_est:* : gb_est:* : em estfun:*	em est		em_988	em gas pro:* em gas plo:* em gas plo:*	em_gss_vrl:* gb_gssl:* gb_gssl:*	7 22	analysis of the total score distribut SIMMARTES			i.8 834 12 BI766766 BI766766 603056866 i.9 948 13 BQ707185 BQ707185 AGENCOURT i.4 963 13 BQ671259 BQ671259 AGENCOURT

15 80 741

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information of
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLAM11517 row. column: 18
High quality sequence stop: 772.
High quality sequence stop: 772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 834)
  GGCACTAAGAGGGGCTGGACCTGGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGGCC
                                                                                                                                                                                                                                                                                     BI766766 834 bp mRNA linear EST 25
03056866F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 CCCAGGAGGAGCTGGTGGCAGAGGAGGACCAGGACCCGTCGGAACTGAATCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCCAGGAGGAGCTGGTGGTGGCAGAGGACCAGGACCCGTCGGAACTGAATCCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 AAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGT
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                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                                                                                              1320 ITITIAAAACAGAIATIATITITIATIATIATIGIGACAAAATGITGAIAAATG
                                                                                                                                                                                    721 TITITAAAACAGATATTATTITATTATTATTGNGACAAAATGITGATAAATGG
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Pred. No. 7.3e-134;
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/db_xref="taxon:9606"
/clone="IMAGE:5206217"
                                                                                                                                                                                                                                                                                                                                                                           BI766766.1 GI:15758344
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Homo sapiens
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BI766766
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BI766766
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                                                          îone is available royalty-free from RZPD;
FXPD (clone@rzpd.de) for further information. Seq primer:
Primer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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                                                                                                                                                                                                                             clone="IMAGp998E15243 ; IMAGE:154742"
                                                                                                                                                                   organism="Homo sapiens"
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'db_xref="taxon:9606"
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8353983 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278608
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a; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                       TGGACAGGACGCAGGCAGGTGTGGACGGGACAGTGAGTGGCTGGGAGGAA
                                                                                                                                    SAATCAACAGCTCCAGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTC
                                                                                                                                                                                                                            GGCTGGGCTCTACTACCTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTC
                                                                                                                                                                                                                                                                                                                    GAAGCTGGACTTGCTGGTGGATGTGCTGGCCCTGCGCCTGCGTGCAATTC
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Institutes of Health, Mammalian Gene Collection (MGC)
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Procurement: Dr. Mark Watson
Library Preparation: Rubin Laboratory
duencing by: The I.M.A.G.E. Consortium (LINL)
quencing by: Agencourt Bioscience Corporation
distribution: MGC clone distribution information can larged the I.M.A.G.E. Consortium/LLNL at:
LLCM2466 row: n column: 17
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: Robert Strausberg, Ph.D.
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/uni_type="maxNa"
/ub_xref="taxon:9606"
/ulone="lwaRNa"
/ub host="billoB (phage-resistant)"
/ulone=lib="WHH MGC_113"
/ulone="Organ: spleen; Vector: pOTB7; Site_1: XhoI Ecoff; cDNA made by oligo-dr priming. Directional into EcoRI/XhoI sites using the following 5' adap GGCACGAG(G). Library constructed by Ling Hong in laboratory of Gerald M. Rubin (University of Cal Berkeley) using ZAP-cDNA synthesis kit (Stratagen Supersoript II RT (Life Technologies). Note: this NIH_MGC Library."
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                                                                            organism="Homo sapiens"
quality sequence start: 24 quality sequence stop: 550. Location/Qualifiers
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Sequencing by: Agencourt Bioscience Corporation
e distribution: MGC clone distribution information can lthrough the I.M.A.G.E. Consortium/LLNL at:
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quality sequence stop: 565.
Location/Qualifiers
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                                                                                   240 CTTTGATGAGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGTGT
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National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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/ido. lib= NHH MGC 115."

/note= 'Organ: pooled brain, lung, testis; Vector:
pcWV-SPORT6; Site_1: Nor1; Site_2: EcorV (destroyed); RNA

source anonymous pool of 6 male brains, age range 23-27; I
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (BroxV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
erriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NH_MGC Library."
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Library Preparation: Life Technologies, Inc.
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
aquencing by: Incyte Genomics, Inc.
distribution: MGC clone distribution information can lithrough the I.M.A.G.E. Consortium/LLNL at:
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LLAM11437 row: 1 column: 03
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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5175698"

/lab_host="DH108"
                                                                                                                                                                                                     lality sequence stop: 759.
Location/Qualifiers
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/lab host="DH108"
/clone lib="NHH MGC 115"
/clone lib="NHH MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
pOWV-SPORTS; Site_1: NotI; Site_2: EcoRV (destroy source anonymous pool of 6 male brains, age range male lung, age 27; and 1 male testis, age 69. Li oligo-dT primed and directionally cloned (EcoRV s destroyed upon cloning). Average insert size 1: insert size range 1-3 kb. Library is normalized a enriched for full-length clones and was conserue.
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Email: cgapbs-r@mail.nih.gov

Irisue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information ca

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12786 row: p column: 02
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sapiens cDNA clone IMAG
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                                                                                      948 ICTITGCICCAGACCIGCCCCICCTAGAGGCIGCCIGGGCCTGTICACGIGIT
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                                                                                                                                                                                                                                                    733 ATCCCACAT-AATACAGTATICCCACTCTTATCTTCAAATCCCCC 776
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ial Institutes of Health, Mammalian Gene Collection (MGC) ished (1999)
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equencing by: Incyte Genomics, Inc.
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Procurement: ATCC
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/db xref="taxxon:9606"
/clone="IRAGE:5405478"
/tissue_type="adenocarcinoma, cell line"
/tab host="Bh108 (phage-resistant)"
/clone_lib="NIH MGC 90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1
Site_2: Sall; Cloned unidirectionally; oligo-dT l
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Techno
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Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov
Plate: LiAM12034 row: b column: 07
High quality sequence stop: 728.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
II (bases 1 to 728)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (1
Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car
flound through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLMM.2034 row: a column: 12
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/clone="IMAGE:2605459"
/tissue type="adenocarcinoma, cell line"
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/mol_type="mRNA"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                           cgapbs-r@mail.nih.gov
Procurement: Miklos Palkovits, M.D., Ph.D.
ibrary Preparation: Michael J. Brownstein (NHGRI), Shiraki
iki and Piero Carninci (RIKEN)
ibrary Arrayed by: The I.M.A.G.E. Consortium (LINL)
distribution: MGC clone distribution information can be
hrough the I.M.A.G.E. Consortium/LINL at:
image.llnl.gov
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| Institutes of Health, Mammalian Gene Collection (MGC)
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                                               /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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99.0%; Pred. No. 3.1.
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30563490 5', mRNA sequence.

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Email: bento-goare@quiowa.edu
Tissue Procurement: Mary Hendrix
CDNA Library preparation: Dr. M. Bento Soares, University
CDNA Library Arrayed by: Dr. M. Bento Soares, University
DNA Sequencing by: Dr. M. Bento Soares, University
DNA Sequencing by: Dr. M. Bento Soares, University
DNA Sequencing by: Dr. M. Bento Soares, University
The following repetitive elements were found in this cDN
Sequence: 37-144, SGC_rich#Low_complexity
Location/Qualifiers

Location/Qualifiers
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/lab host="DHLOB (TI phage resistant)"
/clone lib="NIH_MGC_214"
/clone lib="NIH_MGC_214"
/note="Organ: Lung; Vector: pYX-Asc; Site 1: Ecoi Site 2: Not 1; The library was constructed accorr Bonaldo, Lennon and Soares, Genome Research, 6:75:196. Denatured RNA was size fractionated on a liggel. First strand cDNA synthesis was primed with primer containing a Not I site. Double strand cDN size selected according to mRNA size fraction, libwith Ecok I adaptor digested with Not I and their directionally into pX-Asc vector. The library to sequence located between the Not I site and the I is GATAAAGGCCA. Tissue was provided by Mary Hendri
                                                                                                     1 (bases 1 to 697)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilita
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                                                                           University of Iowa
The Newton Road, 4156 MEBRF, Iowa City, IA 52242,
TH: 319 335 9565
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                 Contact: Soares, MB Coordinated Laboratory for Computational Genomics
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30563490"
                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
Homo sapiens (human)
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ibrary preparation: Dr. M. Bento Soares, University of Iowa
ibrary Arrayed by: Dr. M. Bento Soares, University of Iowa
cycunching by: Dr. M. Bento Soares, University of Iowa
Distribution: Distribution information can be found at
genome.uiowa.edu/distribution/humanfl.html
                                                                                                                                                                                                                                                                                                                                                       713
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/clone="IMAGE:10559317"
/tisume_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH10B (TI phage resistant)"
/clone lib="NIH_MGC_214"
/note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
Site_2: Not I; The library was constructed according
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"M.F., Lennon, G. and Soares, M.B.
zation and subtraction: two approaches to Res. 6 (9), 791-806 (1996)
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$T0-avw-m-22-0-UI.r1 NIH MG
$659317 5', mRNA sequence.
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/db xref="taxon:9606"
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Bonaldo, Lennon and Soares, Genome Research, 6:79
1996. Denatured RNA was size fractionated on a 18
gel. First strand cDNA synthesis was primed with
primer containing a Not I site. Double strand cDN
size selected according to mRNA size fraction, II
with EcoR I adaptor, digested with Not I and then
directionally into pYX-Asc vector. The library ta
sequence located between the Not I site and the p
is GATAAGGCCA. Tissue was provided by Mary Hendri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B1966060 609 bp mRNA linear EST 12-16-2204.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo se CDNA clone IMAGE:5672623 3' similar to TR:054907 054907 TNI WEAK INDUCER OF APOPTOSIS ;, mRNA sequence.
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98.9%; Pred. No. 2.5e-113;
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Best Local Similarity 98.9
Matches 659; Conservative
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sapiens (human)

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/clone_lib="Human"
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Institute of Pathology
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Matches 577; Conservative
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/dev stage="Adult"
/dev stage="Adult"
/lab_nost="Nation"
/lab_nost="Nation"
/clone_lib="Metton Normalized Human Islet 4 N4-HIS 1"
/clone_lib="Metton Normalized Funantist Site_1: Not 1;
Site_2: Sal 1: Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). CDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on Solid Support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Pandreas Consortium of University, Howard Hughes Medical Institute of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                            ota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                       1,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., 1ka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., St.,. Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A., it,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., 1as,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., 1ms,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCCCTGGGCCCATCTCAAGGCTGCCCCTTCCTCACCTACTTCGGACTCTTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                t: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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Pred. No. 9.7e-100;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="IMAGE:5672623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                      rine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.6%;
99.7%;
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                                                                                                          uses 1 to 609)
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AF163779 luman Homo sapiens genomic clone BAC750E14, genor
369 TICCCACTCTTATCTTACAACTCCCCCACCGCCCACTCTCCACCACCTCAGTAGCTCC
                                                                                                    cccrgacccrrrraaggccccccagraarcrcaacrccccccrggccacagacccc
                                                                                                                                                                                                                                                    1147 ATTGFGTFCACTGTACTCTGTGGGGCAAGGATGGGTCCAGAAGACCCCCACTTCAGG
                                                                                                                                                                                                                                                                                                  249 ATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTTCAGAAGACCCCCACTTCAGG
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Cousin, P., Billotte, J., Chaubert, P. and Shaw, P. H. Physical map of 17p13 and the genes adjacent to p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     785 GCACCCTCCCCTGGGCCCCATCTCAAGGCTGCCCCCTTCCTCACCTACTTCGGACT
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sub_clone=AB2R Asc-BamHI PSL1180
Class: BAC subclone.
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8; Mismatches 4
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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1144
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/dev stage="Adult"
/dev stage="Adult"
/lab_host="RMU108"
/clone_lib="Human Retinal pigment epithellum/choroid cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 540
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a; Butheria; Primates; Catarrhini; Hominidae; Homo.
es 1 to 567)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 .yl Human Retinal pigment epithelium/choroid cDNA malized, unamplified): cs Homo sapiens cDNA clone cs80h07
CCCTCTAGAGGCTGCCTGGCCTGTTCACGTGTTTTCCATCCCACATAAATACAG
                                                                                                                                                                                      CCACTCTTATCTTACAACTCCCCCACGCCCACTCTCCACCTCACTAGCTCCCCA
                                                                                                                                                                                                                                        CCACTCTTATCTTACAANNNYCCACCCCCACTCTCCACCTCACTAGCTCCCCA
                                                                                                                                                                                                                                                                                         TGACCCTTTGAGGCCCCCCAGTGATCTCGACTCCCCCCTGGCCACAGACCCCCAGG
                                                                                                                                                                                                                                                                                                                       TGACCCTTGAGGSCCCCAGTGATCTCGACTCCCCCCTGGCCACAGACCCCCAGG
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mer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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(Un-normalized, unamplified): cs"
/note="Organ: Eye; Vector: pCmVSPORTG; Two differe
eyes (75-80 years old) yielded approximately 600 t
dissected RPB/choroid tissue. This in turn yielde
of total RNA and 7 ug of mRNA. A directionally cl
library in the pCMVSPORTG vector was constructed
interary fallowing the protocols of the Superson Possentially following the protocols of the Superson Plant (Intirogen Corp.
chttp://www.invirtogen.com/>). The library code
designation was cs. For this library, cDNA inserted cloned into the Not!/Mull sites of the vector. ES;
analysis was performed on the unamplified library
NIH Intramural Sequencing Center (NISC)."
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IMAGE:6197488 5', mRNA sequence.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ct. Robert Strausberg, Ph.D.

cgapbs.rémail.nih.gov

brocurement: Dr. James R. Lupski

Library Preparation: Life Technologies, Inc.

Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing by: Agencour Bioscience Corporation

c distribution: MGC clone distribution information can be

through the I.M.A.G.E. Consortium/LINL at:

Library Arrayed by: Agencour Strain LIP

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Search completed: April 7, 2004, 23:15:25 Job time : 3339.48 secs

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CRGANISM unidentified
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      GAGGCTGCCTGGCCTGTTCACGTGTTTTCCATCCCACATAAATACAGTATTCCCA
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Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A.,
Stone,D.M., Watanabe,C.K. and Wood,W.I.
Compositions and methods for the treatment of tumour
Patent: WO 0153486-A 3 26-JUL-2001;
Genetiech, Inc. (US)
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Sequence 3 from Patent W00153486.
AX201324
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Best Local Similarity 99.8
Matches 1322; Conservative
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AGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGGTGGTG 240  MAGGAGGACCAGGACCGGAACTGAATCCCCAGACAGAAGAAAGA		CAGGCAGGTGTGGAGCAGGAGCTGAGAGGAAGCCAGAATCAACACTCC 528	CTCTGCGCCTACAACCGCCAGATTTATAGTCACCCGGGCTGGGCTTTACTCTAC CTCTGCGCTCACACTTTGATGAGGGGAGTTTATAGTCACCCGGGCTGGGGCTCTAC CTGTACTCTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGACTTG CTGTACTCTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTG CTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTG CTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACTGAAGCTGGACTTG CTGTACTGTCAGATGAGGGGAAGGCTGTCTACTAACTGAAGCTGGACTTG CTGTACTGTA			:TCGGACTCTTCCAGGTTCACTGAGGGCCCTGGTCTCCCCAGGCT 888 			CATAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCAGTGATCTCGACTCCCCCTG 1128	ACAGACCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAG 1188	AGCCAPAGAGACTGGGC	GCCAGGAGTICCCAAATGIGAGGGGCGAGAAACAAGACTCCTCCCTTGAGAA 1308 GCCAGGAGTICCCAAATGIGAGGGCGAGAAACAAGACCAAGCTCCTCCCTTGAGAA 1260	CCGGGGATTTTTAAAACAGATATTATTTATTATTATTATGGAAAATGTTGATA 1368 

Db   1201 CTAGGCCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAAGCTCCTCCTTG.	AF055872 Homo sapie AF055872.1 AF055872.1 Homo sapie Homo sapie Eudensycla; Marmalia;	REPRENCE 1 (bases 1 to 1368) AUTHORS Marsters.A.A. Sheridan,J.P., Pitti,R.M., Brush,J., Goddar Ashkenazi,A. TITLE Adentification of a ligand for the death-domain-containing Apol DOURNAL Curr. Biol. 8 (9), 525-528 (1998) MEDLINE 98228355 PUBMED 95603133 PUBMED 95603133	Marsters, S.A., Sheridan, J. Ashkenazi, A. Ashkenazi, A. Direct Submission Submitted (25-MAR-1998) M South San Francisco, CA 9 Location/Qualifice	/ Organism= "Mono Saplens"   / Mol Lype= "MRNA"   / Ab_xref="taxon:9606"   / Ab_xref="taxon:9606	/gene="ArOin" /gene="ArOin" Apol/DR3" /note="TMF homolog" /codon start=1 /product="Apol/DR3 ligand" /protein_id="Apol/DR3 ligand" /protein_id="AAC39724.1" /db_refe=[8] 13.108231"		Indels CACAGCCC	Db 1 CGATCCCTCGGGATGGGGGGGGGGGGGGGGGGGGGGGGG
							ACIAGETECCEAGACCETTGAGACCETTGAGACCECCAGAGATCGACCCCCEGGGGGGGGGAGGGTGGGCTCCCCCCGGGGGGGGGG	CACTTCAGGCACTAAGAGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGC 1248

	Z E	PUBMED 9405449  REFERENCE 2 (bases 1 to 1306)  AUTHORS Bourdon, P., Heesion, C., Tizard, R. and Browning, J.  TITLE Direct Submission JOURNAL Submitted (14-OCT-1997) Cell Biology, Biogen, 12 Cambridge MA 02142, USA  FEATURES Location/Qualifiers 1. 1306   Organism "Homo sapiens"   mol. Lype="mRNA"   db xref="taxon:9606"   chromosome="17"   map="17p13"   fissue type="tonsil"   tissue type="tonsil"   tissue type="ligand in the INF family; secreted protein codon not verified experimentally"		Best Local Similarity 100.0%; Pred. No. 2.4e-225;   Matches 1285;   Conservative 0; Mismatches 0; Indels 0;   Matches 1285;   Conservative 0;   Mismatches 0;   Indels 0;   Conservative 0;   Mismatches 0;   Conservative 0;   Conservative 0;   Indels 0;   In
CCGCTCGCGCTCGGCCTCGCCTCGCCTCCGCCTCCGCCTCCT	CCTTTCCTGAACCGGCTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACA 408	GTGGATGGTGTGCTGGCCTGCTGCTGGAATTCTCAGCCAGAGCTTG 600 GTGGATGGTGTGCTGGCCTGCTGCTGGAGGAATTCTCAGCCACTGGAGCTGG GTGGATGGTGTGTGGCTGCCTGCTGCTGGAGGAATTCTCAGCCACTGCGGCCAGT 708 GTGGATGGTGCTGGCCTGCCTGCCTGCTGGAGGAATTCTCAGCCACTGCGGCCAGG 768 CTCGGGCCCCAGCTCCGCTCTGCCAGGTGTCTGGGCTTTGGCCCTGCGGCCAGG 768 CTCGGGCCCCAGCTCCCCTCGCCAGGTGTCTGGGCTTTGGCCCTTCCTGCGGCCAGG 720 TCCCTGCGGATCCGCCCTCTGCCAGGTGTCTGGGCTTTGGCCCTTCCTCACC 828 TCCCTGCGGATCCGCCCCCCCCTGGGCCCTTCTAAGGCTGCCCCTTCCTCACC 780 TTCGGACTCTTCCAGGTTCACTGAGGGCCCTGGTCTCCCCAGGCT 888 TTCGGACTCTTCCAGGTTCACTGAGGGCCCTGGTCTCCCCAGGCT 888 TTCGGACTCTTCCAGGTTCACTGAGGGGCCCTGGTCTCCCCCAGGCT 840	GGCTCCCCTCGACAGCTCTCTGGGCACCCGGTCCCCTTGCCCCACCCTAAGCCGCCT 948	CACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCGTGATCTCGACTCCCCCTG 1128

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RE FE	REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE ORIGIN	Wiley,S.R. to 1236) Wiley,S.R. to family useful for treatment and diagnosi disease Patent: US 6207642-A 1 27-MAR-2001; Location/Qualifiers 1. 1236 /organism="unknown" /mol_type="unassigned DNA"
	Query Matc Best Local Matches 12	Match B9.3%; Score 1226.4; DB 6; Length 1236; Local Similarity 99.5%; Pred. No. 1.3e-214; es 1230; Conservative 0; Mismatches 6; Indels 0; C
S G	106	ATGGCCGCCGTCGGAGCCAGAGGCGGAGGGGGC 
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₹ da	2 1	26 GIGGTCAGITIGGGGAGCCGGGCATCGCTGTCCGCCAGGAGCCTGCCCAGGAGGF
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ර් සි	346	6 CCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCCC
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Matches 1230; Conservative
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205 Query Match Source FEATURES CDS ORIGIN qq à ò g ò g à g Š 셤 ò g ò erg R.L. Feingold, E.A., Grouse, L.H., Derge, J.G., r.R. D. Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., I.S.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haish, F., nko, L., Marusina, K., Farmer, A.A., Eurin, G.M., Hong, L., T.E., Boransen, M.B., Bonaldo, M.F., Casavant, T.L., T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., I.P., Prange, C., Raha, S. S., Loquellano, N.A., Peters, G.J., J.R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Gunaratne, P.H., Richards, S., C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Haleon, E., Marny, D.M., Sodergreen, E.J., Lu, X., Gibbs, R.A., Haleon, E., Ketteman, M., Madan, A., Rodrigues, S., M.C., Ralesseley, R.W., Touchman, J.W., Green, E.D., M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., 1G.G., Blakesley, R.W., Touchman, J.W., Schmutz, J., Myers, R.M., Schein, J.E., Krzywinski, M.I., Skaleka, U., Smailus, D.E., J.A., Schein, J.E., Jones, S. J. and Marra, M.A., Gode, Soi., U.S.A., Schein, J.E., Jones, S. J. and Marra, M.A., Gode, Sci. U.S.A., 99 (26), 16899-16903 (2002) CTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCGAGTGATCTCGACTCCCCC 1020 CCACAGACCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAG 1185 SCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGGAGGAAAGAAGAGACTG 1245 PRI 04-OCT-2003 7 1642 bp mRNA linear PRI 04-OCT-2003 plens tumor necrosis factor (ligand) superfamily, member 12, ipt variant 2, mRNA (cDNA clone MGC:20669 IMAGE:4766071), ta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ubmission a (07-DEC-2001) National Institutes of Health, Mammalian lection (MGC), Cancer Genomics Office, National Cancer e, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, Butheria; Primates; Catarrhini; Hominidae; Homo. gapbs-r@mail.nih.gov

courement: Louis Staudt

rary Preparation: Rubin Laboratory

rary Arrayed by: The I.M.A.G.E. Consortium (LLNL)

encing by: National Institutes of Health Intramural

burg, Maryland; 2003 this sequence version replaced gi:17512138 ICCCTGTGGATTTTTAAAACAGATATTATTTT 1341 Project URL: http://mgc.nci.nih.gov GI:33874709 MGC help desk piens (human) es 1 to 1642) B 1 to 1642) ipt cds. 7.2

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Akhter, N., Ayelle, K., Becketrom-Sternberg, S.M., Benjamin, B. Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Broc Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legas McDowell, J., Pearson, R., Stantingop, S., Thomas, P.J., McClos Tsurgeon, C., Yogut, J.L., Walker, M.A., Wetherby, K.D., Wiggin Young, A., Zhang, L.-H. and Green, E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 chadachadacccccccardaccccccardaccccarcadacchadadacadadadacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 GGGGAGCCGGCCTGCTGGTCCCGCTCGCGCTGGGCCTGGGCCTGGGCCTGGCGTGC
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Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
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Matches 1347; Conservative
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QY         1286 AAGACAAGCTCCTCCAGAATTCCCTGTGGATTTTTAAAACAGATATTATTT           Db         1516 AAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAACAGATATTTT           QY         1346 ATTATTGTGACAAAATGTTGATAAATGG           Db         1576 ATTATTGTGACAAAATGTTGATAAATGG	RESULT 10 AC016876/C LOCUS AC016876 AC016876 AC016876 AC016876 AC016876 ACCESSION How sapiens chromosome 17, clone RP11-186B7, complete sevents and access access and access and access access and access acce	irren, B., Lint aldwin, J., Baa aldwin, J., Baa cown, A., Castl booke, P., DeArr erreira, P., Fi erreira, P., Fi erreira, P., Fi bloczky, J., Li Jbhoczky,	Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Naylor,J., Naylor,J., Naylor,J., Nobil,D., Oliver,J., Peterson,J. Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rock, Smith,C., Spencer,B., Schupback,R., Seaman,S., Sev, Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Tai Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,J. Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainc Direct Submitted (00-OCT-2002) Whitehead Institute/MIT Center for Referench, 320 Charles Street, Cambridge, MA 02141, USA AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Andersc Barra,N., Basselien,V., Bloom,T., Boguslavkiy,L., Boukhgalter Camarata,J., Chang,J., Chaze,D., Chosepl,Y., Diaz,J.S., Dodg Barra, J., Chang,J., Charg,J., Charg,J., Charg,J., Charg,J., Charg,J., Charg,J., Garadapha,J., Gardyma,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ted (31-OCT-2002) Whitehead Institute/MIT Center for Genome ch, 320 Charles Street, Cambridge, MA 02141, USA 31, 2002 this sequence version replaced gi:23592141.

Peats were identified using RepeatMasker:

/ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nter: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o site: http://www-seq.wi.mit.edu
ltact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iter project name: L3849
iter clone name: 186_B_7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nter code: WIBR
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le first 60.3 kilobases of this clone are being submitted. Lainder overlaps accession number AC113189 [WIGGR project

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S6.0%; Score 768.2; DB 9; Length 60268;
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Strausberg, R.
Direct Submission
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                 Best Local Similarity
Matches 26; Conserv
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INAT RAMI SYALITER, ELENA FEINSTEIN
C12N15/09, A61K31/711, A61K45/00, A61K48/00, A61P9/00, A61P9/10, PC
                                                                                                                                                                                                                                                                                     nce characteristic to gene transcription controlled by hypoxia t: JP 2002525081-A 10 13-AUG-2002; BIOTECH INC
                                                           195 486 bp DNA linear PAT 17-JUL-2003 are characteristic to gene transcription controlled by
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nalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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100.0%; Pred. No. 0.022;
cive 0; Mismatches 0; Indels
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ence 729 from Patent W00229103.
8082
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27-AUG-1998 US 60/0981
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B. (bases 1 to 495)

E. (bases 1 to 495)

Strausberg,R.L. Feingold,E.A., Grouse,L.H., Derge,J.G.,
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Sch
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bl
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsi
hopkins,R.F., Jorden,H., Moore,T., Max,S.I., Wang,J., Hong
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong
Stapledron,M., Soares,M.B., Bonaldo,M.F., Tosasvan,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peter
Abramaon,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malak,J.A., Gunaratne,P.H., Richards,S.W.,
Worley,K.C., Hale,J.S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,K., Gibbs,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
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Akhter,N., Ayele,K. Becketrom-Sternberg,S.M., Benjamin,
Alakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Bl
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Le
Maduro,Q.L., Maskerli,B., Mastrian,S.D.,MCC
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Vig
Young,A., Zhang,L.H. and Green,B.D.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Ensure Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI
CDNA Library Narional Institutes of Health Intramu
Sequencing Center (NISC),
Gaithersburg, Maryland;
Meb site: http://www.nisc.nih.gov/
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Gene Collection (MGC), Cancer Genomics Office, National
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002
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0
                                                                                                                                                                                                                                                                                                                                                                                                           495 bp mRNA linear
Homo sapiens cDNA clone IMAGE:3879577, partial cds.
BC060315
    Length 487;
1.9%; Score 26; DB 6; Length 48; ilarity 100.0%; Pred. No. 0.022; Conservative 0; Mismatches 0; Indels
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07-AUG-2000 JP 2000280989
05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN
                                                                           PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N C12N1/21, PC C12N1/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5 C12N15/00 C12N15/00 CC EST and encoded human protein FW Key Location/Qualifiers FT CDS 338. .499.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 0.022;
tve 0; Mismatches 0; Indels
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1.9%; Score 26; DB 6; Length 516;
Best Local Similarity 100.0%; Pred. No. 0.022;
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343. .>516
/note="unnamed protein product"
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AX885407
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1.9%; Score 26; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 26; Conservative 0; Mismatches
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Homo sapiens
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PF 07-AU
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PI JEAN
GIORDANO
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ia; Butheria; Primates; Catarrhini; Hominidae; Homo.
IRAK Plate: 134 Row: c Column: 18
.one was selected for full length sequencing because it
the following selection criteria: Hexamer frequency ORF
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100.0%; Pred. No. 0.022;
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/clone lib="NIH MGC 68"
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3.J.-B.D.M., Jobert,S. and Giordano,J.-Y.
and encoded human proteins
3 to 6639063-A 1162 28-OCT-2003;
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s,J.B.D.M., Jobert,S. and Giordano,J.E.
d encoded human protein
JP 2002010789-A 1155 15-JAN-2002;
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25 1162 from patent US 6639063.
25.1 GI:40168635
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P 2002010789-A/1155
5-JAN-2002
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BD111487.1 GI:23206305
JP 2002010789-A/3564.
Homo sapiens (human)
Homo sapiens (human)
Homosapiens (human)
Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteli
Ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (baes 1 to 522)
Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
EST and encoded human protein
BST and encoded human protein
GENSET CORP
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                                           JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN
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1.9%; Score 26; DB 6; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels
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1.9%; Score 26; DB 6; Length 522;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels
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Key Location/Qualifiers
CDS 341. :517.
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CORIXA CORPORATION (US)
Location/Qualifiers
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Sequence 877 from Patent WO0212280.
AX381939
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/mol type="unassigned DNA"
/db_xref="taxon:9606"

    .522
    /organism="Homo sapiens"

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JP 2002010789-A/3564
15-JAN-2002
07-AUG-2000 JP 2000280989
05-AUG-1999 US 60/147499
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/db_xref="taxon:9606"
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C12N15/00
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AX381939
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12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
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                                              offs, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, ia; Eutheria, Primates, Catarrhini, Hominidae, Homo.uses 1 to 516)
is,J.B.D.M., Duclair,E. and Jordan,J.Y.
ce tag and encoded human protein
i. JP 2001269182-A 1263 02-OCT-2001;
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FEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
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100.0%; Pred. No. 0.022;
vative 0; Mismatches 0; Indels
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ds,J.B.D.M., Jobert,S. and Giordano,J.-Y.
accorded human proteins
t: US 6639063-A 3571 28-OCT-2003;
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Conservative 0; Mismatches
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/mol type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
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Location/Qualifiers
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26-FEB-1999 US 60/12248
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                                                                                                                                                                                                           IP 2001269182-A/1263
)2-OCT-2001
                                                                                                                                                                                        fomo sapiens (human)
fp 2001269182-A/1263
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934.1 GI:40171044
              apiens (human)
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Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Eutele Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I (bases I to 538)
Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
EST and encoded human protein
Patent: JP 2002010789-A 3561 15-JAN-2002;
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                                                                                                                                                       Length 534;
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                                                                                                                                                       1.9%; Score 26; DB 9; Length 534
100.0%; Pred. No. 0.022;
iive 0; Mismatches 0; Indels
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Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 3568 28-OCT-2003;
/tissue type="Brain, glioblastoma"
/clone lib="NIH MGC_57"
/lab_host="DH10B"
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                                                                            /note="Vector: pDNR-LIB'
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/wol_type="genomic DNA"
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BD111484
BD11484.1 GI:21206302
JP 2002010789-A/3561.
Homo sapiens (human)
Homo sapiens
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05-AUG-1999 US 60/1474
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JP 2002010789-A/3561
15-JAN-2002
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Best Local Similarity 100.0
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Unclassified.
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GENSET CORP
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C12N15/00
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lu, S.P., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

ul, S.P., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,

s, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heish, F.,

enko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

ton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

z, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

ci, P., Prange, C., Raha, S.S., Loquellano, M.A., Peters, G.J.,

on, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

an, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

on, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

J., Helton, E., Ketteman, M., Madan, A., Rodriques, S.,

rd, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

n, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

field, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,

ch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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-lone was selected for full length sequencing because it the following selection criteria: Hexamer frequency ORF
                                                                                  PRI 14-NOV-2003
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ia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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ibrary Arrayed by: The I.M.A.G.E. Consortium (LLNL)
quencing by: Genome Sequence Centre,
cer Agency, Vancouver, BC, Canada
cgsc.bc.ca
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                                                                               22 534 bp mRNA linear apiens cDNA clone IMAGE:3839189, partial cds.
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Procurement: ATCC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 540)
Einat, P., Skaliter, R. and Feinstein, B. Sequence characteristic to gene transcription controlled Patent: JP 2002525081-A 9 13-AUG-2002;
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DN JP 2002525081-A/9

DD 13-AUG-2002

PP 27-AUG-1999 JP 2000571058

PR 27-AUG-1999 US 60/038158,05-MAY-1999 US 60/132

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PC CILLIS/09,A61K31/711,A61K45/00,A61K48/00,A61P9/00,A6
                 02-0CT-2001
24-FEB-2000 JP 2000118773
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JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JE
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ds,J.B.D.M., Duclair,B. and Jordan,J.Y.
nce tag and encoded human protein
t: JP 2001269182-A 1262 02-0CT-2001;
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ive 0; Mismatches 0; Indels
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Submitted (02-0AN-2003) National Institutes of Health, Man
Submitted (02-0AN-2003) Cancer Genomics Office, National Ca
Gene Collection (MGC), Cancer Genomics Office, National Ca
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratance, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulse
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanay
A.N., Gibbs, R.A.
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                                                                                                                                                                                                                                                                       Homo sapiens, clone IMAGE:5285034, mENA.
BC042807
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1.9%; Score 26; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 26; Conservative 0; Mismatches
         0; Mismatches
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/db_xref="taxon:9606"
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AR415932.1 GI:40171042
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         26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo saplens
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AR415932
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                                                                                                                                                                                                                            RESULT 68
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5-AUG-1999 US 60/147499
EAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
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12NS/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
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ia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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: US 6639683-A 3572 28-OCT-2003;
Location/Qualifiers
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s,J.B.D.M., Jobert,S. and Giordano,J.E.
d encoded human protein
JP 2002010789-A 3565 15-JAN-2002;
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35.1 GI:40171045
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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CATTGTTAGACTTTGAAATTTC 512
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/mol_type="genomic DNA"
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NEDO human cDNA sequencing project supported by Ministry Economy, Trade and Industry of Japan; CDNA full insert se Research Association for Botecohnology (RAB); cDNA librar construction and 5'-end one pass sequencing: Institute of Science, University of Tokyo, Laboratory of Genome Struct Genome Center; 3'-end one pass sequencing: RAB; clone selfull insert sequencing: RAB and Helix Research Institute.
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Homo sapiens mRNA; cDNA DKFZp762B195 (from clone DKFZp762
AL359585
                                                                                                                                                           Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura Fukuzumi, Y., Fujimori, Y., Komiyama, M., Suzuki, Y., Hata, H. Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyam Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.
                                                                                                                                                                                                                                                                                                                                                     Sugano, S. and Suzuki, Y.
Direct Submission
Submitted (31-JUL-2003) Sumio Sugano, Institute of Medica University of Tokyo, Laboratory of Genome Structure, Huma Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, (E-mail:flodna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (15-JUN-2000) MIPS, Am Klopferspitz 18a, D-8215
Martinsried, GERNANY
Clone from S. Wiemann, Molecular Genome Analysis, German
Kesearch Center (DKFZ); Email s. WiemannoGKfz-heidelberg:
Sequenced by GBF (National Research Center for Biotechnol
Braunschweig/Germany) within the CDNA sequencing consorti
                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butel
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homc
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Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. a
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This clone (DKFZp762B195) is available at the RZPD in Ber
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100.0%; Pred. No. 0.025;
ative 0; Mismatches 0; Indels
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/clone lib="LNF"
/note="cloning vector: pME1BSFL3"
                    oligo capping, fis (full insert sequence).
Homo sapiens (human)
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_tref="taxon:9606"
/clone="LNF01586"
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AK130060.1 GI:34526798
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                                                                                                                                                                                                                                                                                                             Unpublished
2 (bases 1 to 1822)
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Best Local Similarity
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lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 0.022;
rative 0; Mismatches 0; Indels
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0.022;
0; Indels
                                                                                                                                                                                                                                                                                    Length 595;
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                                             isses 1 to 595)
is,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
and encoded human proteins
:: US 6639063-A 3569 28-CT-2003;
Location/Qualifiers
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ds,J.B.D.M., Jobert,S. and Giordano,J.E.
de ncoded human protein
t: JP 2002010789-A 3562 15-JAN-2002;
T CORP
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Key Location/Qualifiers
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larity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
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/mol_type="genomic DNA"
/db xref="taxon:9606"
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                                                                                                                                                                                                                  /mol_type="genomic DNA"
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Location/Qualifiers
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07-AUG-2000 JP 2000280989
05-AUG-1999 US 60/14745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded human protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595
                                                                                                                                                                                         /organism="unknown"
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JP 2002010789-A/3562
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Conservative

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485.1 GI:23206303 02010789-A/3562. sapiens (human)

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Direct Submitted (1-MAR-2001) Sanger Centre, Hinxton, Cambridges CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clon requests: clonerequest@sanger.ac.uk
On Aug 24, 1999 this sequence version replaced gi:5730221.
During sequence assembly data is compared from overlapping where differences are found these are annotated as variatitogether with a note of the overlapping clone name. Note to variation annotation may not be found in the sequence subm corresponding to the overlapping clone, as we submit seque only a small overlap as described above.

The following abbreviations are used to associate primary numbers given in the feature table with their source datab Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Info on the WORMPEP database can be found at the their source was fin follows unless otherwise noted all regions were either double-stranded or sequenced with an alternate chemistry oby high quality data (i.e., phred quality >= 30); an attem made to resolve all sequencing problems, such as compressing repeats; all regions were covered by at least one plasmid or more than one MIS subclone; and the assembly was confirmed that a sequencial from part that the sequence was generated from part that the sequence was generated from part that the sequence was generated from part that the sequence was generated from part that the sequence was generated from part that the sequence was generated from part that the sequence was generated from part than the sequence was generated from part than the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSDJ686N3 110293 bp DNA linear PRI 06 Human DNA sequence from clone RP4-686N3 on chromosome 20q1 Contains the 3' part of the gene for a novel ATP dependent helicase (contains conserved C-terminal helicase domains a DEAD/DEAH boxes), the KIAA1404 gene, a putative novel gene ATSs, GSSs and two CpG islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bacterial clone contigs of human chromosome 20, constructed Sanger Centre Chromosome 20 Mapping Group. Further inform be found at http://www.sanger.ac.uk/HGP/Chr20 RP4-686N3 is from the library RPC14 constructed by the grapheter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL049766.14 GI:5763746
HTG; CpG island; DEAD box; DEAH box; KIAA1404; RNA helicas
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110293)
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/gene="dJ686N3.1"
join(<207. .266,518. .683,2195. .2241,2363. .2449
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                                                                                                   1.9%; Score 26; DB 9; Length 2650; 00.0%; Pred. No. 0.026;
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                                                                                                                      100.0%; Preu.
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/db_xref="taxon:9606"
/chromosome="20"
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                                                                                                                                                                                        26; Conservative
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                                                                                                   Query Match
Best Local Similarity
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KEYWORDS
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contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 -Charlottenburg, GERMANY; Email: clone@rzpd de Further ition about the clone and the sequencing project is available it/www.mips.blocham.mpg.de/proj/cDNA/.
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Juman cDNA sequencing project supported by Ministry of
// Trade and Industry of Japan; cDNA full insert sequencing:
// Trade and Industry of Japan; cDNA full insert sequencing:
// Trade and Industry of Japan; cDNA full insert sequencing:
// Association for Biotechnology (RAB); cDNA library
// Licion: Helix Research Institute (HRI) (supported by Japan
// Diotechnology Center, National Institute of Technology and
// Industrion: HRI and RAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="melanoma (MeWo cell line)"
/clone lib="762 (synonym: hmel2). Vector pSport1; host
DH10B; sites NotI + SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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/clone Tib="THYMU2"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapping; fis (full insert sequence).
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                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="DKFZp762B195"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                   /map="20q13.2-13.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
2140. .2145
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59656138,74497599,1055610655,1081810959, 1218512338,1340013481,1358313760,1619916305, 1648616588,1914319237,1933319456,1984419931,	repeat_region	56905809 /note="AluSq/x repeat: matches 14133 of conse AluSq/x repeat: matches 14133 of consensus"
.21327)	repeat_region	peat: matches 1303
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join(<207266,518683,21952241,23632449,36803785, 59656138,74497599,1055610655,1081810959,	region	matches 48174 of
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CEIRS: II:Oz3500 II:Q9Z15Z Sw:P25888 Sw:P32892 Sw:Q099	_region	91269436 /note="AluJo repeat: matches 1308 of consensu
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## ATTGTTAGACTTTGAAATTTC 66465

13 159020 bp DNA linear HTG 27-APR-2000 uplens chromosome 20 clone RP11-564F22 map 20, WORKING DRAFT 15, 21 unordered pieces. ed (25-MAR-2000) Whitehead Institute/MIT Center for Genome in, 320 Charles Street, Cambridge, MA 02141, USA 27, 2000 this sequence version replaced gi:7328901. ota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; a; Butheria; Primates; Catarrhini; Hominidae; Homo. ----- Genome Center ter: Whitehead Institute/ MIT Center for Genome Research This is a 'working draft' sequence. It currently sts of 21 contigs. The true order of the pieces of known and their order in this sequence record is rary. Gaps between the contigs are represented as Nert size: 171000, agaroge-fp Nert size: 157020; sum-of-contigs Nity coverage: 3.9 in Q20 bases; agarose-fp Nity coverage: 4.2 in Q20 bases; sum-of-contigs r.F.A. & Green, P. (1996-1997) ftp.genome.washington.edu/RM/RepeatMasker.html tact: sequence\_submissions@genome.wi.mit.edu B., Linton, L., Nusbaum, C. and Lander, E. upiens chromosome 20, clone RP11-564F22 site: http://www-seq.wi.mit.edu 3.2 GI:7651931 GS\_PHASE1; HTGS\_DRAFT. ies 1 to 159020) ses 1 to 159020) ter code: WIBR ipiens (human)

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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon it is available and the accession number will be preserved:
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7 4 8 5 8 9 6 9 C	5', mRNA sequence.  ON BM921213.1 GI:19371592  SET.  Homo sapiens (human)  ISM Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  CE 1 (bases 1 to 1071)  National Institutes of Health, Mammalian Gene Collection (M  AL Unpublished (1999)  Contact: Robert Strausborg, Ph.D.  Email: Gapbs-r@mail.nih.gov  Tissue Procurement: Life Technologies, Inc.	CDNA CDNA DNA S Clone found httpu Plate: High q	Anote="Organ: pooled brain, lung, testis; vector: pcWv-SpORT6; Site 1: Not1; Site 2: EccRV (destroye source anonymone) of 6 male brains, age range male lung, age 27; and 1 male testis, age for Lib oligo-dT primed and directionally cloned (EccRV sidestroyed upon cloning). Average insert size 1: 8 insert size range 1-3 kb. Library is normalized an enriched for full-length clones and was construct Gruber (Invitrogen). Research Genetics tracking 021. Note: this is a NIH-MGC Library."  Query Match 44.6%; Score 613; DB 12; Length 1071; Best Local Similarity 99.7%; Pred. No. 4.88-301; Matches 713; Conservative 0; Mismatches 2; Indels 0; Ga
OY  Db  Qy  Db  Qy  Db  Qy  Db  Db  Db  Db  Db  Db  Db  Db  Db  D	ACCESSION VERYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	FEATURES	ORIGIN Query M Best Lo Matchee
Ta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; a; Eutheria; Primates; Catarrhini; Hominidae; Homo. at 1 to 777)  http://mgc.nci.nih.gov/.  l Institutes of Health, Mammalian Gene Collection (MGC) shed (1999)  shed (1999)  Robert Strausberg, Ph.D. cgapbs r@mail.nih.gov  Procurement: Life Technologies, Inc. ibrary Preparation: Life Technologies, Inc. ibrary Preparation: Life Technologies, Inc. ibrary Arrayed by: The 1.M.A.G.E. Consortium (LLNL) thencology by: Incyte Genomics, Inc. ibrary Arrayed by: Consortium/Linl. at: ibrary Arrayed by: The 1.M.A.G.E. Consortium (LLNL) therough the I.M.A.G.E. Consortium/Linl. at: ibrary sequence stop: 759.  Linger.linl.gov  Linger.linl.gov  Location/Qualifiers  location/Qualifiers  location/Qualifiers  location-location/Gualifiers  location-location	/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: EccRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (BcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."  45.8%; Score 629; DB 12; Length 777; rity 99.7%; Pred. No. 3.1e-309; nservative 0; Mismarches 2; Indels 0; Gaps 0;	TCGGAACTGAATCCCCAGACAGAAGAAAGCCAC	

Plate: LLCM2456 row: 1 column: 13 High quality sequence stop: 565. Location/Qualifiers Location/Qualifiers  963	ORIGIN  ORIGIN  Query Match  44.1%; Score 605; DB 13; Length 963; Best Local Similarity 100.0%; Pred. No. 5.7e-297; Matches 605; Conservative 0; Mismatches 0; Indels 0; G  Qy 408 ACGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACAGG  Dh 39 ACGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTTCATCCACCACAGGGGGGGG	. 466 99 99 99 1528 99 158 99 59 59 59 59 59 59 59 59 59 59 59 59	648 279 279 708 339	Db   399 GTCCTCCTGGGGATCGCACCCTCGGGCCCATCTCAAGGCTGCCCCTTCC	OY 948 TCTTTGCTCCAACCTGCCCTCCTAGAGGCTGCGGGCTGTTCACGTGTT
		CCTCAGCCGCTCTT CCTCAGCCGCTCTT CCTCAGCCGCTCTT CCTCAGCCGCTCTT CGTGTTTTCCATCC CGTGTTTTCCATCC CGTGTTTTCCATCC CGTGTTTTCCATCC CGTGTTTTCCATCC	CTCCACT CCC 1126 CCC 726 CCC 726	is cDNA clone ertebrata; Ev Hominidae;	al Institutes of Health, Mammalian Gene Collection (MGC) ished (1999).  ished (1999)  is Robert Strausberg, Ph.D. cgapbs-r@mail.nih.gov Procurement: ATCC Library Preparation: Rubin Laboratory Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) equencing by: Agencourt Bioscience Corporation distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: //mage.llnl.gov

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/note="Organ: Eye; Vector: pCWVSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCWVSPORT6 vector was constructed at Life rechnologies (Rockville, MD; now part of Invitrogen Corp, essentially following the protocols of the SuperScript Plasmid System (Invitrogen Corp, Plasmid System (Invitrogen Corp, Plasmid System (Invitrogen Corp, Plasmid System (Invitrogen Corp, Chtp://www.invitrogen.com/>). The library code designation was cs. For this library, cDNA inserts were cloned into the Not!/Mull sites of the vector. EST analysis was performed on the unamplified library at the NH Intramural Sequencing Center (NISC)."
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                                                                                                                                                                                                                                                                              G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A., n.J.W., Bouffard, G., Smith, D. and Peterson, K. ed sequence tag analysis of human RPE/choroid for the Project: Over 6000 non-redundant transcripts, novel genes ice variants
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a, Butheria, Primates, Catarrhini, Hominidae, Homo.
.yl Human Retinal pigment epithelium/choroid cDNA nalized, unamplified): cs Homo sapiens cDNA clone cs80h07
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Eye Institute
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mer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/dev_stage="Adult"
|lab_host="EMDH10B"
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db_xref="taxon:9606"
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/sex="M"
/cell line="CK-KI"
/lab_host="ToplOF"
/clone lib="Li5CKKI"
/clo
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Kim, M. S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., R Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S.
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GAGGACCAGGACCCGTCGGAACTGAATCCCCAGACAGAAGAAGCCAGGATCCTGC
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Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
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21C Frontier Korean EST Project 2001
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Email: yongsungemail:kribb.re.kr
Plate: 30 row: E column: 06
High quality sequence stop: 545.
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/db xref="taxon:9606"
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EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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39.7%; Score 545; DB 14; L
100.0%; Pred. No. 2.1e-266;
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81 828 bp mRNA linear EST 07-SEP-2001 254F1 NIH MGC\_96 Homo sapiens cDNA clone IMAGE:5285892 5', equence.
81 81.1 GI:15489620 apiens (human) apiens (human) cota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ia; Butheria; Pimates; Catarrhini; Hominidae; Homo.

2525

uses 1 to 828)

% http://mgc.nci.nih.gov/.

al Institutes of Health, Mammalian Gene Collection (MGC)

ished (1999)

t: Robert Strausberg, Ph.D.

cgapbs-ramail.nih.gov

? Procurement: Wiklos Palkovits, M.D., Ph.D.

Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

/lone liberary WGC 96"
//clone liberary WGC 96"
//clone liberary Nation Westor: pBluescriptR (modification of the context of t CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11722 row: k column: 13 TCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGAGACGATCG 223 ATTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACC 343 TGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGCTGC GCGCTGCCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGGGCCCCCAGCTCC CTGCCAGGTGTCTGGGCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGGATCCGC creccassigniciasecretrescerecasecasesicerecerecasarecea CCCCTGGGCCCATCTCAAGGCTGCCCCCTTCCTCACCTACTTCGGACTCTTCCAGG cccridedcccarcrcaadgcrccccrrccrcaccracrrcagacrcrrcag CTGAGGGGCCCTGGTCTCCCCACAGTCGTCCCAGGCTGCCGGCTCCCCTCGACAGC CTGAGGGCCCTGGTCTCCCCGCAGTCGTCCCAGGCTGCCGGCTCCCCTCGACAG GGAACTGAATCCCCAGACAGAAGAAGCCAGGATCCTGCGCCTTTCCTGAACCGA GGAACTGAATCCCCAGACAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGA 372 TCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCC 492 AGTGAGTGGCTGGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACC GATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTACTACCTGTACTGTCAGGTG 283 GATCGGGGGGTTTATAGTCACCCGGGCTGGGCTCTACTACTGCTGTACTGTCAGGTG TGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTG GCGCTGCCTGGAGGAATTCTCAGCCACTGCGGCCCAGTTCCCTCGGGGCCCCAGCTC . 0 Length 828; 2; Indels Score 518; DB 12; Pred. No. 1.4e-252; 0; Mismatches 2; /clone="IMAGE:5285892" /tissue\_type="hypothalamus" /lab\_host="DH108" Toshiyuki and Piero Carninci (RIKEN) /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" High quality sequence stop: 776. Location/Qualifiers Query Match 37.7%; Best Local Similarity 99.7%; Matches 618; Conservative ( 43 552 672 403 163 612 732 463 792 852 FEATURES ORIGIN q q qq ð g ö d ð g à 셤 à g à ö à ð g ð qq

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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12034 row: b column: 07
High quality sequence stop: 728.
Location/Qualifiers
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/lab host="DH108" (phage-resistant)"
/clome_lib="NIH_MGC_90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally; oligo-dT pr
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technol
Note: this is a NIH_MGC Library."
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MHI-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (N Unpublished (1999)
374 TITATAGTCACCCGGGCTGGGCTCTACTACCTGTACTGTCAGGTGCACTTTGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       603395825F1 NIH_MGC_90 Homo mapiens cDNA clone IMAGE:540547 mRNA sequence.
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                                                                                                                                                                              434 AAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGTGCTGCCCTGCCCTGC
                                                                                                                                                                                                                                                                                           494 GAGGAATICTCAGCCCACTGCGGCCAGTICCCTCGGGCCCCCAGCTCCGCCTCTGCCAC
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                                                                                                                                                                                                                                                   682 GAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGGGCCCCCAGCTCCGCCTCTGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 554 TCTGGGCTGTTGGCCCTGCGGCCAGG 579
                                                                                                                                                                                                                                                                                                                                                                                              742 TCTGGGCTGTTGGCCCTGCGGCCAGG 767
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/db_xref="taxon:9606"
/clone="IMAGE:5405478"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/note="Organ: Left Pelvis, Vector: pT7T3-Pac (Pharmacia)

with a modified polylinker; Site 1: BcoR I; Site 2: Not I;

NCI_CGAP_Ch1 is a cDNA library containing the following

NCI_CGAP_Ch1 is a cDNA library containing the following

tissue(s): Chondrosarcoma Grade II. The library was

constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 5 bp . mRNA linear EST 07-NOV-2002 Z0-bap-i-03-0-UI.81 NCI_CGAP_Ch1 Homo sapiens cDNA clone Z0-bap-i-03-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgapbs-r@mail.nih.gov
Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
                                                                                                                                                                                                                AGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGCCAGATCGGGGAG 373
                                                                                                                                                                                                                                                                         621
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                                                                                                   radroaccedededecroracracreterererereserecerringareages 433
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GTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATGAA 253
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ia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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al Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATTCTCAGCCACTGCGGCCAGTTCCCTCGGGCCCCCAGCTCCGCCTCTGCCAGGTG
                                                                                                                                                            AGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGCCAGATCGGGGAG
                                                                                                                                                                                                                                                                      TAGTCACCCGGGCTGGGCTCTACTACTGTACTGTCAGGTGCACTTTGATGAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                   r. M. Bento Soares, bento-soares@ulowa.edu
ollowing repetitive elements were found in this cDNA
ce: 1-84, >AI rich#Low_complexity (matched compliment)
imer: Mi3 PORWARD
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/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
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'db_xref="taxon:9606"
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synthesis was primed with an oligo-dr primer cont
Not I site. Double stranded cDNA was ligated to a
adaptor, digested with Not I, and cloned directic
into pryrab-pac vector. The oligonucleotide used t
the synthesis of first-strand cDNA contains a lit
sequence that is located between the Not I site a
(dT)18 tail. The sequence tag for this library is
TGATCACGCT.
TAG TISSUE-grade-2-chondrosarcoma
TAG LIBSUH-H-EZO
TAG LIBSUH-H-EZO
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestne Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Cliftc Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Bliste Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvil
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Bütelec Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 666)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate
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                                                                                                                                                                                                                                     CF126539 666 bp mRNA linear EST 05-
UI-HF-ET0-avw-m-22-0-UI.rl NIH_MGC_214 Homo sapiens cDNA cl
MAGB:30559317 5', mRNA sequence.
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                                           303 GGACCCGTCGGAACTGAATCCCCAGACAGAAGAAAGCCAGGATCCTGCGCCTTTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Tissue Procurement: Mary Hendrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coordinated Laboratory for Computational Genomics
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High quality sequence stop: 451.  Location/Qualifiers  1. 474   organism="Homo sapiens"     mol_type="mRNA"     db_xref="taxon:9606"     clone="IMAGE:6128001"     /clone="type="Purified pancreatic islet"     /lab_host="PH10B"     /clone=lib="HR85 islet"     /note="Corgan: Pancreas; Vector: pBluescript SK(-)     Not1; Site_2: Xho1; cDNA made by oligo-dT priming Size-selected on agarose gel. Average insert size Xize-selected once. Contact information: Hiroshi Inou Metabolism Div. (Alan Permutt Lab), Washington Ur School of Medicine, Box 8127, 660 South Bucclid Av Louis. Mo 63110, B-mail: hinoue@imqate, wusel.edu,	314-362-1916, Fax: 314-747-2692."  Query Match 33.6%; Score 462; DB 13; Length 474;  Best Local Similarity 100.0%; Pred. No. 4.8e-224;  Matches 462; Conservative 0; Mismatches 0; Indels 0; C	Oy 912 TGGGCACCCGGTCCCCTCTGCCCCACCCTCTTTGCTCCAGACCTGCCC  Db 474 TGGGCACCCGGTCCCCTCTGCCCCACCCTCTTTTGCTCCAGACCTGCCC  Oy 972 CTCTAGAGGCTGCCTGGCCTGTTTACCATCCCACATAAATACAGTA1  Db 414 CTCTAGAGGCTGCCTGGGCCTGTTTACCATCCACATAAATACAGTA1	QY 1032 ACTCTTATCTTACAACTCCCCACCGCCACTCTCCACTCACT	QY         1152         GTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAF           Db         234         GTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAF           QY         1212         GGCTGGACCTGGCGCAGAAGCCAAAGACACTGGGCCTAGGCCAGAAGTTCCCAF           Db         174         GGCTGGACCTGGCGCAAGGAAGCCAAAGACCTAGGCCTAGGCCAAGAGTTCCCAF	Qy         1272         GAGGGCGAGAAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAA           Db         114         GAGGGCGAGAAACAAGACAAGCTCCTCCCTCTGAGAATTCCCTGTGGATTTTTTAAA           Qy         1332         ATATTATTTATTATTGTGACAAAATGTTGATAAATGG         1373           Db         54         ATATTATTATTATTGTGACAAAATGTTGATAAATGG         1373           Db         54         ATATTATTTATTATTATTGTGACAAAATGTTGATAAATGG         13	RESULT 14 CB529199/C CB529199/C CB529199/C CB529199/C CB529199/C CB529199/C CB529199/C DEFINITION UI-H-FT2-bjf-k-03-0-UI.sl NCI CGAP_FT2 Homo sapiens CDNA C ACCESION CB529199/C ACCESION CB529199/C BS7. KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) AURHORS 1 to 569 AUTHORS AUTHORS AUTHORS AUTHORS TITLE NALICGAP http://www.ncbi.nlm.nih.gov/ncicgap. TITLE TI
CCGTCGGAACTGCACCAGACGAAGAAGCCAGGATCCTGCGCCTTTCCTGAA 71  CTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTTGCAAGAG 422	CACTITGATGAGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGTGGTG	CGCCTCTGCCAGGTGTTCGGGCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGGGT 782		15 474 bp mRNA linear EST 21-OCT-2002 15.X1 HR85 islet Homo sapiens cDNA clone IMAGE:6128001 3', 115.1 GI:24203667 125.1 GI:24203667	optures and the state of the st	ine Pancreas Consortium Divers); ine Pancreas Consortium ished (2000) it Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue it Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue ine Pancreas Consortium id University, Howard Hughes Medical Institute )f Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, 7 17-495-1812 il7-495-8557 dmelton@bioth.harvard.edu if was constructed by Dr. Hiroshi Inoue DNA sequencing by: igcon University Genome Sequencing Center For information on ing a clone please contact: Dr. Hiroshi Inoue ie@im.wwstl.edu) imer: -40UP from Gibco

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GGGCCCCAGCTCCGCCTCTGCCAGGTGTCTGGGCTGTTGGCCCTGCGGCCAGGGTCC
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99.8%; Pred. No. 3.2e-211;
tive 0; Mismatches 1;
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/clone="IMAGE:6278608"
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                               47 GACAAAATGTTGATAAATGG 28
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Homo sapiens
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/mol_type="mRNA"

/db_xref="taxxon:9606"

/clone="UT-H-FT2-bjf-k-03-0-UI"

/tissue_type="Aveolar Macrophage"

/dev stage="Adult"

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/lab_host="DH10B (Life Technologies)"

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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Book I; Site_2: Not I;

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Book I; Site_2: Not I;

/note="Organ in the different treatments. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of lowa.

TAG_IISUE-Human Lung Aveolar Macrophage

TAG_LIB=UT-H-FT2

TAG_SED_GGCCATGCCG"
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llowing repetitive elements were found in this cDNA is: 1-82, AT rich#Low_complexity (matched compliment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 569;
                                             : Robert Strausberg, Ph.D.
gapbs-r@mail.nih.gov
Procurement: Dr. Gary W. Hunninghake, U of I
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Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Matson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2466 row: n column: 17
High quality sequence start: 24
High quality sequence start: 24
High quality sequence stores
AGENCOURT 8353983 NIH MGC_113 Homo sapiens cDNA clone IMAGE BQ707185
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//clone lib="NIH WGC 113.
//clone lib="NIH WGC 113.
//note="Organ: spleen; Vector: pOTB7; Site_1: Xhol; ScoR1; cDNA made by oligo-dr priming. Directionall into BCORNIXhol sites using the following 5' adapt GGCACGAG(G). Library constructed by Ling Hong in laboratory of Gerald M. Rubin (University of Cali Berkeley) using ZAP-CDNA synthesis kit (Stratagene Superscript II RT (Life Technologies). Note: this NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleo
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 948)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (M
Unpublished (1999)
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QY         301 CAGGACCCGTCGGAACTGAATCCCCAGACAGAAGAAAGCCAGGATCCTGGGCCTTT           Db         1 CAGGACCCGTCGGAACTGAATCCCCAGAAGAAAAGCCAGGATCCTGGGCCTTT           QY         361 AACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCG           Db         61 AACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCG           QY         421 GCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGACGGAGGCCAGGCCAGGCCAGACGCAGCCCAGACTCACCAGCCTCACCAGCCCAGACCAGACCAGACCAGACCAGACCAGACCAGACGAGCCAGGCCAGACCAGACCAGACCAGACCAGACCAGACCCAGACCCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACCACAGACACAGACACAGACACAGACACAGACACAGACACAGACACAGACACAGACACAGACACAGACACAGACACACAGACACAGAC	QY         601 CAGGEGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGA           Db         301 CAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGAAGCTTGCTGGTGGA           QY         661 GTGCTGGCCTGCGCGTGGAAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGG           Db         361 GTGCTGGCCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGG           QY         721 CAGCTCCGCCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGG           QY         721 CAGCTCCGCCTCTGCC 736           Db         421 CAGCTCCGCCTCTGCC 436	RESULT 17 CF126932 CF126932 CF126932 CF126932 CF126932 CF126932 UI-HF-ETO-avx-k-19-0-UI.rl NIH_MGC_214 Homo sapiens CDNA C IMAGE: 30563490 5', mRNA sequence. ACCESSION CF126932.1 GI:33204664 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human)  NGMANISM Homo sapiens (human)  NGMANIA (hare)  CORDANOPAL  CONTACT: Lennon,G. and Soares,M.B.  AUTHORS  NGMANIN  GENOWAY  JOURNAL  GENOWAY  GONDAL LAPARED  CONTACT: Soares, MB  CONTACT: Soares, MB  CONTACT: Soares, MB  CONTACT: Soares (1966)  FAX: 319 335 9826  FAX: 310 335 9826  FAX: 310 7010 7010 7010 7010 7010 7010 7010	http://genome.uiowa.edu/distribution/humanfl.html The following repetitive elements were found in this cDNF sequence: 37-143, sGC_rich#Low_complexity Seq primer: pYx-5, Location/Qualifiers 1. 697 source /.organiam="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"
CCCAGCTCCGCCTCTGCCAGGTGTCTGGCCCTGCGGGCCAGGGTCCTCC 466   GGATCCGCACCTCCCTGGCCCATCTCAAGGCTGCCCCTTTCCTCACCTTCTC 834	URT 8682031 Lupski sciatic_nerve Homo sapiens CDNA clone 6197488 5', mRNA sequence.  31. GI:22276239  apiens (human) apiens (human) apiens caraitata; Vertebrata; Buteleostomi;	ses it to 940.  Chttp://mgc.nci.nih.gov/.  al Institutes of Health, Mammalian Gene Collection (MGC) ished (1999)  t: Robert Strausberg, Ph.D. cgapbs-remail.nih.gov Procurement: Dr. James R. Lupski library Preparation: Life Technologies, Inc. Library Preparation: Life Technologies, Inc. Library Preparation: Life Technologies, Inc. Library Arrayed by: The I.M.A.G.E. Consortium (LINL) equencing Dy: Agencourt Bioscience Corporation distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: Limanistor row: j column: 17 unality sequence stop: 453. Location/Qualifiers I. 940    organism="Homo sapiens"     organism="Homo sapiens"     db xref="taxon:9606"     corganism="MRAGE: 6197488"     db xref="taxon:9606"     clone="tMAGE: 6197488"     dev stage="adult, 70 yr"     tissue_type="sciatic nerve"     clone=lib="upung   cloned using the following adaptors:     clone=lib="vector: pCMV-SQRGGGCCCT(15)-3'. Size selected     clone=lib="adult   cloned using the following adaptors:     clone=lib="vector: pCMY-SQRGGCCCT(15)-3'. Size selected     clone=lib="adult   clone   clo	Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."  31.8%; Score 436; DB 13; Length 940; arity 100.0%; Pred. No. 1e-210; onservative 0; Mismatches 0; Indels 0; Gaps 0;

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/ Organism: Among Saptens / Organism: Among Saptens / Organism: Among Saptens / Organism: Among Saptens / Organism: S266217"

/ Lab host="Undlos"

/ Lab host="Undlos"

/ Lone_lib="NIH_MGC 122"

/ Inote="Crgan: pooled lung and spleen; Vector: pCM Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week fem spleen, and 20-22 week male spleens. Library is continued and directionally cloned (EcoRV site_is destupon cloning). Average insert size 1.4 kb, inser range_1-3 kb. Library is normalized and enriched if
cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    full-length clones and was constructed by C. Gruk (Invitrogen). Research Genetics tracking code 02
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                                                                                               found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov
Plate: LLAMISIST row: c column: 18
High quality sequence stop: 772.
Location/Qualifiers
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                  /tissue_rype="Chondrosarcoma Lung Metastasis cell lines"
/lab host="MulloB (T1 phage resistant)"
/lab host="MulloB (T2 phage resistant)"
/clone lib="NIH_MGC 12 phage resistant)"
/clone lib="NIH_MGC 12 phage resistant)"
/note="Organ: Lung; Vector: pXx-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a I* agarose
gel: First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pXx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATAAAGGCCA. Tissue was provided by Mary Hendrix."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 834 bp mRNA linear EST 25-SEP-2001
66F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5206217 5',
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l Institutes of Health, Mammalian Gene Collection (MGC)
shed (1999)
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Procurement: Life Technologies, Inc.
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4e-205;
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100.0%; Pred. No. 4c.
... 0; Mismatches
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  clone="IMAGE:30563490"
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University of Iowa
University of Iowa Med Labs, Iowa City, IA 52242, USP
2024 University of Iowa Med Labs, Iowa City, IA 52242, USP
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University
CDNA Library Arrayed by: Dr. M. Bento Soares, University
UNA Sequencing by: Dr. M. Bento Soares, University
Clone Distribution: Researchers may obtain clones from Re
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this CDN
sequence: 1-82, AMI_rich#Low_complexity (matched complimer
Seq primer: M13 FORWARD
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/mol_type="mtMA"
/db_xref="taxon:9606"
/clone="UI-CF-ECI-abl-p-06-0-UI"
/tissue_type="Lung"
/dev stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage rf /lab_host="DH10B (Life Technologies) (T1 phage rf /lab_host="DH10B (Life Technologies) (T1 phage rf /lab_host="DH10B (Life Technologies) (T1 phage rf /lab_host="DH10B (Life Technologies) (T1 phage rf /lab_host="DH10B (Life Technologies) (T1 phage rf /lab_host="DH10B (Life Technologies) (T1 phage rf /lab_host="DH10B (Life Technologies) (T1 phage rf /lab_host="Dh10B (Life Technologies) (T2 )lab_host="Dh20B (Life Technologies) (T2 )lab_host="Dh20B (Life Technologies) (T2 )lab_host="Dh20B (Life Technologies) (T3 )lab_host="Dh20B (Life Technologies) (T3 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="Dh20B (L1 )lab_host="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Eutele Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I. (bases 1 to 568)
Bonaldo, M.F., Lemnon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitat
                                                                                        1220 CTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGG
                                                                                                                                                                                     1280 AGAAACAAGACAAGCTCCTTCCCTTGAGAATTCCCTGTGGATTTTAAAAACAGATAT
                                                                                                                                                                                                                                                                                                                                             113 AGAAACAAGACAAGCTCCTTCACAAATTCCCTGTGGATTTTTAAAACAGATAT
233 TACTICTGTGGGCAAGGATGGGTCCAGAAGACCCCCACTTCAGGCACTAAGAGGGGCT
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Genome Res. 6 (9), 791-806 (1996)
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/lab nost="bulbe fulle leconologies" / clone libe "Note "Corgan: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Ec (Pharmacia) with a modified polylinker; Site_1: Ec Site_2: Not I; NoT CGAP FE1 is a normalized cDNA ] derived from a pool of mRNA obtained from 3 cell lrom grade II chondrosarcoma tissues. The library constructed according to Bonaldo, Lennon and Soare Genome Research, 6:791-806, 1996. First strand cDN synthesis was primed with an oligo-dr primer conte Not I site. Double stranded cDNA was ligated to adaptor, digested with Not I, and cloned direction into pT7T3-Pac vector. The oligonucleotide used to the synthesis of first-strand cDNA contains a libr sequence that is located between the Not I site ar (GT) R ail. The sequence that is located between the Not I site ar (GT) at all these were provided by Dr Jan Martin from the University of lowe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_TISSUB=Human grade 2 chondrosarcoma cell line
TAG_LIB=UI-H-FB1
TAG_SEQ=CGCTACGGAC"
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                                                                                                                     /clone="UI-H-FB1-bdu-c-24-0-UI"
/tissue type="Cell lines"
/dey stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                       /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGIGACAAAIGIIGAIAAAIGG 1373
                                                                                                xref="taxon:9606"
  Location/Qualifiers
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99.8%;
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Best Local Similarity
Matches 443; Conserva
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                                                                                                                                                                                                                                                                             Score 394; DB 12; Length 568; Pred. No. 2.5e-189;
                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                          100.0%; Pred. ...
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Procurement: James Martin
                                                                                                                                                                       TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"
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Length 569; 1; Indels

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отвитания linear EST 04-603038693F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:51799: mRNA sequence.

28

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Contact: Robert Strausberg, Ph.D.

Contact: Roadl.nih.gov

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hansson

CDNA Library Preparation: Michael J. Brownstein (NHGRI) w

and advice from Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information ca

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: Nnamgo.llnl.gov

Plate: Now: b column: 09

High quality sequence stop: 415.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 824)
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National Institutes of Health, Mammalian Gene Collection (
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/lab_host="DH10B_TonA"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30348032"
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1187 AGACCC 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_MGC_115".
/note="Organ: pooled brain, lung, testis; Vector: pcMv-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 18 kb, insert size range 1-3 kb. Library is normalized and erriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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Procurement: Life Technologies, Inc.
Library Preparation: Life Technologies, Inc.
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
equencing by: Incyte Genomics, Inc.
distribution: MGC clone distribution information can be
through the I.M.A.G.E. Consortium/LLNL at:
LLAM11447 row: j column: 23
uality sequence stop: 529.
Location/Qualifiers
                                                                                                                                                ota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
ia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Chttp://mgc.nci.nih.gov/.
al Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                               Robert Strausberg, Ph.D.
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/lab_host="DH108"
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/db_xref="taxon:9606"
   GI:15935993
                                                                          piens (human)
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GGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGCTGGTGGCA 309

**製造技術** 

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/note="Organ: Pancreas; Vector: psPoRT1; Site 1: Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation, average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
                                                                                                                                                                                                                                                                                                                                                                                                            9 440 bp mRNA linear EST 12-MAR-2002 .yl Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens one IMAGE.5675843 5' similar to TR:054907 054907 TNF-RELATED DUCER OF APOPTOSIS ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was constructed by Dr. Douglas Melton DNA sequencing by:
ton University Genome Sequencing Center For information on
ng a clone please contact: Juliana Brown
fas.harvard.edu) This sequence now available from the IMAGE
iuw, for clone orders contact: info@image.llnl.gov
ality sequence stop: 415.
Location/Qualifiers
                                                sgaccaegacccgrcggaacrgaarccccagacagaagaaagccaggarccrgcg 369
                                                                                                         IGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGG 411
                                                                                                                                                            cergaacegacragricggeeregaagaagrgecaeeraaaggeegegaaaacaegg 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University, Howard Hughes Medical Institute
Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
ta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., a.I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., A., Theising, B., Ritter, E., Ronko, I., Bennett, J., s, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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                                                                                                                                                                                                                   AAGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s, T., Jackson, Y. and Bowers, Y.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5675843"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dmelton@biohp.harvard.edu
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|lab_host="DH108"
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Bukaryota; Metazoa, Chordata, Craniata, Vertebrata; Butelec Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 951) MHF.MGC http://mgc.nci.nih.gov/.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LINLA at:
http://image.lnl.gov
Plate: LLCM2459 row: d column: 01
20. Single-stranded (unhybridized) plasmids were by hydroxyapatite chromatography and used to make library."
                                                                                                                                                                                                                                                                                   808 AAGGCTGCCCCCTTCCTCACCTTCGGACTCTTCCAGGTTCACTGAGGGGCCCTG
                                                                                                                                                                                                                                                                                                                                                    38 AAGGCTGCCCCTTCCTCACCTACTTCGGACTCTTCCAGGTTCACTGAGGGCCCTG
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/lab_host="DH10B (phage-resistant)"
                                                                                                                                                        Length 440;
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                                                                                                                                                           Score 352; DB 12;
Pred. No. 6.6e-168;
0; Mismatches 1;
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/db_xref="taxon:9606"
/clone="IMAGE:6275664"
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Tissue Procurement: ATCC
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                                                                                                                                                           Query Match 25.6%;
Best Local Similarity 99.8%;
Matches 402; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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488 GATGAGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGGC 300 CGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGC 428 CATTATGAAGTTCATCCACGACCTGGACAGGACGGAGGCGCAGGTGTGGACGG 120 GTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCG 548 GIGAGIGGCIGGGAGGAAGCCAGAAICAACAGCICCAGCCCICTGCGCIACAACCG 180 ATCGGGGGAGTTTATAGTCACCCGGGCTGGGCTCTACTACCTGTACTGTCAGGTGCA 608 Arcesesagirraragicaccesscresscrictacraccestreracterateras GATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGGC 668 9 CGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGC CATTATGAAGTTCATCCACGACCTGGACAGGACGCAGGCGCAGGCTGTGGACGG Gaps . 0 CGCTGCCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGGG 349 CGCTGCCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGGG 717 Length 951; 0; Indels 25.4%; Score 34%; b. ... 100.0%; Pred. No. 2.6e-166; rive 0; Mismatches 0; onservative

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EST 15-FEB-2002 5.yl Human insulinoma Homo sapiens cDNA 5', mRNA sequence. linear **MRNA** 377 bp 16.1 GI:18680159

ished (2000)
ESTS: ihl5b05.x1
it: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
id: Douglas Consortium
in Pancreae Consortium
id University, Howard Hughes Medical Institute
of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ia; Butheria; Primates; Catarrhini; Hominidae; Homo. .ses 1 to 377) (LD., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., ka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Er, L., Marra, M., Pape, D., Wylle, T., Marrin, J., Blistain, A., t, A., Theising, B. Ritter, E., Ronko, I., Bennett, J., ans, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., ms, T., Jackson, Y. and Bowers, Y. ine Pancreas Consortium apiens (human)

/tisue type="insulinoma"
/lab host="HH10B (phage-resistant)"
/lone\_lib="Human insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-;
Xho1; Site\_2: EcoRI; Constructed with lambda ZAPI
(Stratagene) by Dr. J. Ferrer, in vivo mass-excis pBluescript SK- by Dr. H. Inoue following the Walliniversity protocol (http://genome.wustl.edu/est/lambda\_protocol.shtm Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division Laboratory, Washington University School of Medi 127, 660 S Buclid Ave, St. Louis, MO 63110) NC is a Washington University Pancreas EST project l 1093 CCCTTTGAGGCCCCCCAGTGATCTCGACTCCCCCCTGGCCACAGACCCCCAGGGCAT CCCTTTGAGGCCCCCAGTGATCTCGACTCCCCCTGGCCACAGACCCCCAGGGCAT 128 TICACTGIACTCIGIGGGCAAGGAIGGGICCAGAAGACCCCACTTCAGGCACTAAC 188 geriggaceregegegagagecaaagagacriggeceraggecaaggrirecaaa 1273 AGGGGGAGAAACAAGACAAGCICCTCCCTTGAGAATTCCCTGTGGATTTTAAAA 248 AGGGGGGAGAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAA CTCTTATCTTACAACTCCCCCACGCCCACTCCCCACCTCACTAGCTCCCAATCC cretraretracaderececadedeceacierecacereaciadereceaare 1153 TTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCCACTTCAGGCACTAA GCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAA . 0 Length 377; Indels 1333 TATTATTTATTATTATTGTGACAAAATGTTGATAAATGC 1373 TATTATTTTTTATTATTATTGTGACAAAATGTTGATAAATGG 348 Score 341; DB 12; I Pred. No. 2.6e-162; .. 0 24.8%; Scor. 100.0%; Pred. No. 2... '... 0; Mismatches organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" Seg primer: -40RP from Gibco. location/Qualifiers 341; Conservative Similarity 1033 1213 œ 308 68 Query Match Best Local BE858778/c LOCUS Matches RESULT 27 FEATURES ORIGIN d à 셤 ò 셤 ò d ò d ð 8 d

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (Dases I to 710)
NCI/NINDS-CGAP, http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurolog Blorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998) BE858778 110 bp mRNA linear EST 2: 7f95b06.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:3: similar to contains element MER32 repetitive element; ml Email: cgapbs-r@mail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfe Contact: Robert Strausberg, Ph.D. BE858778.1 GI:10374165 Homo sapiens (human) sapiens sequence. BE858778 ORGANISM REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS JOURNAL COMMENT

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: dmelton@biohp.harvard.edu
:y was constructed by Dr. J. Ferrer In vivo mass-excised to
script SK- by Dr. H. Inoue DNA sequencing by: Washington
script Genome Sequencing Center For information on obtaining a
please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)

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/docume="Utn=-CQ1-acs-a-05-0-U1"
/tissue_type="optic nerve"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="bdult"
/dev_stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy
CDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowe
Clone Distribution: Researchers may obtain clones from Ref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics (www.resgen.com).

The following repetitive elements were found in this CDNA sequence: 1-94, AT_rich#Low_complexity (matched compliment Seq primer: M13 Forward
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Normalization and subtraction: two approaches to facilitate
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                                                                                                                                                                                                                                                                                                        University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 9565
Email: bento-soares@uiowa.edu
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100.0%; Pred. No. 1.1e-155;
ive 0; Mismatches 0;
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/organism="Homo sapiens"
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Genome Res. 6 (9), 791-806 (1996)
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                                                                                                               'Ph.D. ibrary Arrayed by: Greg Lennon, Ph.D. ibrary Arrayed by: Washington University Genome Sequencing Center distribution: NCI-CGAP clone distribution information can be hrough the I.M.A.G.E. Consortium/LLNL, send email to:
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                                                  lbrary Preparation: M. Bento Soares, Ph.D., M. Fatima
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Location/Qualifiers
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mer: -40UP from Gibco
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/clone=lib="NGI CGAP_Kid11"
/clone=lorgan: Kidney, Vector: pT7T3D-Pac (Pharmace a modified polylinker; Site 1: Not 1; Site 2: Ecc plasmid bnA from the normalized library NCT_CGAP prepared, and ss circles were made in vitro. Foll purification, this DNA was used as tracer in a st purification reaction. The driver was PCR-amplifican a pool of 5,000 clones made from the same 1: (cloneIDs 1322376-1323911, 1456007-1456775, and 150052-1502855). Subtraction by Bento Soares and Fatima Bonaldo.
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Seq primer: -40UP from Gibco
High quality sequence stop: 330.
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AMISG12.XI NCI_CGAP_Kidl1 Homo sapiens cDNA clone IMAGE:26
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NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (
                                        226 recechaggaregarecagaagaceceacricaggeacraagagggeregaeere
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Mic
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Library Arrayed by: Greg Lennon, Ph.D.
equencing by: Washington University Genome Sequencing Center
distribution: NCI-CGAP clone distribution information can be
through the I.M.A.G.E. Consortium/LLNE, send email to:
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Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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The sequence contained an oligo-dT track that was present contained that was used to prime the synthesis of fin strand cDNA and therefore this may represent a bonafide potail. cDNA Library Preparation: M.B. Soares Lab Clone distinct. CARP clone distribution information can be found throw. I.M.A.G.E. Consortium/LIML and strand contains and the following repetielements were found in this cDNA sequence: 49-81,
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23.7%; Score 326; DB 10; L 100.0%; Pred. No. 1.2e-154; iive 0; Mismatches 0;
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quencing Arrayed by: Greg Lennon, Ph.D.
quencing by: Washington University Genome Sequencing Center
distribution: NCT-CGAP clone distribution information can be
hrough the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 345 bp mRNA linear EST 29-NOV-2000 4.X1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:3406302 3' to contains element MSR1 repetitive element ;, mRNA
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    CTCGACTCCCCCCTGGCCACAGACCCCCAGGCATTGTGTTCACTGTACTCTGT 1167
                                                                                                                                                                                        SCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAA 1287
                                                                                                AGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGC 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgapbs-r@mail.nih.gov
Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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ta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
a; Butheria; Primates; Catarrhini; Hominidae; Homo.
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DS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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/lab_host="DH108"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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mer: -40UP from Gibco
ality sequence stop: 333.
Location/Qualifiers
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/Ida nost="Data Julia Fermiologies" / Jebn nost="Data Described for the polylinker; Site 1: Not 1; Site 2: Eco RI; The polylinker; Site 1: Not 1; Site 2: Eco RI; The NOT CGAP Sub4 library is a subtracted library derived from the NOT CGAP Sub1 library; which is subtracted derived from the NOT CGAP Sub1 library, which is subtracted of Idrary derived from Bi. Bi constitut mixture of 21 normalized or subtracted NOT CGAP CO10, NOT CGAP CO10, NOT CGAP CO10, NOT CGAP Kid3, NOT CGAP Kid1, NOT CGAP Libraries NOT CGAP End2, NOT CGAP End2, NOT CGAP Libraries were pooled armigned erranded DNA preparation of the resulting was used as a tracer in a subtractive hybridizat a driver whose composition is detailed below: NOT CGAP End2 Kid3 pool 1: LLAM 334-337, 3682-3683, 3798-3803 (IMAGE ClonelDe 1322376-1323911, 152091-1323911, 152091-1323911, 152091-1323911, 152091-1323911, 152091-1323911, 152091-1323911, 152091-1323911, 152091-1323911, 152091-1323911, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 152091-132391, 
                                                                                                                                                                Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
The sequence contained an oligo-dr track that was present oligonucleotide that was used to prime the synthesis of fistered one this may represent a bonafide potarial cDNA and therefore this may represent a bonafide potarial. CDNA Library Preparation: M.B. Soares Lab Clone distribution information can be found throut NCI-CGAP clone distribution information can be found throut www-bio.llnl.gov/bbrp/image/image.html The following repet elements were found in this cDNA sequence: 61-93,
         1 (bases 1 to 364)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (
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/lab_host="DH10B (Life Technologies)"
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TAG_SEQ=ATTC"
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/db_xref="taxon:9606"
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NCI CGAP Co4, NCI CGAP Fr22, NCI CGAP Pr28, NCI CGAP Co10, NCI CGAP Kid5.

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NCI CGAP Kid1.

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NCI CGAP Kid1.

NCI CGAP LA12,

NCI CGAP LA13,

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NCI CGAP LA14920-1417991,

14504-1470983,

147592-1476743);

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Discovery. Genome Research 6, 791-806.
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TAG_SEO=AAACc"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev stage="Adult"
/lab_host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS
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B19672694 Human Islet 4 N4-HIS 1 Homo sa cDNA clone IMAGE:5672623 5' similar to TR:043508 043508 TNF WEAK INDUCER OF APOPTOSIS ;, mRNA sequence.
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Unber_ESTS: ie72g04.x1
Conteat: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                               287 TGATCTCGACTCCCCCCTGGCCACAGACCCCCCAGGGCATTGTGTTTCACTGTACTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                    227 GCAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGG
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1050 CCCCACCGCCCACTCTCCACTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCC
                                               347 CCCCACCCACTCTCCACCTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCC
                                                                                                                                                               TGATCTCGACTCCCCCTGGCCACAGACCCCCAGGGCATTGTGTTCACTGTACTCT
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
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Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
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/db_xref="taxon:9606"
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Location/Qualifiers
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Homo sapiens
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/clone lib="NCI CGAP Kid11"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and se circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDS 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     orgaphs remainingly for the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the sta
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                                                                                                                                                                                                                                                                                                                                       SCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGGGAAAAAA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAACAGATATTATTTTTTATTAT 1347
        CTCGACTCCCCCTGGCCACAGACCCCCAGGGCATTGTGTTTCACTGTACTCTGT 1167
                                                                                                                                                                       NGGATGGGTCCAGAAGACCCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGC 1227
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a; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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P http://www.ncbi.nlm.nih.gov/ncicgap.
I Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                           GGATGGGTCCAGAAGACCCCACTTCAGGCACTAAAGAGGGGCTGGACCTGGCGGC
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                                                                                 cresacreseceresecacasasacececasesearrerererererererer
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'db_xref="taxon:9606"
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shed (1997)

별목본

nservative

GI:5633396 piens (human)

piens

quence.

Can

University of Washington

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Site 2: Sall; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA made by oligo-dT priming. Size-selected by column fractionation, average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
'note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
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           Length 456;
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23.6%; Score 324; DB 12; 99.7%; Pred. No. 1.3e-153; ive 0; Mismatches 1;
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., A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and GSS 27-AUG-1998 Al H03 MF CIT Approved Human Genomic Sperm Library D Homo genomic clone Plate=3054 Col=5 Row=O, genomic survey ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ia; Butheria; Primates; Catarrhini; Hominidae; Homo. 18es 1 to 367) :as,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., ice-tagged connectors: A sequence approach to mapping and Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) linear ot: Mahairas GG, Wallace JC, Hood L Chroughput Sequencing Center DNA 367 bp human genome 65.1 GI:3471394 apiens (human) ing the apiens , ē

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/db_xref="taxon:9606"
/db_xref="plate=3054 Col=5 Row=O"
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/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Libr
/note="Uorgan: sperm; Vector: pBeloBAC11; BAC Clon
B-Coli DH10B"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
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INH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 367;
401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3054 row: O column: 5
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                        23.4%; Score 321; DB 28; L ilarity 100.0%; Pred. No. 4.2e-152; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                  High quality sequence stop: 367.
Location/Qualifiers
1..367
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/note="Organ: pancreas; Vector: pBluescript SK-; & XhoI; Site 2: EcoRI; Constructed with lambda ZAPI] (Stratagenē) by Dr. J. Ferrer, in vivo mass-excist pBluescript SK- by Dr. H. Inoue following the Wat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University protocol

(http://genome.wusl.cdu/est/lambda_protocol.shtm.)

Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division Laboratory, Washington University School of Medical Colid Ave. St. Louis, MO 63110). Not is a Washington University Pancreas EST project 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI695776 329 bp mRNA linear BST 17
wb/7907.xl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:231
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                                 & Hiroshi Inoue
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                                                                  Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human_insulinoma"
                                    Contact: Douglas Melton, Klaus H. Kaestner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_114"
/clone_lib="NIH_MGC_114"
/incte="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male_brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (BcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Intl-tengen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
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ia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ses 1 to 374)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Ka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., E., Marria, M., Pape, D., Wylie, T., Marrin, T., Blistain, A., t., A., Theising, B., Ritter, E., Ronko, I., Bennett, J., as, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., ine Pancreas Consortium in Pancreas Consortium ished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCACTCTCCACCTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGA
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Pred. No. 5.9e-152;
0; Mismatches 0; Indels
       prough the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.4%; buc. 100.0%; pred. No. ...
                                                image.llnl.gov
LLAM12814 row: n column: 16
                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                  ality sequence start: 74 ality sequence stop: 420. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      clone="IMAGE:5763279"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATGTTGATAAATGG 1373
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//oco="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plannid DNA from the
normalized library NCI CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
this DNA was used as tracer in a subtractive hybridization
caction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                              cgapbs-r@mail.nih.gov
Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Puck, M.D., Ph.D.
Library Preparation: M. Bento Soares, Ph.D.
Library Preparation: M. Bento Soares, Ph.D.
Library Arrayed by: Greg Lennon, Ph.D.
Library Arrayed by: Greg Lennon, Ph.D.
Library Arrayed hy: Magentium/Library Arrayed Center
distribution: NCI-CGAP clone distribution information can be
through the I.M.A.G.B. Consortium/Library
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AP http://www.ncbi.nlm.nih.gov/nciogap.
al Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 340)

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurolog Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. bys Sequencing by: Washington University Genome Sequencin Clone distribution: NCI-CGAP clone distribution informatifound through the I.M.A.G.E. Consortium/LLNL, send email tinfo@image.llnl.gov.
7H17g12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:35
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                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fati
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                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-667239,
726408-728711, and 729096-31339. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCTGGCCACAGACCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGAT 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGAAGACCCCACTICAGGCACIAAGAGGGCTGGACCTGGCGGCAGGAAGCCAA 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTEGECCTAGECCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAAGACAAGCTCC 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITGAGAATICCCIGIGGAITITIAAAACAGAIAIIAITITITATIAITATIGIGACA 1357
                                                                                                        407 bp mRNA linear EST 30-NOV-1998
.X1 Soares NFL T GBC S1 Homo sapiens cDNA clone
842906 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGAGAATTCCCTGTGGATTTTTAAAACAGATATTATTTTTTATTATTATTGTGACA 36
                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                               http://www.ncbi.nlm.nih.gov/ncicgap.
Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                actegecctageccageagtrcccaaatereagegegegagaaaacaagacaad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robert Strausberg, Ph.D. cgapbs-r@mail.nih.gov cgapbs-r@mail.nih.gov one is available royalty-free through LLNL; contact the onsortium (inf@image.llnl.gov) for further information. Length: 610 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ceceresecacaesececassesarrererrererererererersessesassar
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a, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'clone="IMAGE:1842906"
'lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ality sequence stop: 401.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mol_type="mRNA"
'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 610 Std Erro
mer: -40UP from Gibco
                                                                                                                                                                                                                                      5.1 GI:3804188
          IGTTGATAAATGG
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Umpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Mich
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Clone distribution: NCI-CGAP clone distribution informatic
found through the I.M.A.G.E. Consortium/LLNL at:
qm86c02.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:18956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 rccaccrcacracrcccaarccraaccrrraaggcccccagrarcrcaacr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 CCTGGCCACAGACCCCCCAGGGCATTGTGTTTCACTGTACTCTGTGGGCAAGGATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1185 GAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 GAAGACCCCACTTCAGGCACTAAGAGGGGCTCGACCTGGCGGCGCAGGAAGCAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1245 GGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAAGACAAGCTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 GGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAAGACAAGCAACCCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1065 TCCACCTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGATCTCGACT
                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 416;
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100.0%; Pred. No. 5.7e-146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www-bio.llnl.gov/bbrp/image/image.html
lnsert Length: 649 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 411.
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1895618"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .416
                                                                                                                   AI291866.1 GI:3934640
                                                                                                                                                                Homo sapiens (human)
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                                            DEFINITION
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Enkarycia; Metazoa; Chordata; Craniata; Vertebrata; Eutele Enkarycia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 317)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute / National Institute of Neurolog Disorders and Stroke, Brain Tumor Genome Anatomy Project Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencir
Clone distribution: WCI-CGAP Clone distribution informati
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbprp/image/image.html
Insert Length: 1005 Std Brror: 0.00
Seq primer: -40UP from Gibco
Bigh quality sequence stop: 308.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131; double-stranded cDNA was ligated to Ecoladaptors (Pharmacia), digested with Not I and Co. RI sites of the modified pTTT. Library is normalized, and was constructed by Be Soares and M. Patima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                        AI202121 317 bp mRNA linear EST 02
qi52c03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      867 CICCCCACAGICGICCCAGGCIGCCGGCICCCCICGACAGCICTCIGGGCACCCGG
                       240 CTCCCCACAGTCGTCCCAGGCTGCCGGCTCCCCTCGACACTCTCTGGGCACCCGG
                                                                                                                                                                                                                 360 GGGCTGTTCACGTTTTCCATCCCACATAAATACAGTATTCCCACTCTTATCTT
                                                                                    300 crcrecceaccreacecererrrecrecacacececerecece
                                                                                                                                                                           987 GGGCCTGTTCGATGTTTTCCATCCCACATAAATACAGTATTCCCACTTTATCTT
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100.0%; Pred. No. 6.3e-143;
iive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:1860100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI202121.1 GI:3754727
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Homo sapiens
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                                                                                                                                                                                                                                                                         1047 CTCCCCA 1054
                                                                                                                                                                                                                                                                                                                 420 CTCCCCA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                           63 910 bp mRNA linear EST 30-JAN-2001
667Fl NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4367225 5',
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                            TTCCCTGTGGATTTTTAAAACAGATATTATTTTTTATTATTGTGACAAAATGTT 1364
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ia; Butheria; Primates; Catarrhini; Hominidae; Homo.
ses 1 to 910)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:4367225"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC 86"
/note="Organ: bone; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dr primed.
Average insert size 1:533 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                   TCAGCCACTGCGGCCAGTTCCCTCGGGCCCCCAGCTCCGCCTCTGCCAGGTGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36CTGCCCCTTCCTCACCTACTTCGGACTCTTCCAGGTTCACTGAGGGCCCTGGT
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al Institutes of Health, Mammalian Gene Collection (MGC)
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Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ished (1999)
t: Robert Strausberg, Ph.D.
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Location/Qualifiers
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                       63.1 GI:12603569
                                                                                                                                                                                                                                                                                                                                                                                                                 apiens (human)
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/dev stage="adult"
/lab_host="DH10B (Life Technologies) (Tl phage resistant)"
/clone lib="UI-B-CL1"
/clone lib="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1; UI-B-CL1 is a normalized DNA library containing the
                                                                                                                                                                                                                                    1250
                                                                                                                                                                                                                                                                                                                                                       1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGGATTTTTAAAACAGATATTTTTTTTTTTTTTTTGTGACAAATGTTGATAAA 1370
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                                                                                                                  ACCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGAC 1190
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1130
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ia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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),M.F., Lennon,G. and Soares,M.B.
ization and subtraction: two approaches to facilitate gene
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AGCTCCCCAATCCCTGACCCTTTGAGGCCCCCAGTGATCTCGACTCCCCCCTGGC
                                                                                                                                                          TTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCT
                                                                                                                                                                                                                                                                                AGGAGTTCCCAAATGTGAGGGGGGGAAAAAAAAGAGAAAGCTCCTCCCTTGAGAATT
                                                       Agenceceaanecengaceenringaggeeeceegaganeregacreeceergge
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.1-afe-m-20-0-UI.rl UI-E-CL1 Homo sapiens CDNA clone
.1-afe-m-20-0-UI 5', mRNA Bequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wcon Road , 4156 MEBRF, Iowa City, IA 52242, USA 19 335 8250
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/mol_type="mRNA"
/db_xref="taxon:9606"
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following tissue(s): retina. The library was const according to Bonaldo, Lennon and Soares, Genome RK 6:791-806, 1996. First strand CDNA synthesia was I with an oliqo-dr primer containing a Not I site. I stranded cDNA was ligated to an ECOR I adaptor, d: with Not I, and cloned directionally into prime the vector. The oligonucleotide used to prime the synt first-strand cDNA contains a library tag sequence located between the Not I site and the (d7)18 tail sequence tag for this library is CCGCG. This libric created for the program, Gene Discovery in the Vii System, supported by National Eye Institute (NEI)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa
Tays Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8265
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9665
Fax: 319 336 966
Fax: 319 336 966
Fax: 319 318 966
Fax: 319 318 966
Cibrary Preparation: Dr. M. Bento Soares, University DNA Library Arrayed by: Dr. M. Bento Soares, University DNA Sequencing by: Dr. M. Bento Soares, University of Iow Clone Distribution: Researchers may obtain clones from Re
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UI-E-CL1-afe-m-20-0-UI.sl UI-E-CL1 Homo sapiens CDNA clone
UI-E-CL1-afe-m-20-0-UI 3', mRNA sequence.
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The following repetitive elements were found in this CDNA sequence: 60-92, AT_rich#Low_complexity (matched complime
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100.0%; Pred. No. 2.3e-140;
tive 0; Mismatches 0;
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Homo sapiens
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TITLE
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University of Iowa
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761: 319 335 9565
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Email: bento-scaresceniowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy
DNA Sequencing by: Dr. M. Bento Soares, Univeristy
DNA Sequencing by: Dr. M. Bento Soares, Univeristy
Clone Distribution: Researchers may obtain clones from Re
Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Jab nose="Onto (Little fermiologies") (II progets (Clone libe-UT-E-CQ1" (note="Organ: eye; Vector: pry73-pes (Pharmacia) modified polylinker; Site_1: BCOR I; Site_2: Not UT-E-CQ1 is a normalized cDNA library containing tollowing tissue(8): optic nerve. The library was constructed according to Bonaldo, Lennon and Soar Genome Research, 6:791-806, 1996. First strand Genome Research, 6:791-806, 1996. First strand Conton I site. Double stranded cDNA was ligated to adaptor, digested with Not I, and cloned directic into pry73-Pac vector. The oligonucleotide used the synthesis of first-strand cDNA contains a libracy expense that is located between the Not I site a (d7)18 tail. The sequence tag for this library is CATTAAGTC. This library was created for the prog Discovery in the Visual System, supported by Natil Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ul-E-CQ1-acs-a-05-0-UI"
/cissue_type="optic nerve"
/dev_stage="adult"
/lab_host="DH10B (life Technologies) (T1 phage re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   582 GCTCTACTACTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTG1
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21.1%; Score 290; DB 12; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.7e-136;
Matches 290; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        702 GGCCAGTTCCCTCGGGCCCCCAGCTCCGCCTCTGCCAGGTGTCTGGGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .298
/organism="Homo sapiens"
   Genome Res. 6 (9), 791-806 (1996)
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                                                                                       Contact: Soares, MB
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                                                                                                                                                                                                                                                                                                                                  /clone llb="Ul-E-Clu!"
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR 1; Site_2: Not 1; modified polylinker; Site_1: EcoR 1; Site_2: Not 1; Ul-E-Cll is a normalized cDNA library containing the Ul-E-Cll is a normalized cDNA library containing the following tissue(8): retina. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, ei.79-806. 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGGC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_INB=UL-E-CLI
TAG_ESEQ=CCGCG"
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                                                                                                                                                                                                                                                /dev_stage="adult"
/lab_host="DHLOB"
/lab_host="DHLOB"
/clone_lib="UI-E-CL1"
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lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ases 1 to 298)
Ao, M.F., Lennon, G. and Soares, M.B.
lization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITAAAACAGAIAITAITITITAITAITAITGIGACAAAAIGIIGAIAAAIGG 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 201-acs-a-05-0-UI.rl UI-E-CQ1 Homo sapiens cDNA clone cQ1-acs-a-05-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.6%; Score 296; DB 13; I
100.0%; Pred. No. 2.4e-139;
iive 0; Mismatches 0;
                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-CL1-afe-m-20-0-UI"
                                                                                                                                                                                                                                          tissue_type="human retina"
                                                                                                                              organism="Homo sapiens"
                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346.1 GI:19002204
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 1027)
Chases 1 to 1027)
Chasin, P., Billotte, J., Chaubert, P. and Shaw, P. H.
Physical map of 17p13 and the genes adjacent to p53
Genomics 63 (1), 60-68 (2000)
                                                                                                                                                                                                                                    AF163779 Innear GSS 29-AF163779 Human Homo sapiens genomic clone BAC750E14, genomi
1052 CCACCGCCCACTCTCCACCTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 CCACCCCACTCTCCACCTCACCTCACTCCCCAATCCCTGACCCTTTGAGGSCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1232 AGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448 AGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1292 AGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAACAGATATTATTATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  508 AGCICCTCCTTGAGAATTCCCTGTGGATTTTTAAAACAGATATTTTTATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 Arcresacrececeresecacadaececeasesearrererererererer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1172 AAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 AAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1112 ATCTCGACTCCCCCCTGGCCACAGACCCCCAGGGCATTGTGTTCACTGTACTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.7%; Score 271; DB 28; Length 1027; 99.7%; Pred. No. 1.7e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rue du Bugnon 25, Lausanne, VD 1011, Switzerland
sub_clone=AB2R Asc-BamHI PSL1180
                                                                                                       437 TCATCCACGACCTGGACAGGACGCAGGCAG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1352 GTGACAAATGTTGATAAATGG 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               568 GTGACAAATGTTGATAAATGG 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="17p"
/clone="BAC750E14"
/clone lib="Human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaw PH
Experimental Oncology
Institute of Pathology
                                                                                                                                                                                                                                                                                                            AF163779
AF163779.1 GI:5726439
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: BAC subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 321; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Best Local Similarity
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AI760777/c
                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
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PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                        AF163779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
              32F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766071 5'
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46 CAAAATGTTGATAAATGG 29

77 346 bp mRNA linear EST 24-JUN-1999 5.X1 NCI\_CGAP\_Kid12 Homo sapiens cDNA clone IMAGE:2398377 3',

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LOCUS ORGANISM BF940141/c REFERENCE AUTHORS TITLE ACCESSION JOURNAL VERSION KEYWORDS RESULT 51 FEATURES ORIGIN g à à g à ò 셤 /clone lib="NCI CGAP Kid12"
//clone lib="NCI CGAP Kid12"
//oloe="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polyliher; Site1: Not 1; Site 2: Eco R1; Plasmid DNA from the normalized library NCT CGAP Kid5 was prepared, and sg circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and HAP2104-1493255). Subtraction by Bento Soares and M. Patima Bonaldo. " Cgapbs.remail.nih.gov
Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.,
Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.,
Library Preparation: M. Bento Soares, Ph.D.
Library Arrayed by: Greg Lennon, Ph.D.
Library Arrayed by: Washington University Genome Sequencing Center
equencing by: Washington University Genome Sequencing Center
distribution: MCI-CGAP Clone distribution information can be
through the I.M.A.G.B. Consortium/LLNL at:
0.1Nhl.gov/Pbrp/fmage/image.html
Location/Qualifiers CICCCCCCTGGCCACAGACCCCCAGGCCATTGTGTTCACTGTACTCTGTGGGCAAGG 1175 BETCCAGAAGACCCCACTTCAGGCACTAAGAGGGCTGGACCTGGCGGCAGGAAGCC 1235 SAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAAGACAAGCT 1295 ö 287 CICCCCCTGGCCACAGACCCNCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGG 227 gerecagaagaceeeaerreaggeaeraagaggeriggaeergeeggeaaggee 167 ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ia; Eutheria; Primates; Catarrhini; Hominidae; Homo. ses 1 to 346) AP http://www.ncbi.nlm.nih.gov/ncicgap. al Cancer Institute, Cancer Genome Anatomy Project (CGAP), CCACTCCCACCTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCAGTGATCT SCACTCTCCACCTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGATCT 0; Gaps /clone="IMAGE:2398377" /tissue\_type="2 pooled tumors (clear cell type)" /lab\_host="DH10B" Length 346; 1; Indels 19.4%; Score 267; DB 9; L 99.7%; Pred. No. 1.5e-124; 0; Mismatches /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" t: Robert Strausberg, Ph.D. Fatima Bonaldo. 77.1 GI:5176444 apiens (human) Conservative ished (1997) Gene Index equence. apiens arity

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Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Bukaryota, Metazoa, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 346)

NOT/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurolog
Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAR), Tumor Gene Index

Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Core distribution information through the I. W.A.G.E. Consortium/Libri, send email info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 321.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfe
BF940141 1inear EST 22 nac68906.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:3 similar to contains element MSR1 repetitive element ;, mRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fati
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 3']; double-stranded cDNA was ligated to Eco adaptors (Pharmacia), digested with Not I and c the Not I and Eco RI sites of the modified pT/TI Library is normalized, and was constructed by B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1168 GGGCAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 receedadeecearrereactreactractacearecearecerates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 Adreanciceacrececeredecacadadececadadecaridioricacidade
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.1%; Score 262; DB 10; Length 34
100.0%; Pred. No. 5.4e-122;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="glioblastoma (pooled)"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soares and M.Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1MAGE:3439667"
                                                                                                                                                   BF940141.1 GI:12357461
                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 262; Conservative
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/ Mol type="RANA"

// Mol type="RANA"

/ Mol type="RANA"

/ Mol type="RANA"

/ Lab host="NANGE:258160"

/ Lone="IMAGE:258160"

/ Lone="Corpan: pooled." Vector: pr7:3D-Pac (Pharmac nodified polylinker; Site 1: Not 1; Site 2: Eco Equal amounts of plasmid DMA from three normalize libraries (fetal lung NbHL19W, testis NHT, and B-Ibraries (fetal lung NbHL19W, testis NHT, and B-NCI CGAP GCBH) were mixed, and ss circles were may viro. Following HAP purification, this DNA was utracer in a subtractive hybridization reaction. Twas PCR-amplified cDNAs from pools of 5,000 clone from the same 3 libraries. The pools consisted of I.MA.G.E. clones 297480-302087, 682632-687239, 726408-728111, and 729086-731399. Subtraction by Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                   xb70a02.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2581610 3' Similar to contains element MSR1 repetitiv AW081731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelec
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 318)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact
This clone is available royalty-free through LLNL; contact
This clone is available royalty-free through LLNL; contact
Seq primer: -400P from Gibco
High quality sequence stop: 314.
Location/Qualifiers
1. .318
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1318 GATTITTAAAACAGATATTATTTTATTATTATTGTGACAAAATGTTGATAAATGG
                 AATTCCCTGTGGATTTTTAAAACAGATATTATTTTTTTATTATTGTGACAAAATGT
                                                               1138 CCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 ccccadadecarrererreracreracrerereresecaagaaraderecagaagaeeee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1198 CAGGCACTAAGAGGGGTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 GAGTICCCAAATGIGAGGGGGGAGAACAAGACAAGCTAGCTCCTCCCTTGAGAATTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.2%; Score 236; DB 9; Le
100.0%; Pred. No. 9.9e-109;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW081731.1 GI:6036883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                  TAAATGG 1373
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                                                                                                                                                                                         31 TAAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                       1307
                                                                                                                                     1367
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Matches
                                                                                                                                                                                                                                                                          RESULT 53
AW081731/c
                                                                                                                                                                                                                                                                                                                                                            DEFINITION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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/lab_host="nDH10B"
/lab_host="nDH10B"
/lab_host="nDH10B"
/cloon=lib="MCI CGAP Brn23"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a nodified polylinker; Site=1: Not I; Site 2: Eco RI; Ist strand cDNA was primed with a Not I - oligo(AT) primer [5' strand cDNA was primed with a Not I - oligo(AT) primer [5' strand cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ibrary Arrayed by: Greg Lennon, Ph.D.

quencing by: Washington University Genome Sequencing Center
distribution: NCI-CGAP clone distribution information can be
ihrough the I.M.A.G.E. Consortium/LINL, send email to:
mage.llnl.gov
.mer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCACTTCAGGCACTAAGAGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGG 1246
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                                                                                                                                                                                                                                             561 bp mRNA linear EST 25-JAN-2001 .xl NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3441742 3'to TR:Q9UK76 Q9UK76 HN1 PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cacagacccccagggcarrererrereracrererrergggcaaggarggerccaga 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aggecaggagireceaaargreagggggggggagaaagaagagaggreereerigag 92
SCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGGGGAGAAAAA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ia, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
a, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACAGACCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
1 Cancer Institute / National Institute of Neurological
rs and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ibrary Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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100.0%; Pred. No. 2.7e-114;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nality sequence stop: 260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'clone="IMAGE:3441742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                            SCICCICCTIGAGAAT 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                    SCICCICCCTIGAGAAT
                                                                                                                                                                                                                                                                                                                                                                    8.1 GI:12512043
                                                                                                                                                                                                                                                                                                                                                                                                                        piens (human)
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41.1 GI:7454367 apiens (human)

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uses 1 to 264)

apiens

.ished (1997) Gene Index

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Email: cgapber@mail.nih.gov
Tissue Prourement: Christopher Moskaluk, M.D., Ph.D., Mic
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencir
Clone distribution: NCI-CGAP clone distribution informati
found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 669 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone libe "NOI CGAP Kidl2"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharma note="Organ: Kidney; Vector: pT7T3D-Pac (Pharma modified DNA from the normalized library NOI CGAP prepared, and ss circles were made in vitro. Follourification, this DNA was used as tracer in a simply hypridization reaction. The driver was PCR-amplificm a pool of 5,000 clones made from the same 1 (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares an Fatima Bonaldo. "
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 253)
wjl7g05.xl NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:24 similar to contains element PTRS repetitive element ;, mRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1145 GCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCCACTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 TAAGAGGGCTGGACCTGGCGGCAGGAAGCCAAAGAACTGGGCCTAGGCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1265 CAAATGTGAGGGGGGAGAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l. .253
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2403128"
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                                                                                                           AI863563.1 GI:5527670
                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                Homo sapiens
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                                                              sequence.
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                                                                                     AI863563
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AI682487/c
LOCUS
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        DEFINITION
                                                                                                                                                                                                ORGANISM
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TITLE
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KEYWORDS
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/clone libe_Soares NPL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-667239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                         ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
.ia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              it: Robert Strausberg, Ph.D.
cgapbs-r@mail.nih.gov
lone is available royalty-free through LLNL; contact the
consortium (info@image.llnl.gov) for further information.
climer: -dom Gibco.
uality sequence stop: 263.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'AP http://www.ncbi.nlm.nih.gov/ncicgap.
nal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                            EST
                                                                                                                                                              41 264 bp mRNA linear ES' 0.x1 Soares NFL T GBC_S1 Homo sapiens CDNA clone 2978587 3', mRNA sequence.
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'organism="Homo sapiens" /mol\_type="mRNA" /db\_xxef="taxon:9606" /clone="IMAGE:2978587" /lab\_host="DH10B"

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1 (bases 1 to 698)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (M
                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information car found through the I.M.A.G.E. Consortium/LLNL at: http://inage.llnl.gov
                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelec
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 CAGGAGCCTGCCCAGGAGGAGCTGGTGGCAGAGGAGGACCAGGACCGTCGGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 CAGGAGCCTGCCCAGGAGGAGCTGGTGGCAGGAGGAGGACCAGGACCCGTCGGAACT
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                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%; Score 217; DB 12;
100.0%; Pred. No. 5.8e-99;
tive 0; Mismatches 0;
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 613.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5213480"
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                      BI906850.1 GI:16169619
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                                                                    Homo sapiens (human)
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  ACCESSION
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/lab_host="adult"
/lab_host="blt08"
/clone_lib="NCI_CGAP_Pr28"
/clone_lib="NCI_CGAP_Pr28"
/note="Organ: prostate; Vector: pl773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NIT_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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ibrary Arrayed by: Greg Lennon, Ph.D.
durary Arrayed by: Greg Lennon, Ph.D.
quencing by: Washington University Genome Sequencing Center
distribution: NCI-CGAP clone distribution information can be
hrough the I.M.A.G.B. Consortium/Link at:
Length: 223 Std Error: 0.00
Length: 240P from Gibco.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                   : Robert Strausberg, Ph.D. cgapbs-r@mail.nih.gov Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Buck, M.D., Ph.D.
.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2322405 3',
                                                                                                                                                                         ta, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
a, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                       Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Pred. No. 3.6e-104;
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100.0%; Pred. No. --
0; Mismatches
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2322405"
                                                                                7.1 GI:4892669
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Mi
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Clone distribution informatifound through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Lenght 438 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
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/lab_host="nH10B"
/lab_host="nH10B"
/lone_lib="NCI_CGAP_Pr28"
/note="forgan: prostate; Vector: pT7T3D-Pac (Pharn with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, at circles were made in vitro. Following HAP purific this DNA was used as tracer in a subtractive hybireaction. The driver was PCR-amplified cDNAs from of 5,000 clones made from the same library (clone of 5,000 clones made from the same library (clone Stage Sept59, 1101192-1101959, and 1217928-12206 Subtraction by Bento Soares and M. Fatima Bonalde
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                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Chases I to 391.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo mapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2315088"
AI669243.1 GI:4834017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="male"
                                              Homo sapiens (human)
Homo sapiens
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Unpublished (1997)
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                                                                                                                                                                                                                                                          cgapbs-r@mail.nih.gov
Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                       ora; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
ia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                   ses 1 to 351)
NDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
al Cancer Institute / National Institute of Neurological
ers and Stroke, Brain Tumor Genome Anatomy Project
shed (1998)
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o, Ph.D.
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imer: -40UP from Gibco·
uality sequence stop: 339.
Location/Qualifiers
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IMAGE:1651448 3' similar to contains MSRI.t3 MSR1 repetitivelement;, mRNA sequence. AI091441

AI091441.1 GI:3430500

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EST 16-OCT-2001

4 1.00T-200 B94 bp mRNA linear EST 16-OCT-200 26F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5217367 5',

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ta; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
a, Butheria, Primates, Catarrhini, Hominidae, Homo.
4.1 GI:16171193
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/uctone_line_nai_wor_line
/note="rube" nai_wor_spore; site 1: Not1; Site_2: EccRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dr primed
and directionally cloned (EccRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
lu_2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
                                                                                                                                   cgapbs-r@mail.nih.gov
procurement: Life Technologies, Inc.
ibrary Preparation: Life Technologies, Inc.
ibrary Arrayad by: The I.M.A.G.E. Consortium (LLNL)
quencing by: Incyte Genomics, Inc.
distribution: MGC clone distribution information can be
hrough the I.M.A.G.E. Consortium/LINL at:
http://mgc.nci.nih.gov/.
Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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/clone="IMAGE:5217367"
/tissue_type="leukocyte"
/lab_host="mH108"
/clone_lib="NIH_MGC_118"
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/organism="Homo sapiens"
                                                                                                       : Robert Strausberg, Ph.D.
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                                                    Gaps
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  Length 894;
                                                    Indels
15.0%; Score 206; DB 12;
100.0%; Pred. No. 2.5e-93;
iive 0; Mismatches 0;
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National Cancer Institute, Cancer Genome Anatomy Project (Content of the content of the con
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BF222608
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This clone is available royalty-free through LLNL; contact
TMAGE Consortium (info@image.llnl.gov) for further informat
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 465.
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/clone="IMAGE:1651448"
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ses 1 to 224)

ished (1997)

Gene Index

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1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-511. (ex.315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly t
Re are not submitting the same ciformation of clones with t
sequence in this library and as well as in other 3'-direct
libraries, see 'http://www.imcb.osaka- u.ac.jp/bodymap'.
sequences of the clones represented by this GS sequences:
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 282)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 ACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0407 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI)
and advice from Piero Carninci (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 1064)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF994566
AGENCOURT 15621154 NIH MGC_147 Homo sapiens CDNA clone IMAGE:30520331 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.3%; Score 182; DB 13; Length 282; 100.0%; Pred. No. 3.5e-81; ative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="texon:9606"
/db_xref="adult"
/clone lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"
                                                                                                                                                                                Institute for Molecular and Cellular Biol
                                                                                                   BodyMap; human gene expression database Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                              Contact: Okubo, K.
                                                                                                                                                                                                                   Osaka University
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                                                                                     Okubo, K.
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CF994566
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/lab_host="DH10B"
/lab_host="DH10B"
/clone lib="MCI CGAP_Pr28"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NOT CGAP Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDS
985608-986759; Il01192-1101959; and 1217928-1220615)
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 282 bp mRNA linear EST 31-DEC-2002
30003761 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
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Library Arrayed by: Greg Lennon, Ph.D.
Library Arrayed by: Washington University Genome Sequencing Center
Lequencing by: Washington University Genome Sequencing Center
cincernibution: NCI-CGAP clone distribution information can be
through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgapbs-r@mail.nih.gov
Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.-
Buck, M.D., Ph.D.
                                                                                                             ota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; ia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                              AP http://www.ncbi.nlm.nih.gov/ncicgap.
al Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Conservative 0; Mismatches
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'mol_type="mRNA"
'db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                 t: Robert Strausberg, Ph.D.
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                  08.1 GI:11129886
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sapiens

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column: 14

Plate: NDAM612 row: o

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/tissue_type="Human Placenta"
/lab host="DH10B TonA"
/lab host="DH10B TonA"
/clone_lib="NIH MGC 12"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
alr_xhol; Site_2: BamH; Oligo-dT primed using primer
alr_xhol; Site_2: BamH; Oligo-dT primed using primer
insert size 2: 3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This is
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Library Preparation: Michael J. Brownstein (NHGRI) with help
vice from Floro Carninci (RIKEN)
Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
equencing by: Agencourt Bioscience Corporation
distribution: MGC clone distribution information can be
through the I.M.A.G.E. Consortium/LLNL at:
//mage.llnl.gov
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    http://mgc.nci.nih.gov/.
1 Institutes of Health, Mammalian Gene Collection (MGC)
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31 Rm10A07 Bethesda, MD 20892
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:: Daniela S. Gerhard, Ph.D.
                                                                                                                                      NDAM593 row: e column: 12
                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                   clone="IMAGE:30520331"
                                                                                                                                                                 ality sequence stop: 249.
                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                       Location/Qualifiers
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Journal Jacobies, Vector: pBluescriptR; Site all Aboles. Site 2: Band; Oligo-dT primed using print all Abol; Site 2: Band; Oligo-dT primed using print of TTTTTTTTTTTTVN-3', size-selected for avera insert size 2.3 kb and normalized to ROT 5. This primary library enriched for full-length clones are constructed using the Cap-trapper method (Carning preparation). Library constructed by M. Brownstein NIMM/NHGRI, National Institutes of Health). Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:8606"
/clone="IMAGE:1525511"
/lab_host="DH10B"
/clone lib="Soares NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmac a modified polylinker; Site_1: Not I; Site_2: Eco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Chases I to 338 I to 338 I to 338 I to 338 I to 34 Maw.ncbi.nlm.nih.gov/nciogap.
Not.CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contac
This clone is available royalty-free through LLNL; contac
InAGE Consortium (info@image.llnl.gov) for further informa
Insert Length: 330 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 332.
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IMAGE:1525511 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                     /tissue type="Human Placenta"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_147"
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                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                    /clone="IMAGE:30527869"
High quality sequence stop: 287.
Location/Qualifiers
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Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was were as tracer in a subcractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made Iron the same 3 libraries. The pools consisted of Iron the same 3 libraries. The pools consisted of Iron the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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99.7%;
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EST 04-AUG-2000 .97 104-AUG-200 UP DP NRNA linear EST 04-AUG-200 S.x1 NCI\_CGAP\_GC6 Homo sapiens cDNA clone IMAGE:3221115 3', sequence.

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.97.1 GI:9703605

sapiens (human)

apiens

ota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; lia; Butheria; Primates; Catarrhini; Hominidae; Homo.

nal Cancer Institute, Cancer Genome Anatomy Project (CGAP), ases 1 to 196) 3AP http://www.ncbi.nlm.nih.gov/ncicgap.

lished (1997)

ct: Robert Strausberg, Ph.D.

do, Ph.D.
Library Arrayed by: Greg Lennon, Ph.D.
Sequencing by: Washington University Genome Sequencing Center
Sequencing by: Washington University Genome Sequencing Center
e distribution: NT-CGAP clone distribution information can be
through the I.M.A.G.E. Consortium/LINL, send email to: : cgapbs r@mail.nih.gov B Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael nert-Buck, M.D., Ph.D. Library Preparation: M. Bento Soares, Ph.D., M. Fatima

quality sequence stop: 175. Location/Qualifiers image.llnl.gov rimer: -40UP from Gibco

/organism="Homo sapiens" /clone="IMAGE:3221115" /mol\_type="mRNA" /db\_xref="taxon:9606"

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/tissue type="pooled germ cell tumors"
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/lab_host="DH10B"
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/note="Vector: pT73D-Pac (Pharmacia) with a modi
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmi
from the normalized library NCI CGAP GC4 was preg
ss circles were made in vitro. Following HAP puri
this DNA was used as tracer in a subtractive hybr
reaction. The driver was PCR samplified CDNAS from
of $5,000 clones made from the same library (clone
of $5,000 clones made from the same library (clone
1257096-1258631, 1469064-1470983, and 1475592-147
Subtraction by Bento Soares and M. Fatima Bonaldc
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
I bases 1 to 422)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestn
Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clift:
Hillier, L., Marra, M., Pape, D., Mylie, T., Martin, J., Blist:
Schnitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvi
Williams, T., Jackson, Y. and Bowers, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library was constructed by Dr. J. Ferrer In vivo mass-exc paluescript SK- by Dr. H. Inoue DNA sequencing by: Washin University Genome Sequencing Center For information on obsclone please context: Dr. Hiroshi Inoue (hinoue@im.wustl. Seq primer: -40UP from Gibco High quality sequence stop: 416.
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BI677255
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
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/lab_host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"
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Fax: 617-495-8557
Email: dmelton@blohp.harvard.edu
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/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
Xho1; Site_2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.ed/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."
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12.2%; Score 167; DB 12; Length 422;

rity 100.0%; Pred. No. 1.7e-73;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

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372 bp mRNA linear BST 17-SEP-2001 yl Human insulinoma Homo sapiens CDNA 5', mRNA sequence.

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y was constructed by Dr. J. Ferrer In vivo mass-excised to cript SK- by Dr. H. Inoue DNA sequencing by: Washington sity Genome Sequencing Center For information on obtaining a please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) imer: -40RP from Gibco.

Location/Qualifiers
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1 University, Howard Hughes Medical Institute
f Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                      ota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, a, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                               D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., ca, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., J., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., A., Theising, B., Ritter, E., Ronko, I., Bennett, J., 38, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., ns, T., Jackson, Y. and Bowers, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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/db_xref="taxon:9606"
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GI:15630163
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3STB: id87a02.x1
                                                                piens (human)
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/clone\_lib="Human insulinoma" /note="Organ: pancreas; Vector: pBluescript SK-; Site\_l:

/lab\_host="DH10B (phage-resistant)" /clone lib="Human insulinoma"

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(Stratagene) by Dr. J. Ferrer, in vivo mass-excise pBluescript SK- by Dr. H. Inoue following the Was DBluescript SK- by Dr. H. Inoue following the Was (http://genome.wustl.edu/est/lambda protocol.shtml please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Laboratory, Washington University School of Medic 18127, 660 S Euclid Ave, St. Louis, MO 63110). Not is a Washington University Pancreas EST project li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele-Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 436) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzm Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HS 3188 B1 F05 MR CIT Approved Human Genomic Sperm Library sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="CIT Approved Human Genomic Sperm Libz /note="Organ: sperm; Vector: pBeloBAC11; BAC Clor
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XhoI; Site_2: EcoRI; Constructed with lambda ZAPII
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Plate: 3188 row: L column: 9
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Class: BAC ends
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Length 409; Indels EST 22

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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra, Parsons,C., Riktin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. a
                                                                                                                                                                    1216 GGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATG1
                                                                                                                                                                                                        184 GGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGI
                                                                                                                                                                                                                                                 1276 GGCGAGAAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAACAG
                                                                                                                                                                                                                                                                           124 GGCGAGAAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAACAC
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 bp mRNA linear EST 2 yj77a08.rl Soares breast 2NbHBst Homo sapiens cDNA clone IBAGE:154742 5', mRNA sequence.
Average insert size 1.69 kb. Life Technologies 11549-011"
                                                                                                                                                                                                                                                                                                                                    1336 TATTTTTTTTTTTTTTGTGACAAAATGTTGATAAATGG 1373
                                                                                                                                                                                                                                                                                                                                                                           64 TATTTTTATTATTGTGACAAATGTTGATAATGG 27
                                                                                   Query Match
11.5%; Score 158; DB 10;
Best Local Similarity 100.0%; Pred. No. 6.8e-69;
Matches 158; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:556839"
/db_xref="taxon:9606"
/clone="IMAGE:154742"
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Contact: Wilson RK
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JOURNAL
COMMENT
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s cgapbs-r@mail.nih.gov

s procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

b Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Library Preparation: Life Technologies, Inc.

Library Arrayed by: Greg Lennon, Ph.D.

Sequencing by: Washington University Genome Sequencing Center
e distribution: NCI-CGAP clone distribution information can be
through the I.M.A.G.E. Consortium/LLML at:
io.lln.gov/bbrp/image/image.html
rimer: -40UP from Gibco
quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 409 bp mRNA linear EST 27-OCT-1999
34.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622510 3',
                                                                                                                                                                                                                                                                                                                                                                                                       GCAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGGCTGGACCTGGCG 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGGGGAAAAC 1285
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/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                 ò
                                                                                                                                                       CCTGTTCACGTGTTTTCCATCCCACATAAAAAAGAGTATTCCCACTCTTATCTTACA 1045
                                                                                                                                                                                                                                      CCCCACCGCCCACTCCCACCTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCC 1105
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lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ases 1 to 409)
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signet ring cell features"
/lab_host="DH10B"
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                                                                                                                   Gaps
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0
                                                                            Length 436;
                                                                                                                   3; Indels
                                                                          Score 162; DB 28;
Pred. No. 6.2e-71;
0; Mismatches 3;
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/db_xref="taxon:9606"
/clone="IMAGE:2622510"
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                   E-Coli DH10B"
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/lab host="DH10B"
/lab host="DH10B"
/lone_lib="NCI_CGAP_Pr22"
/norte="Corgan: prostate; Vector: pT7T3D-Pac (Pharm with a modified polylinker; 1st strand cDNA was p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 bp mRNA linear BST 30 mRNA sequence.
A1865482
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179)
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National Cancer Institute, Cancer Genome Anatomy Project (
                                                                                                                                                                                365 GACTAGTICGGCCTCGCAGAAGIGCACCTAAAGGCCGGAAAACACGGGGCTCGAAGAG
                                                                                                                                                                                                                              345 GACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGGCTCGAAGAC
                                                                                                                                                                                                                                                                                                                   465 ACGGBACAGTTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGC
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Gruber (Invitrogen). Research Genetics tracking 023, Note: this is a NIH_MGC Library."
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H
                                                                                       Length 785;
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Email: cgapbs-remail.nth.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.
Tissue Procurement: Michael J. Brownstein, M.D., Ph. Bemer-Buck, M.D., Ph.D.
Emmer-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing by: Washington University Genome Sequencing the I.M.A.G.B. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco:
                                                                                                                                     1; Indels
                                                                                       Score 132; DB 12;
Pred. No. 1.4e-55;
0; Mismatches 1;
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/db_xref="taxon:9606"
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1. .179
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                                                                                            Query Match 9.6%;
Best Local Similarity 99.3%;
Matches 302; Conservative (
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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TITLE
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KEYWORDS
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/note="Organ: pooled colon, kidney, stomach; Vector:
pcMv-SpoRT6; Site 1: Not1; Site 2: BcoRv (destroyed); RNA
pcMv-SpoRT6; Site 1: Not1; Site 2: BcoRv (destroyed); RNA
gource anonymous pool 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT prinned and directionally cloned (EcoRv site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 785 bp mRNA linear EST 25-SEP-2001 66F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188168 5',
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ibrary Arrayed by: The I.M.A.G.E. Consortium (LLNL)
squencing by: Incyte Genomics, Inc.
distribution: MGC clone distribution information can be
                                                                                                                                                                                            GTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATG
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Institutes of Health, Mammalian Gene Collection (MGC)
    230. Library constructed by Bento Soares and M.Fatima Bonaldo."
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                                                                                                Score 140; DB 14; Length 345;
Pred. No. 1e-59;
                                                                                                                                              3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgapbs-r@mail.nih.gov
Procurement: Life Technologies, Inc.
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                                                                                                                                              0; Mismatches
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/db_xref="taxon:9606"
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Harrow W

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from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo. "
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ö cciaggeccaggaricccaaargigagggggggaaacaagacaagcicciccii 112 0; Gaps Length 179; 0; Indels 9.5%; Score 130; DB 9; L 100.0%; Pred. No. 1.1e-54; iive 0; Mismatches 0; onservative

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AAATGG 1373 AAATGG 42

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1 210 bp mRNA linear EST 13-AUG-1998 s1 NCI\_CGAP\_Br2 Homo sapiens cDNA clone IMAGE:1632506 3', equence.

희무결함

61.1 GI:3418453

(human)

ota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; 19es 1 to 210) apiens

AP http://www.ncbi.nlm.nih.gov/ncicgap.

uished (1997) et: Robert Strausberg, Ph.D.

crange of the control

1. .210 /organism="Homo sapiens"

/mol\_type="mRNA" /db\_xref="taxon:9606" /clone="IMAGE:1632506"

/cisue\_type="breast"
/lissue\_type="breast"
/lissue\_type="breast"
/lissue\_type="breast"
/lobe\_i="billor"
/clone\_lib="NCI\_GARP\_Br2"
/note="Vector: pT7T3D-pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I
breast tumor tissue, and was then primed to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Bco RI sites of the modified pT7T3
vector. This library is the normalized version of
NCI\_GAP\_Br1.1. Library was constructed by Bento Soares
and M. Fatima Bonaldo. "

1246 GGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAAGACAAGCTCCTCCC 150 eeccraeeccaeeacricccaarereaececcaaaacaaeaacaaecraeccicc Length 210; Query Match
9.3%; Score 128; DB 9; I
Best Local Similarity 100.0%; Pred. No. 1.2e-53;
Matches 128; Conservative 0; Mismatches 0; 1366 ATAAATGG 1373 30 ATARATGG 23 ORIGIN g ð d à 엄

Search completed: April 8, 2004, 23:42:07 Job time : 3973 sec8

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n 5.1.6 Compugen Ltd. Search time 654 Seconds (without alignments) 8918.618 Million cell updates/sec	67477	ARIES  Description  Description  Description  Description  Aav18600 Homo sapi  Aav25587 Polyuucle  Aav18600 Human TWE Adc57901 Human TWE Adc49717 Human PRO Aba49717 Human PRO Aba69888888988889888898888988889888898888
GenCore version 5.1.6 opyright (c) 1993 - 2004 Compt c search, using sw model il 8, 2004, 19:06:21; Search (without general search sear	UC 0.0 , Gapext 60.0 seqs, 2124099041  tisfying chosen ps 200000000 g first 100 summan seq 29Jan04:* teseqn1990s:* teseqn2000s:* teseqn2001bs:* teseqn2001bs:* teseqn2001bs:* teseqn2001bs:* teseqn2001bs:* teseqn2003s:* teseqn2003s:* teseqn2003s:* teseqn2003s:* teseqn2003s:*	Then number of regults preduce that of by analysis of the total secore od by analysis of the total secore of by analysis of the total secore of by analysis of the total secore of by analysis of the total secore of by analysis of the total secore of by analysis of the total secore of by analysis of the total secore of by analysis of the total secore of the total secore of the total secore of the total secore of the total secore of the total secore of the total secore of the total secore of the total secore of the total secore of the total secore of the total secore of the total secore of the total secore of the total secore of the total secore of the total secore of the total secone of the total se

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## ALIGNMENTS

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> BP dard; cDNA; 1373

(first entry)

necrosis factor related ligand; tnf; treatment; cancer; sease; immune system; stimulation; suppression; on; ds.

tumour necrosis factor related ligand (TRELL) gene.

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/note= "tumour necrosis factor related ligand" Location/Qualifiers 1. .852 \*tag=

96US-0028515P. 97US-0040820P. 97WO-US013945. 96US-0023541P.

GENEVA FACULTY MEDICINE.

N.

Y, Browning JL; ĕ

5619/13.

is factor related ligand - useful for, e.g. treating cancer, lisease and immune responses to tissue grafts.

3 48-50; 69pp; English

al compositions to treat cancer, autoimmune diseases or as uses to tissue grafts, or to stimulate or suppress the immune is useful to screen for TRELL receptors, by labelling with a shell and screening compositions for binding. Agents with TRELL receptor binding can also be screened for, can nistered, optionally with interferon gamma, to induce cell at, suppress or alter immune responses (sepecially involving a recinoma cells) involving a signal pathway between TRELL and The DNA sequence can be used in gene therapy for TRELL repars in mammals (sepecially involving the second of the s amounts is that encoding human tumour necrosis factor related ligand rders in mammals (especially humans), e.g. tumours, nd inflammatory diseases or inherited genetic disorders, by into cells, and expressing, therapeutically effective amount e.g. a virus comprising a gene encoding TRELL. It may also the preparation of prepare probes for screening hetic DNAs for TRELL-encoding sequences and for antisense or active fragments can be included with a carrier in

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ard; DNA; 1306 BP

first entry)

tumour necrosis factor; osteopathic; bone; gene; ds. encoding tumour necrosis factor superfamily member.

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002WO-US033022

:001US-0329393P.

3-JEWISH HOSPITAL

346/40.

F, Teitelbaum SL;

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c comprising a core, and at least one external loop, useful processes of bone formation or inhibiting bone resorption, a treatments for disease or condition characterized by loss

ge 66-67; 78pp; English.

aquence is that of a polynucleotide encoding a non-RANKL tummour necrosis factor (TNF) superfamily. The invention naturally-occurring proteins that contain one or more of the protein core of RANKL (see ABR42066-70) in combination with a protein core obtained from a non-RANKL member of the TNF Also provided are polynucleotides encoding such proteins. bind to RANK, acting as mimics of RANKL. They can be used to formation by either inhibiting bone resorption or inducing thus providing treatment for diseases or conditions by loss of bone mass

BP; 247 A; 434 C; 368 G; 257 T; 0 U; 0 Other;

ery Match 93.6%; Score 1285; DB 7; Length 1306; st Local Similarity 100.0%; Pred. No. 0; tches 1285; Conservative 0; Mismatches 0; Indels 0; Ge	89 CACAGCCCCCCCCCCATGGCCGCCCGTCGGAGCCAAGGCGGAGGGGGCGCCGGG 	149 AGCCGGGCACCGCCCTGCTGGTCCCGCTCGCGCTGGGCCTGGGCCTGGCCTTGGCCTTGGCCTTGGCCTTGGCCTTGCCCTTGCTCCCGCTCGCGCTGGGCCTGGGCCTGGCGCTGGCCTGGCCTGGGCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCGCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCCTGCCCCTGCCCCTGCCCCCTGCCCCCTGCCCCCTGCCCCCC	209 TCGGCCTCCTGCTGGCCGTGGTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGG	CGGCCTCCTGCCGGCGTGATTTGGGAAGCCGGGCATCGCTGT	69	AGGAGGAGGATCCTGCTGCTTTCCTGAACCGACTAGTTCGGC	41 CAG	8 0	301 CACCIMANGGCCGGGAHANCACGGGCTCGANGGGCGGATCGGAGGGGGGGGGGGGGG	61	509 AAGCCAGATCAACAGCTCCAGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTTT	421 AAGCCAGAATCAACAGCTCCTCTGCGCTACAACGGCCAATTTT	9	81	29	41	689 TCTCACCACTGCGGCCAGTTCCCTCGGGCCCAGCTCCGCCTCTGCCAGGTCTCTGCCAGGTCTCTGCCAGGTCTCTGCCAGGTCTCTGCCAGGTGTCTCTGCCAGGTGTCTCTGCCAGGTGTCTCTGCCAGGTGTCTCTGCTGCTGCTGCTGTGTGTCTTGTGCTGCTGTGTGTCTTGTGCTGTGTGTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	49	661 TGTTGGCCCTGCGGCCAGGGCCTCCCTGCGGATCCGCACCCTCCCCTGGGGCCCAT	09 AGGCTGCCCCTTCCTCACCT	21 AGGCTGCCCCTTCCTCACCTACTTCGGACTCTTCCAGGTTCALTGAGGGGCCCTT	869 CCCCACAGTCGTCCCAGGCTGCCGGCTCCCCTCGACACCCTCTGGGGACCCCGGTCTCTGGGCTCTCTGGGCTCTCTGGGTCTCTCTGGTCGGCTCTCTGGTCGGCTCTCTGGGTCGCGGCTCCTC	ccacadrocadocadocadoracecadorada da contra do contra do como contra do como como como como como como como c	929 CIGCCCCACCCTCAGCCGCTCTTTGCTCCAGACCTGCCCCTCCTCTAGAGGCTGC	ceccacecterendadesecteringesectedesectedesecteradadesecte	ည္ပ <u></u>	CCTGTTCACGTGTTTTCCATCCCACATAAATACAGTATTCCCACTCTTATCTTA	1049 CCCCCACCGCCCACTCTCCACTCACTCACTCACAATCCCTGACCCTTTGAGGCC	61 CCCCCACCGCCCACTCTCCACTAGCTCCCCAATCCCTGACCTTTGAGGC	1109 GIGAICICGACICCCCCTGGCCACAGACCCCCAGGGCAIIGIGIICACIGIACIC
Query Best L Matche	Qy Dp	à g	λ	Db	۵. م	9 8	유	ب م	g 8	· 음 ·	δ	qq	λό ti	gg	δλ	Dp	දු පු	\ \d	Dp Q	ολ	Д	ζ	qq	δ	qq	ζ	Ωþ	δ	QQ	Š

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	XX SQ Sec	Sequence 1306 BP; 247 A; 434 C; 368 G; 257 T; 0 U; 0 Other;
AGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCA 1228	Query Best 1 Matche	Query Match 93.6%; Score 1285; DB 7; Length 1306; Best Local Similarity 100.0%; Pred. No. 0; Matches 1285; Conservative 0; Mismatches 0; Indels 0; 6
GCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAAG 1288	දු පු	89 CACAGCCCCCGCCCCCATGGCCGCCCTCGGAGCCAGGGGGGGG
GCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAACAGATATTATTTTTATTATT 1348	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	149 AGCGGGGACCGCCTGGTGGTCCGCTCGCGCTGGGCCTGGGCCTGGCGCTGGCCTGGCCTGGCCTGGCCTGGCCTTGCCCTGCTCCCGCTCGCGCTCGGCCTGGGCCTGGGCCTGGGCCTGGGCCTGGGCCTGGGCCTGGCCTTGCTGC
######################################	දු පු	209 TCGGCCTCCTGCTGGTGGTCAGTTTGGGGAGCCGGGGATCGCTGTCGCCCCAC
	À q	269 CTGCCCAGGAGGAGCTGGTGGCAGAGGAGGACCAGGACCCGTCGGAACTGAATCCC
ıdard; cDNA; 1306 BP.	& ga	329 CAGAAGAAAGCCAGGAICCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAG; [
(first entry)	ò	389 CACCTAAAGGCCGGAAAAACACGGGCTCGAAGAAGAGCGATCGCAGCCCATTATGAAGT
soding sequence.	r do	301 CACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGT
<pre>; tumour necrosis factor; ligand; cytostatic; ior; osteopathic; gene; ss.</pre>	oy Op	449 CACGACCTGGACAGGACGGAGCGCAGGTGTGGACGGGACAGTGAGTG
Location/Qualifiers 18. 767 /*teg= a	දු පු	509 AAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTT
/product= "Human TWEAK" -A2.	که <del>د</del>	569 TCACCGGGCTGGCTCTACTACTGTACTGTCAGGTGCACTTTGATGAGGGGAA 1481 TCACCGGGCTGTACTGTGTGTGTGTGTGACTGTACTGTCAGGTGCACTTTGATGAGGGGAA
2002WO-US023782.	8 8 8	
2001US-0307838P	2 2	5*1 ICIACCIGANGCIGGACITACCICACIGGACCACCAGCACCACACACACACACACACATGACACACAC
N GENOME SCI INC.	ž 8	
Rosen CA; 0659/40.	λ Q	749 IGTIGGCCCTGCGGCCAGGTCCTCCCTGCGGATCCGCACCTCCCCTGGGCCCAGGTCCTGCGGATCCGCACCCTCCCT
ltimeric complex having a first polypeptide member of the is factor (TNF) ligand family, and a second different member d family, useful for treating cancer, osteoporosis or an	o d	809 AGGCTGCCCCTTCCTCACCTACGTCGACTCTTCCAGGTTCACTGAGGGCCCT
isease	λõ	869 CCCCACAGTCGTCCCAGGCTGCCGGCTCCTCGACAGCTCTTCTGGGCACCCGGT
Page 367-368; 388pp; English.	ορ	781 CCCCACAGTCGTCCCAGGCTCCCGTCGACAGCTCTCGACAGCTCTCGACGCACCCGGT

989 GCCTGTTCACGTGTTTCCATCCCACATAAATACAGTATTCCCACTCTTATCTTA 901 GCCTGTTCACGTGTTTTCCATCCCACATAAATACAGTATTCCCACTCTTATCTTT

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sequence is that of a polynucleotide encoding human TWEAK. In relates to compositions comprising heterotrimeric complexes orcosis factor (TNF) ligand family members, and their use in prevention and treatment of disease. In one embodiment, imeric complex comprises full-length or extracellular TWEAK and full-length or extracellular portions of other TNF y members, preferably VEGI or VEGI-SV. The heterotrimeric the invention are useful for treating an autoimmune disease, iteoporosis, and particularly for inhibiting cancer cell m, increasing B cell proliferation, or inducing apoptosis of

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929 CIGCCCCACCCICAGCCGCICTIIGCICCAGACCIGCCCCICCCCCTCIAGAGGCIC

1049 CCCCCACCGCCCACTCTCCACTCACTCCCCAATCCCTGACCCTTTGAGGC

ACGECCAACTCTCCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCA 1020 STCGACTCCCCCCTGGCCACAGGCATTGTGTTCACTGTACTCTGTG 1168	888 <b>x</b> 8	antibody that binds specifically to endokine alpha polypeptide. The present sequence represents a cDNA encoding a tumour necrosis fact family ligand.  Sequence 1306 BP; 247 A; 434 C; 368 G; 257 T; 0 U; 0 Other;
GGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCA 1228 	ÕĎĔ	Query Match 93.6%; Score 1285; DB 9; Length 1306; Best Local Similarity 100.0%; Pred. No. 0; Matches 1285; Conservative 0; Mismatches 0; Indels 0; Ga
CCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGGGAAAAAAG 1288 	QY DP	89 CACAGCCCCCGCCCCCATGGCCGCCGTCGGAGCCAGAGGCGGAGGGGGGCCCGGGC
CTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAACAGATATTATTTTTATTTT 1348 	δ. du	149 AGCCGGGCACCGCCCTGCTGGTCCCGCCTCGCGCTGGGCCTGGGCCTGGCGCTGGCCT 
GACAAATGTTGATAATGG 1373                    GACAAATGTTGATAAATGG 1285	op op	209 TCGGCCTCCTGCTGGCCGTGGTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGG
	Qy	269 CTGCCCAGGAGGTGGTGGCAGAGGAGCAGCACCCGTCGGAACTGÀATCCCC
ard; cDNA; 1306 BP.	8 %	329 CAGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGA?  241 CAGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGA
<pre>first entry) oding INF ligand family member #12.</pre>	& <u>8</u>	389 CACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTT( 
n; tumour necrosis factor; TNF ligand; endokine alpha; resorption disorder; osteoporosis; Paget's disease; fication.	Qy du	449 CACGACCTGGACAGGACGGAGGCAGGCAGGCACGGGACAGTGAGTG
т·	Sy da	509 AAGCCAGAATCAACGCCTCTGCGCTACAACGCCAGATCGGGAGTTT7
.002US-00218547.	는 성 -	569 TCACCCGGGCTGGGCTCTACTGCTGTCAGGTGCACTTTGATGAGGGAAGG
.001US-0312542P. .001US-0330761P.	9 G	629 TCTACCTGAAGCTGGACTTGCTGGATGGATGCTGGCTGCCTGC
CA. II B.	yo dd	689 TCTCAGCCACTGCGGCCAGTTCCCTCGGGCCCCAGCTCCGCCTCTGCCAGGTGTCTCCCCAGGTCTCTCCCTCGGGCCCCCAGCTCCGCCTCGGCCTCTGCCAGGTGTCCTCGGGCCCCAGGTCCGGCCTCGGCCTCGGCCTCGGCCTCGGCTCTCGCAGGTGCTCCCTCGGGCCCCAGGTTCCCTCGGGCCCCAGGTCCGCCTCGGCCTCGGCCTCGGCCTCGGCCTCTGCCAGGTGCTCTCGCCAGGTGCCTCGGGCCCTCGGCCTCGGCCTCGGCCCTCGGCCTCCT
Rosen CA, Nardelli B; )72/66. 306.	8 8	749 TGTTGGCCTGCGGCCAGGGTCCTGCGGATCCGCACCCTCCCT
ulpha gene useful for preparing a composition for treating a lated with excessive or insufficient bone resorption e.g., Paget's disease or arterial calcification.	<i>ò</i> €	809 AGGCTGCCCCTTCCTCACCTACTTCGGACTCTTCCAGGTTCACTGAGGGGCCCTG
3Q ID NO 23; 145pp; English.	λō .	869 CCCACAGAGTCCACAGCTGCCGGCTCCCCTCGACAGCTCTCTGGGCACCCGGTC
relates to an isolated nucleic acid molecule encoding a is factor family ligand. A composition comprising the sody or its fragment is used for treating an individual in ased level of endoxine alpha activity. The endoxine alpha resent in a heterotrimeric complex is used for treating an	40 Q	781 CCCCACAGTCGTCCCAGGCTCCCCCTCAACAGCTCTCTGGGCACCCGGTC 929 CTGCCCCACCCTCAGCCGCTCTTTGCTCCAGACCTGCCCTCTAGAGGCTGC
ving a disorder associated with excessive bone resorption, osis, Paget's disease or arterial calcification. Treating an ving a disorder associated with insufficient bone resorption inistering an endokine alpha antagonist, which is the	<b>장</b> 셤	989 GCCTGTTCACGTGTTTTCCATCCCACATAAATACAGTATTCCCACTCTTATCTTAC 

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CACCGCCCACTCTCCACCTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCA 1108
TCTCGACTCCCCCTGGCCACACCCCCAGGGCATTGTGTTCACTGTACTCTGTG 1168
AGGNTGGGTCCGGAAGACCCCATTCAGGCACTAAGAGGGGCTGGACCTGGCGCA 1228
GCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAAG 1288 
GCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAACAGATATTATTATTATT 1348
:TGACAAATGTTGATAAATGG 1373                     :TGACAAATGTTGATAAATGG 1285

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dard; cDNA; 1364 BP.

(first entry)

acoding secreted protein #19

ed protein, gene; se; nutritional supplement; haemophilia; ion; bacterial infection; fungal infection; diabetes; asthma; isorder; rheumatoid arthritis; multiple sclerosis; tumour; hyroiditis; allergic reaction; neurodegenerative disease; lisease; parkinson's disease; liver fibrosis; cancer; ulcer; disorder; inflammatory disorder; crohn's disease; incision; aration; wound healing; burn; haematopolesis; deficiency; lymphoid cell deficiency.

42.

2001WO-US010224.

2000US-0195582P.

TICS INST INC.

ark HF, Fechtel K, Agostino MJ, Graham JR;

Resnick RJ;

Howes SH,

9321/23.

land ninety two polynucleotides derived from a variety of sources which encode secreted proteins, useful for treating sencies and disorders such as autoimmune disorders.

le 82; 372pp; English.

in relates to 592 polynuclectides which have been derived from human tissue sources and which encode novel secreted is polynuclectides can be used as probes for the on and isolation of full length cDNA and genomic DNA. The des and proteins can also be used as nutritional supplements.

The proteins are useful in the treatment of various immune deficiand disorders such as viral infections, bacterial infections, fun infections, autoimmune disorders (e.g. rheumatoid arthritis, mult sclerosis, autoimmune thyroiditis and diabetes) and allergic read and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Altheimer's disease, parkinson's disease), liver fibrosis, coagulation disorders (e.g. haemophilis inflammatory disorders (e.g. Crohn's disease) and tumours. They a useful for tissue regeneration, for wound healing and in the trea hurns, incisions and ulcers. The proteins are also useful for recharactopolesis and for treating myeloid or lymphoid cell deficier Sequences ABK34863-ABK35454 represent polynucleotides of the inve AGTIGCACCTAAAGGCCCGGAAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATG CTCAAGGCTGCCCCTTCCTCACCTACTTCGGACTCTTCCAGGTTCACTGAGGGC 5 Techerodecoderecetrecetrocedanicerredonecedandos 85 CAGGCACAGCCCCCCCCCATGGCCGCCCGTCGGAGCCAGAGGCGGAGGGGG 65 CAGGCACAGCCCCCCCCCCCATGGCCGCCCGTCGGAGCCAGAGGCGGAGGGGGGC TGCCTCGGCCTCCTGCTGGCCGTGGTCAGTTTGGGGGAGCCGGGCATCGCTGTCCG recercescerecrecescerestrastrasseasecescerescristes GAGCCTGCCCAGGAGGAGCTGGTGGCAGAGGAGCACCAGGACCCGTCGGAACTGA CAGACAGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTC CAGACAGAAAGCCAGGATCTTGGCTTTCCTGAACCAACTAGTTGGCCTT AGTECACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATG 505 GAGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGGCCAGATCGGGG ses atagicaccessseressericiaciacietaristeasserscacitisaisasses 545 ATAGTCACCCGGGCTGTACTACTACTGTACTGTCAGGTGCACTTTGATGAGG 625 GCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGCCCTGCGCTGCC 685 GAATICICAGCCACIGCGGCCAGIICCCICGGGCCCCCAGCICCGCCICIGCCAGG <u> saárricricasciaciascascaastricicricassicicicasciricisciristicas saárricricas sa a sa a sa a sa a sa a sa a s</u> gescrietrescecriscesceagesrecrecersessaareeseacereee esecterrescentececcases concerces establicados es establicados en establicados establicados establicados establicados establicados establicados establicados en establicados establicados establicados establicados establicados establicados establicados establicados establicados establicados en establicados establicados establicados establicados en establicados en establicados en establicados en establicados en establicados en establicados en establicados en establicados en establicados en establicados en establicados en establicados en establicados en establicados en establicados en establicados en establicados en entre en establicados en entre en establicados en establicados en establicados en establicados en entre en establicados en entre en entre en establicados en entre entre en entre en entre en entre en entre en entre en entre en entre en entre en entre en entre en entre entre en entre e gagaaccagacaccaccaracrasrccacrcacacaacaaccraaaccraaaccraaaca 0; DB 6; Length 1364; Sequence 1364 BP; 246 A; 461 C; 394 G; 263 T; 0 U; 0 Other; Indels 5; Mismatches Score 1247; Pred. No. 0; 0; 7 \$8.06 \$8.66 Best Local Similarity 99.9 Matches 1347; Conservative 999 745 725 805 365 185 265 325 305 385 445 205 25 145 Query Match QΩ g 95 PP 95 à g  $\delta$ ∂ 임 à d ò Db q g ð d à g  $\stackrel{>}{\circ}$ a ð g  $\dot{\delta}$ 8 **X** 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 ð ₽ à

99US-0131445P

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                                                                                                                                                                                                                                                                                                 CCTGTTCACGTGTTTTCCATCCCACATAAATACAGTATTCCCACTCTTATCTTAC 1044
GCTGCCCCTTCCTCACCTACTTCGGACTCTTCCAGGTTCACTGAGGGGCCCTG 844
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                                                                                                        cececagicarecadeciacesciecereceaegerereregescaeer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGTGACAAAATGTTGATAAATGG 1373
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lard; cDNA; 1353

(first entry)

; antitumour; tumour; therapy; cytostatic; breast cancer; c; renal cancer; colorectal cancer; uterine cancer; ar; lung cancer; bladder cancer; is system cancer.

Location/Qualifiers 58. .807 58. .177 /\*tag= b 178. .804 /\*tag= c ď /\*tag= a 58. .177

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99WO-US028565
                   98US-0113296P
                             99WO-US005028.
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The present sequence is that of cDNA clone DNA30879-1152 (AICC 205 encoding human PRO207 (see AAY95338), which shows homology to seve members of the tumnour necrosis factor family, especially human [1] in the cDNA was identified in a foetal kidney of library following identification of an expressed sequence tag with homology to human Apo-2 ligand. A claimed method for inhibiting the composity to human Apo-2 ligand. A claimed method for inhibiting the pro207, PRO30, PRO219, PRO221, PRO324, PRO328, PRO301, PRO506, PRO3056, PRO309, or PRO866 (see AAY95337-49), their agonists or chim peptides incorporating them. The tumour cally a cancely selected from breast, ovarian, renal, colorectal, uterine, prostation, bladder and central nervous system cancer, melanoma and leui which continuous encomposition in the recombinant procession.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatin
RO219, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGCAGGCAGGTGTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 GCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAAGGCCGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel composition to inhibit neoplastic cell growth or for treati:
in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219,
PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or PRO866.
                                                                                                                                                                                                                                                                Marsters SA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1353 BP; 257 A; 443 C; 389 G; 264 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                      Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Fig 3; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the antitumour polypeptides
                                                                                                                                                                                                                                                                          Ashkenazi AJ, Goddard A, Godc
Napier MA, Pitti RM, Wood WI;
            990S-01343287P-
990S-0144758P-
990S-0145698P-
99WO-US021090.
99WO-US021547.
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                                                                                                                                                                                                            (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-442668/38.
                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAY95338
                      14-MAY-1999;
20-JUL-1999;
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The present invention relates to the isolation of novel human PR polypeptides and the polynucleotide sequences encoding them. The polypeptides, agonists, antagonists or anti-PRO antibodies are us treating benign or malignant tumours (e.g. renal, kidney, bladdebreast, etc), leukaemias and lymphoid malignancies, other disord as neuronal, glial, astrocytal, hypothalamic, glandular, macroph stromal and blastocolic disorders, inflammatory, immune and ang disorders. The polynucleotide sequences are also useful in gene ABK40254-ABK40288 encode for the human PRO polypeptides of the i leukaemia; neuronal disorder; stromal disorder; blastocoelic disoinflammatory disorder; immune disorder; angiogenic disorder; gene therapy; cytostatic; neuroprotective; gene; ss. 109 GCCGCCCGTCGGAGCCAGAGGCGGAGGGGCGCGGGGGGGAGCCGGGAACCCGCCC greececreactragecragecragecragecragecracereactrage Thirty five nucleic acids encoding PRO polypeptides, useful for benign or malignant tumors, leukemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders. Score 1172; DB 6; Length 1353; Pred. No. 0; Sequence 1353 BP; 257 A; 443 C; 389 G; 264 T; 0 U; 0 Other; 3; Indels Gurney AL, Smith V, 0; Mismatches d A, Godowski PJ, Pitti RM, Roy MA, Claim 50; Fig 3; 302pp; English. 99WO-USO05028. 99US-0123972P. 99US-0133459P. 99WS-0140650P. 99US-0140653P. 99US-0145698P. 99US-0145698P. 99US-014522P. 99US-0145395P. 85.4%; 99.8%; 99WO-US028634 99WO-US021090 99WO-US028313 99WO-US028301 2000WO-US003565 99WO-US020111 Goddard A, Best Local Similarity 99.8 Matches 1322; Conservative Fan J, P Wood WI; (GETH ) GENENTECH INC. WPI; 2002-205567/26. P-PSDB; AAU86129. WO200153486-A1. Ashkenazi AJ, 02-JUN-1999; 22-JUN-1999; 22-JUN-1999; 20-JUL-1999; 26-JUL-1999; 28-JUL-1999; Marsters SA, Watanabe CK, 11-FEB-2000; 17-AUG-1999; 31-AUG-1999; 01-SEP-1999; 15-SEP-1999; 30-NOV-1999; 05-JAN-2000; 11-MAR-1999 11-MAY-1999 DEC-1999 26-JUL-2001 DEC-1999 169 Query Match Ношо g g q ð ð ò 1080 1188 1140 1248 SCCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAAGACAAGCTCCTCCCTTGAGAA 1308 CCTGTGGATTTTTAAAACAGATATTTTTTTTTTTTTTTGTGACAAAATGTTGATA 1368 1020 1128 ACATAAATACAGTATTCCCACTCTTATCTTACAACTCCCCCACCGCCCACTCTCCA 1068 GCTCCAGACCTGCCCCTCCTAGAGGCTGCCTGGCCTGTTCACGTGTTTTCCA 1008 GCTCCCTCGACAGCTCTTGGGCACCCGGTCCCCTCTGCCCCCACCCTCAGCCGCT 948 708 720 828 780 888 TCGGACTCTTCCAGGTTCACTGAGGGGCCCTGGTCTCCCCGCAGTCGTCCAGGCT 840 648 ACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCAGTGATCTCGACTCGCCCTG CAGACCCCCAGGGCATTGTGTTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAG CACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGC rgracrercaderecaerrreardadegegaageerereracerdaageregaetre IGGATGGTGTGCTGGCCTGCCTGGAGGAATTCTCAGCCACTGCGGCCAGT regesececasereceserrerecassisticises in a second consecutation of the second consecutat CCCTGCGGATCCGCACCCTCCCCTGGGCCCCATCTCAAGGCTGCCCCTTCCTCACC cerrecedarecedacerrecerredecedarercaagecrecederrecreace TCGGACTCTTCCAGGTTCACTGAGGGCCCCTGGTCTCCCCCAGGTCGTCCCCAGGCT TCTGCGCTACAACCGCCAGATCGGGGGGTTTATAGTCACCCGGGCTGGGCTCTAC benign tumour; malignant tumour; lymphoid malignancy; human PRO207 polypeptide. BP ndard; cDNA; 1353 (first entry)

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The present sequence encodes a human tumour necrosis factor (TNF) lymphotoxin homologue designated Apo-3 ligand, Apo-3 ligand has sytosteatic activity. Apo-3 ligand can be used to induce apoptosis mammalian cancer cells, to induce NF-kappaB-dependent transcript: to induce UNK/SAPK-dependent responses in mammalian cells
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NF-kappaB-dependent transcription; JNK/SAPK-dependent response; c
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GTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCTGCCCAGGAGGAGCTGGTG
                                                                                                                                           AGGCAGGTGTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCC
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The TNF-related endothelium proliferative agent (TREPA), or its activators or agonists, are used to treat a deficit of TREPA, expremely activators or agonists, are used to treat a deficit of TREPA, expremely also to induce apoptosis for treating cancer and eliminating autor calls, as an adjunct to cancer chemotherapy or antiviral treal TREPA peptides can also be used to target cytotoxic agents or for affinity isolation of the corresponding receptor, the nucleic and affinity isolation of the corresponding receptor, the nucleic and infinity and be used to transform tumour cells to reader them more capponsive to TREPA and to screen for TREPA mimics. Ribozymes, it inflammation or a wide range of autoimmune conditions, condition inflammation or a wide range of autoimmune conditions, condition at the prosclerosis), for bitth control (inhibiting ownlation and process).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ss; TNF; endothelium proliferative agent; TREPA; wound healing;
tissue grafting; vascularisation; apoptosis; autoimmune; birth
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/*tag= a
/product= "TREPA"
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98US-00021706.
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Matches 1208; Conservative
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The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molec designated as TREPA (TNF related endothelium proliferative agent) Soluble biologically active TREPA are used to treat TREPA-associal diseases, tumours or metastases. TREPA is used for inducing angic in human for promoting wound healing and for vaccularising grafts for successful grafting and to promote tissue grafts. The present sequence is a cDNA clone ID #690050 encoding human TREPA
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<u>есвалением вестовния в метом в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо в предпессо</u>
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99.6%; Pred. No. 0;
tive 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD04350
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This invention describes isolated Tumor Necrosis Factor (TNF) fareceptor polypeptides: APO4, APO6, APO8 and APO9 or their active receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands I and 3 TMRLI and I their active fragments APO4 is useful for diagnosing prostate cancer can determining levels of APO4 in an individual. Prostate cancer can determining levels of APO4 in an individual. Prostate cancer can determining aponts linked to a therapeu moiety. APO4 polypeptides are also useful for identifying select binding agents, to the polypeptide/active fragment which is extracellular expressed on the cell surface. The binding is preferably perform vivo. APO4 polypeptides/active fragments are also useful for so vivo. APO4 polypeptides/active fragments are also useful for so vivo. APO4 polypeptides/active fragments are also useful in diagnosis consists and antagonists by binding and observing the change for agonists and antagonists by binding and observing the change cutivity. Effective pharmacological agents useful in diagnosis, continue of disease are also identified using APO4 polypeptides for greated in vivo or in vitro. APO polyte activity. The method is performed in vivo or in vitro. APO polyte are all useful as immunogens for preparing antibodies. APO4 is cuseful for diagnosis/treatment of developmental or gestational abnormalities. APO8 was transfected to human breast carcinoma of MCP-7, and induced apoptosis New Tumor Necrosis Factor family receptor polypeptides and ligan useful for diagnosis and treatment of prostate cancer and develo Example VII; Fig 13A; 156pp; English. or gestational abnormalities. P-PSDB; AAW93590. AAX23424 RESULT ò 셤 GAGGGGGGAGAAACAAGACAAGCTCCTTGAGAATTCCCTGTGGATTTTTAAAA 1328 1148 GITCACTGIACTCIGIGGCAAGGAIGGGICCAGAAGACCCCCACTICAGGCACTAAG 1208 GITCACIGIACICIGIGGCAAGGAIGGGICCAGAAGACCCCACIICAGGCACIAAG 1103 GCCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAA 1163 1043 CICTAGAGGCIGCCIGGGCCIGIICACGIGIIIICCAICCCACAIAAAIACAGIAII 1028 ACTETTATETTACAACTECECEACEGECEACTETCEACTEACTEGETCECEAATEC 1088 923 983 90B 803 896 863 788 683 848 743 548 443 608 503 563 728 623 488 383 203 368 263 428 GGGCTGGACCTGGCGGCAGGAAGCCAAAAGAGACTGGGCCTAGGCCAAGAGTTCCCAAA croadedecertestetecesesatestetecadestacetecesesteteceadades TGGGCACCCGGTCCCCTCTGCCCCACCCTCAGCCGCTCTTTGCTCCAGACCTGCCCC ACTETTATETTACAACAACCCCACCCCACTCTCCACCTCACTAGCTCCCCAATCC ACCCTTTGAGGCCCCCCAGTGATCTCGACTCCCCCTGGCCACAGACCCCCAGGGCAT CCCCTGGGCCCATCTCAAGGCTGCCCCTTCCTCACTACTTCGGACTCTTCCAGGT GTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCG CATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGGC TIGCCAGGIGICIGGGCTGIIGGCCCIGCGGCCAGGGICCTCCCTGCGGAICCGCAC THE AGGGGGCCT GGT CCCCACACT CGT CCCAGGCT GCCGGCT CCCCT CGACAGGCT GAACTGAATCCCCAGACAGAAGAAGCCAGGATCCTGCGCCTTTCCTGAACCGACT GAACTGAATCCCCAGACAGAAGAAGCCAGGATCCTGCGCCTTTCCTGAACCGACT sarcegegagitianagicaccegeciegeciciaciaccegracied gargagggaaaggcrgrcraccrgaagcrgaacrrgcrggrggaaggrgrgcrggc ;cgcrgccrggaggaattcrcagccacrgcggccagrtcccrcggccccagcrccg CCCTGGGCCCATCTCAAGGCTGCCCCTTCCTCACCTACTTCGGACTCTTCCAGGT CTGTCCGCCCAGGAGCCTGCCCAGGAGGAGCTGGTGGCAGAGGAGGACCAGGACCC CGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAAACACGGGCTCGAAGAGAGCGATCGC CTGGCGCTGGCCTCGGCCTGCTGGCCGTGGTCAGTTTGGGGAGCCGGGC 

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developmental abnormality; gestational abnormalitity; prostate carefully APOS; APOS; APOS; TNRL-1; TNRL-3; diagnosis; treatment; therapy; cytoplasmic domain; immunogen; antibody preparation; breast carefapoptosis; human; ss.
1164 rereadedeceadaacaacaacaactccrccrrcaadaarrcccrdrddaarrrr
                                                                                                                                                                                                                                                                                                                                               necrosis factor receptor; signal transducer molecule; TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "TNRL3"
                                                                                                                                                                                              BP
                                                                                                                                                                                              AAX23424 standard; DNA; 1030
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                                                                                                 1224 CAGATATTATTT 1236
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/product= "
                                                                                                                                                                                                                                                                          (first entry)
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                                                             CAGATATTATTT
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                                                                                                                                                                                                                                                                                                                Human TNRL3 DNA.
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ctor pDC409-LZ-TWEAK fusion protein-encoding DNA. (first entry)

Example 1; Page 39-40; 46pp; English. Wiley SR; receptor GCTCCAGACCTGCCCCTCCTCTAGAGGCTGCCTGGGCCTGTTCACGTGTTTTCCA 1008 ö 768 828 600 888 948 288 480 540 240 648 348 408 180 468 528 588 TCTGCGCTACTACCGCCAGATCGGGGGGTTTATAGTCACCCGGGCTGGGCTCTAC 360 9 GCTCCAGACCTGCCCCTCTCTAGAGGCTGCCTGGGCCTGTTCCA caractereacerecaetricareacecaaacecreretracereaacerecae regaresrerececerecerecereceresassaarrereaseeacreseerage resseccedascressecreressassastassecretrassecerasses CCTGCGGATCCGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCTTCCTCACC cerecedarecedacereceresecearereasecrecerecerere reggaetettecaggtteaetgagggeeetggteteeeeaeagtegtecaggeet ressacrerrecassrearsassssceresferececasassere GCTCCCCTCGACACCTCTCTGGGCACCCGGTCCCCTCTGCCCCACCCTCAGCCGCT TCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTAC resegeceaserececeretecasastareresecretesecereteseses ACATAAATACAGTATTCCCACTCTTATCTTACAACTCCCCCACGCCCACT 1063 GTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTG TTTGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGCTGGTG GGAGGACCAGGACCCGTCGGAACTGAATCCCCAGACAGAAGAAGCCAGGATCCT TITICCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAAGGCCGGAAAACA TCGAAGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGACGGA rcgaagagarcgaagcccarrargaagrrcarccacgaccrggacagacga GGCAGGTGTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCC "TTTGGGGAGCCGGGCATCGCTGTCCCCCAGGAGCCTGCCCAGGAGGAGGAGCTGGTG GGAGGACCAGGACCCGTCGGAACTGCCCCAGACAGAAGAAAGCCAGGATCCT Gaps ö DB 2; Length 1030; BP; 223 A; 317 C; 279 G; 211 T; 0 U; 0 Other; Indels 0; Mismatches Score 784; 1 Pred. No. 0; 57.1%; nservative

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TWEAK extracellular domain; tumour necrosis factor; TNF; angiogene ocular neovascularisation, diabetic retinopathy; neovascular glauc retinoplastoma; retinopathy of prematurity; retrolental fibroplas: rubeosis; uveitis; macular dematurity; retrolental fibroplas: rubeosis; uveitis; macular dematurity; retrolental fibroplas: corneal graft neovascularisation; psoriasis; metastatic condition. malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic preneoplastic condition; myocardial angiogenesis; wound granulatiscleroderma; vascular adhesion; telangiectasia; ischaemia; human; atherosclerotic plaque neovascularisation; coronary atheroscleros: peripheral atheroscleros; pDC409-LZ-TWEAK; TWEAK receptor; TWEA /product= "Fusion protein comprising a growth hori leader, a leucine zipper multimerisation domain, human TWEAK extracellular domain" Modulating angiogenesis in a mammal for treating diseases mediate angiogenesis, e.g. solid tumors and vascular deficiencies of card peripheral tissue, by administering antagonist or agonist of TWEA Location/Qualifiers 20-DEC-1999; 99US-0172878P. 10-MAY-2000; 2000US-0203347P. 19-DEC-2000; 2000WO-US034755. /\*tag= (IMMV ) IMMUNEX CORP. WPI; 2001-417975/44. P-PSDB; AAU03499 fusion protein. WO200145730-A2 Homo sapiens. Synthetic. 20-DEC-1999; 28-JUN-2001.

The sequence represents a DNA from the expression vector pDC409-L which encodes a fusion protein comprising a growth hormone leader leuchne sipper multimerisation domain, and the extracellular doma human TWBAK. The fusion protein was used in the isolation of human receptor (TWEAKR) expressing clones from a COS cell human CDNA list receptor (TWEAKR) expressing clones from a COS cell human CDNA list a member of the tumour necrosis factor (TNF) and induces angiogenesis. TWEAKR may therefore be used to screen develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retirence neovascular glaucoma, retinoblastoms, retinoblastoms of premeturity, retrolental fibroplasis, unbeosis, uveitis, macular degeneration corneal graft neovascularisation, and inflammatory diseases such an inflammatory diseases incomparation and menageral corneal graft neovascularisation. malignant and metastatic conditions such as sarcomas and carcinom benign tumours and preneoplastic conditions, myocardial anglogene haemophilic joints, scleroderma, vascular adhesions, atherosclero neovascularisation, telangiectasia, wound granulation, cor atherosclerosis, peripheral atherosclerosis and

Sequence 898 BP; 187 A; 266 C; 267 G; 178 T; 0 U; 0 Other;

Ü .; 0 45.5%; Score 625; DB 4; Length 898; 100.0%; Pred. No. 6e-281; Live 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Matches 625; Conservative

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8 8 à 2. a 309 351 369 411

:GGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGCTGGTGGCA

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729 771 789 831

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equencing by hybridisation, SBH; expressed sequence tag; EST; 19; biodiversity; genetic disorder.

SON M C. S L W.

(first entry)

23-APR-2002

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the interior tenaces to an insurance posture comparing and 38043 CDNA sequences, appearing as ACH12789-ACH50831, whose sequence determined by the technique of SBH (sequencing by hybridisation). Included is a purified polypeptide comprising a sequence correspond a reading frame of the novel polymucleotide. The nucleic acid sequencing frame of the novel polymucleotide. The nucleic acid sequencing frame of the novel polymucleotide. The nucleic acid sequencing frame of the novel polymucleotide. The nucleic acid sequencing expressed genes or for physical mapping of the human in forensics, in assessing biodiversities, or in identifying muta responsible for genetic disorders and other traits. The nucleotid sequences are also useful as hybridisation probes, as oligomers for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified poly is useful for generating antibodies specific for it. The present for this patent did not form part of the printed specification, the obtained in electronic format directly from USPTO at
                                                                                        New polynucleotide sequences obtained from various cDNA libraries as hybridization probes, as oligomers for PCR, for chromosome and mapping, in the recombinant production of protein, or in generati
                                                                                                                                                                                                                                      The invention relates to an isolated polynucleotide comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     874 CAGICGICCCAGGCIGCCGGCICCCCICGACAGCICICIGGGCACCCGGICCCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 994 ITCACGIGITITCCAICCACAIAAAIACAGIAIICCCACICIIAICTIACAACIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 ACCCCCACTCTCCACCTCACTTACTCCCCAATCCCTGACCCTTTGAGGCCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1114 CICGACICCCCCCCCACAGACCCCCAGGGCAITGIGITCACTGIACICIGIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 GGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGGCTGGACCTGGCGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1054 ACCGCCCACTCTCCACTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCAA
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            Jones LW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            447 CCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGGA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.6%; Score 407; DB 8; Length 493; 100.0%; Pred. No. 2.6e-179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 493 BP; 87 A; 180 C; 120 G; 101 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
               Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      segdata.uspto.gov/seguence.html?DocID=20030073623
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                                                                                                                                                                                                   Claim 1; SEQ ID NO 21225; 44pp; English.
                 Stache-Crain B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 407; Conservative
                   Labat I,
                                                                                                                                                            antisense DNA or RNA.
                                                       WPI; 2003-615964/58.
                 Drmanac RT,
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ID ABK2
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AC ABK2
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DT 23-A
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AAT22190:

cinoma-specific cDNA #66.

denocarcinoma; colon cancer; tumour; gene; ss.

001WO-US018574.

000US-0210667P. 000US-0252614P.

CORP.

Secribt H; Xu J, ding GE,

52/13.

olynucleotide encoding a polypeptide comprising a portion : protein, for detection, diagnosis and therapy of human

133; 211pp; English.

relates to an isolated polynucleotide (I) encoding a (II) comprising a portion of a colon tumour protein. A new le (III) that hybridises to (I) is useful for determining a cancer in a patient. (II) or antigen presenting cells are useful for stimulating and/or expanding T cells (tumour protein, by contacting T cells with (I), (II) or uting cells that express (I) are useful for treating colon cancer by incubating CD4+ and/or CD8+ T cells isolated from a (I), (II), or antigen presenting cells that express (II) so yincubating CD4+ and/or CD8+ T cells that express (II), or antigen presenting cells that express (II), or antigen presenting cells that express (II), so proliferated T cells, thus inhibiting the development of a patient. A new composition is useful for stimulating an patient. (I) or (II) is useful in vaccines and compositions for prevention and treatment of colon cancer agnosis and monitoring of the cancers. (I), (II) or an ist (II) is useful for detection, diagnosis and/ or therapy cancer. (I) is useful for detection, diagnosis and or therapy cancer. (I) is useful as a probe or primer for nucleic thous, and in the design and preparation of ribozyme calls. sent human colon adenocarcinoma-specific cDNA sequences of

3P; 49 A; 51 C; 58 G; 37 T; 0 U; 0 Other;

0; Gaps DB 6; Length 195; 0; Indels 13.0%; Score 179; DB 6; I 100.0%; Pred. No. 5.3e-73; ive 0; Mismatches 0; nservative

3666CTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCC 1265 FIGHTCACTGIACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCACTTCAGGCACT 76

FIGHTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCCACTTCAGGCACT 1205

SEGGCTGGACCTGGCGCAGGAAGCCAAAGAGACTGGGCCTAGGCCAAGGAGTTCCC 136 

dard; cDNA to mRNA; 282 BP

A single-stranded DNA (or its complementary strand or the corresp cstranded DNA) which comprises one of the 7837 "GS" sequences give AAT19001-T26817 and which is able to hybridise to part of human g DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences we obtained from 3'-directed cDNA libraries prepared from various huritiseus; synthesis of CDNA was initiated from the 3'-end of mRNA poly!(T) as the sole primer. Since the 3'-untranslated sequence with specific mRNAs a Bach library is constructed so as to reflect accurately the relative abundance of different mRNAs in the partic in a cDNA library can be determined (esp. using primers and probe derived from the GS sequences) as a means of diagnosing abnormal Single-stranded DNA for identifying gene signatures - isolated fradirected human cDNA library that reflects relative abundance of  $\alpha$ Gene signature; messenger RNA; mRNA; relative abundance; frequency human; cloning; mapping; non-biased library; diagnosis; detection, cell typing; abnormal cell function; ss. Claim 1; Page 1067; 2245pp; Japanese. Human gene signature HUMGS03761. mRNA in specific human tissues. 94WO-JP001916. 93JP-00355504. (first entry) Okubo K; (MATS/) MATSUBARA K. (OKUB/) OKUBO K. WPI; 1995-206931/27. Homo sapiens. W09514772-A1. Matsubara K, 11-NOV-1994; 12-NOV-1993; 01-JUN-1995. 27-AUG-1996 

1146 CATTGTGTTCACTGTACTCTGTGGCCAAGGATGGGTCCAGAAGACCCCCACTTCAGG Length 282; 0; Indels DB 2; Les 5.4e-25; 5.5%; Score 76; DB 100.0%; Pred. No. 5.4 itive 0; Mismatches Local Similarity 100. hes 76; Conservative Query Match Best Local S Matches

Seguence 282 BP; 80 A; 62 C; 69 G; 66 T; 0 U; 5 Other;

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36 carrigraricacreracreresescaassareserccasaasaccecacreses 1206 AAGAGGGCTGGACCT 1221 96 AAGAGGGGCTGGACCT RESULT 16 g à d

15-JAN-2004 (first entry) ADC97713;

ВР

ADC97713 standard; cDNA; 1239

ADC97713

Murine FL-TWEAK coding sequence. XEXEX

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cell death;
                                                                                                                                                               nal tract disease; pancreatic disease;
organ disease; neural disease; cartilage disease;
connective tissue disease; cellular death; hepatotropic;
XK; TNF relatedness and weak ability to induce c
prosis Factor; TWEAK; fibrosis; cardiac disease;
lung disease; kidney disease; skin disease;

    gastrointestinal; osteopathic; gene; ss.

                                                                                                                          le disease; adipose tissue disease;
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"FL-TWEAK" Location/Qualifiers /product=

2003WO-US011350.

2002US-0371611P

IN INC.

Hahm K; Zheng T, kubowski A,

256/78.

WEAK-related condition, e.g. liver, gastrointestinal, kidney, atic, cartilage or neural tissue condition in a subject annistering to the subject a TWEAK agonist or antagonist.

ID NO 2; 120pp; English

of fibrosis, cardiac disease, liver disease, lung disease, se, skin disease, skeletal muscle disease; adipose tissue irointestinal tract disease; pancreatic disease; reproductive p; neural disease; cartilage disease; bone disease; sissue disease; callular death; and a pathological condition expressing a TWEAK receptor. sequence is the coding sequence for murine transmembrane FLslatedness and weak ability to induce cell death, where TNF
srosis Factor). TWEAK is a member of the TNF family. TWEAK
integonists are useful for treating a TWEAK-related

BP; 249 A; 386 C; 331 G; 273 T; 0 U; 0 Other;

165 GCCGCCCGTCGGAGCCAAGAGGCGGAGGCGCCCGGGGGGAGCCGGGCACCGCCTG Gaps 0; DB 9; Length 1239; 2e-19; 0; Indels 100.0%; Preu. 4.7%; Score 64; Conservative

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64

ndard; DNA; 60 BP

(first entry)

transcript detection oligonucleotide SEQ ID NO:31596.

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription ugenome, useful for detecting tissue-, pathology-, and development Human, mouse, rat, splice transcript, detection, RNA transcript, splice variant, transcriptome, oligonucleotide library, ss. Faigler S; Mintz L, Mintz E, 20-JUL-2001; 2001WO-IB001903. 28-JUL-2000; 2000US-0221607P. 02-MAY-2001; 2001US-0287724P. Wasserman A, (COMP-) COMPUGEN INC. WPI; 2002-257383/30. WO200210449-A2 Homo sapiens. 07-FEB-2002 Shoshan A, 

The present invention describes oligonucleotide libraries for det messenger RNAs that populate a (sub-)transcribtome, where the (st present inventione comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises oligonucleotides, each capable of hybridising selectively to a sc messenger RNAs transcribed from a given transcription unit of the which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a contract of the sample, in expression profilling studies, in qualitative plological sample, in expression profilling studies, in qualitative cuantitatively characterishing the corresponding transcriptome, and detecting RNA transcripts and splice variants of human or animal cuantitatively characteristing the corresponding transcriptome, and pathology-specific genes such as those genes only expressed pecific tissue under a specific pathological condition; to detection variants of a transcriptome of a patient suffering from a particuation of the sorder. ABN27253 to ABN59589 represent oligonucleotide sequence rates, humans and mice, which are used in the exemplification of the particual or present invention. When the exemplification of the present invention. of the printed specification, but was obtained in electroni directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences Example 1; SEQ ID NO 31596; 47pp; English specific genes.

Sequence 60 BP; 13 A; 16 C; 17 G; 14 T; 0 U; 0 Other;

Length 60; 0; Indela 1.7e-17; DB 6; 100.0%; Pred. No. 1.7 ive 0; Mismatches Score 60; 4.48; 60; Conservative Local Similarity Query Match Matches

1145 GCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCACTTCA 1 GCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCACTTCA

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ABN41049 standard; DNA; 60 (first entry) 15-JUL-2002 ABN41049; RESULT 18 ABN41049 

BP.

Human spliced transcript detection oligonucleotide SEQ ID NO:137

Human; mouse; rat; splice transcript; detection; RNA transcript;

REFRESHERS

transcriptome; oligonucleotide library; ss.

001MO-IB001903.

20-JUL-2001; 2001WO-IB001903.

WO200210449-A2. Homo sapiens.

07-FEB-2002

000US-0221607P 001US-0287724P

Faigler S; Mintz L, щ Mintz sserman A,

octide libraries comprising oligonucleotides which bridize to mRNAs transcribed from a transcription unit of a for detecting tissue-, pathology-, and developmental-

ID NO 13797; 47pp; English.

i. The libraries may also be used as specialised miniletect transcripts of a sub-transcriptome under a particular
pathological state, and so allowing the detection of tissue
ny-specific genes such as those genes only expressed in
le under a specific pathological condition, to detect
specific genes; and to detect RNA transcripts and splice
transcriptome of a patient suffering from a particular
(723 to ABNS589 represent oligonucleotide sequences from
und mice, which are used in the exemplification of the
ion. N.B. The sequence data for this patent did not form
'inted specification, but was obtained in electronic format
WIPO at ftp.wipo.int/pub/bublished\_pct\_sequences vention describes oligonucleotide libraries for detecting that populate a (sub-)transcriptome, where the (sub-)comprises messenger RNAs transcribed from multiple units that populate a genome. The library comprises several les, each capable of hybridising selectively to a set of transcribed from a given transcription unit of the genome, one or more messenger RNA splice variants. The libraries are useful for detecting mRNAs from a ple, in expression profiling studies, in qualitatively or characterising the corresponding transcriptome, and in transcripts and splice variants of human or animal

'; 17 A; 15 C; 15 G; 13 T; 0 U; 0 Other;

0; Gaps DB 6; Length 60; 0; Indels Score 60; DB 6; Le Pred. No. 1.7e-17; 4.4%; bcc. 100.0%; Pred. No. . . . . . 0; Mismatches nservative

0;

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ATGTGAGGGGGGAGAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTT 1322 9 

lard; DNA; 60 BP.

(first entry)

transcript detection oligonucleotide SEQ ID NO:31341.

Human spliced transcript detection oligonucleotide SEQ ID NO:3133

(first entry)

15-JUL-2002

ABN58591;

ABN58591 standard; DNA; 60 BP.

RESULT 20 ABN5859. Human, mouse, rat, splice transcript, detection, RNA transcript, splice variant, transcriptome, oligonucleotide library; ss.

rat; splice transcript; detection; RNA transcript; ;; transcriptome; oligonucleotide library; ss.

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messenger RNAs that populate a (sub)transcriptome, where the (sul

C) transcriptome comprises messenger RNAs transcribed from multiple

transcription units that populate a genome. The library comprises

oligonucleotides, each capable of hybridising selectively to a sel

messenger RNAs transcribed from a given transcription unit of the

which encodes one or more messenger RNA splice variants. The

oligonucleotide libraries are useful for detecting mRNAs from a

piological sample, in expression profiling studies, in qualitative

quantitatively characteriaing the corresponding transcriptome, au

detecting RNA transcripts and splice variants of human or animal

transcriptomes. The libraries may also be used as specialised min

libraries to detect transcripts of a sub-transcriptome under a pa.

C biological or pathological state, and so allowing the detection or

and pathology-specific genes such as those genes only expressed

specific tissue under a specific pathological condition; to detect
                                                                                                                                                                                                                                                                                                                                                                                                                           New oligonuclectide libraries comprising oligonuclectides which selectively hybridize to mRNAs transcribed from a transcription un genome, useful for detecting tissue-, pathology-, and developments specific genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental specific genes; and to detect RNA transcripts and si variants of a transcriptome of a patient suffering from a particul disorder. ABN27253 to ABN59589 represent oligonucleotide sequence rate, humans and mice, which are used in the exemplification of tl present invention. N.B. The sequence data for this patent did not part of the printed specification, but was obtained in electronic directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     979 GGCTGCCTGGGCCTGTTCACGTGTTTTCCATCCCACATAAATACAGTATTCCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGCTGCCTGGCCTGTTCACGTGTTTTCCATCCCACATAAAATACAGTATTCCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes oligonucleotide libraries for det
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

4.4%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.7e-17;
Matches 60; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                   Mintz E, Mintz L, Faigler S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 60 BP; 12 A; 19 C; 10 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 31341; 47pp; English.
                                                                                                                                                                                                            28-JUL-2000; 2000US-0221607P. 02-MAY-2001; 2001US-0287724P.
                                                                                                                                                                                                                                                                                                                                   Shoshan A, Wasserman A,
                                                                                                                                                                                                                                                                                   (COMP-) COMPUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-257383/30.
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2001WO-IB001903.

20-JUL-2001; 2001WO-IB001903

WO200210449-A2.

07-FEB-2002

2000US-0221607P

2001US-0287724P.

Faigler S; Mintz L, Mintz E, asserman A,

eotide libraries comprising oligonucleotides which sybridize to mRNAs transcribed from a transcription unit of a l for detecting tissue-, pathology-, and developmental-

Q ID NO 31339; 47pp; English

nvention describes oligonucleotide libraries for detecting a that populate a (sub-)transcriptome, where the (subwe comprises messenger RNAs transcribed from multiple
units that populate a genome. The library comprises several
des, each capable of hybridising selectively to a set of
a transcribed from a given transcription unit of the genome,
one or more messenger RNA splice variants. The
de libraries are useful for detecting mRNAs from a
miple, in expression profiling studies, in qualitatively or
y characterising the corresponding transcriptome, and in
transcripts and splice variants of human or animal
s: The libraries may also be used as specialised mini
detect transcripts of a sub-transcriptome under a particular
pathological state, and so allowing the detection of tissue
yy specific genes; and to detect confittion; to detect
specific genes; and to detect for a for a for a for a splice
specific genes; and to detect for a for a for a for a for a for a splice ntion, N.B. The sequence data for this patent did not form printed specification, but was obtained in electronic format transcriptome of a patient suffering from a particular 127253 to ABNS9589 represent oligonucleotide sequences from which are used in the exemplification of the WIPO at ftp.wipo.int/pub/published\_pct\_sequences mice,

P; 17 A; 15 C; 15 G; 13 T; 0 U; 0 Other;

0; Gaps 4.4%; Score 60; DB 6; Length 60; 00.0%; Pred. No. 1.7e-17; 0; Indels 100.0%; Pred. ... Conservative

AAATGTGAGGGGCGAGAAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTT 1322 9 MATIGEGGGGGGGGAGAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTT

ndard; DNA; 60 BP.

(first entry)

d transcript detection oligonucleotide SEQ ID NO:31597.

, rat, splice transcript, detection, RNA transcript, nt, transcriptome; oligonucleotide library, ss.

The present invention describes oligonuclectide libraries for det messenger RNAs that populate a (sub-)transcribcome, where the (stranscriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises oligonuclectides, each capable of hybridising selectively to a selection ender the configuration unit of the which encodes one or more messenger RNA splice variants. The oligonuclectide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitative quantitatively characterising the corresponding transcriptome, and quantitatively characterising the corresponding transcriptome, and cutenting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised militaries to detect transcripts of a sub-transcriptome under a pictological state, and so allowing the detection capacitic tissue under a specific pathological condition; to detect specific tissue under a specific pathological condition; to detect specific tissue under a specific pathological condition; to detect specific tissue under a specific pathological condition; to detect specific genes; and to detect RNA transcripts and so variants of a transcriptome of a patient suffering from a particut disorder. ABN27531 to ABN5589 represent oligonucleotide sequence. New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription  $\upsilon$  genome, useful for detecting tissue-, pathology-, and development rats, humans and mice, which are used in the exemplification of tpresent invention. N.B. The sequence data for this patent did not part of the printed specification, but was obtained in electronic directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences Mintz E, Mintz L, Faigler S; Sequence 60 BP; 17 A; 15 C; 15 G; 13 T; 0 U; 0 Other; Example 1; SEQ ID NO 31597; 47pp; English. 28-JUL-2000; 2030US-0221607P. 02-MAY-2001; 2001US-0287724P. Shoshan A, Wasserman A, (COMP-) COMPUGEN INC. WPI; 2002-257383/30. specific genes 

Length 60; 4.4%; Score 60; DB 6; Le ilarity 100.0%; Pred. No. 1.7e-17; Conservative 0; Mismatches 0; Local Similarity les 60; Conserv Query Match Matches

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; 0

RESULT 22 AAX56002

AAX56002; 

AAX56002 standard; DNA; 50 BP.

(first entry) 15-JUL-1999 Human tumour necrosis factor Apo-3 ligand probe SEQ ID NO:4.

Human; tumour necrosis factor; Apo-3 ligand; lymphotoxin; apopto NF-kappaB-dependent transcription; JNK/SAPK-dependent response; hybridisation; probe; ss.

Synthetic.

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98WO-US021407
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97US-0062037P 97US-0069862P

TECH INC.

3- ligand (a tumor necrosis factor) homologue.

evention describes a human tumour necrosis factor (TNF) and omologue designated Apo-3 ligand. Apo-3 ligand has civity. Apo-3 ligand can be used to induce apoptosis in cer cells, to induce NF-kappaB-dependent transcription and /SAPK-dependent responses in mammalian cells. The present seents an Apo-3 ligand probe, which is used in an example ent invention

CCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGG 50

2.

dard; DNA; 50 BP

DNA probe.

; antitumour; tumour; therapy; cytostatic; breast cancer; r. renal cancer; colorectal cancer; uterine cancer; er; lung cancer; bladder cancer; us system cancer; melanoma; leukaemia; neoplasm; probe; ss.

99WO-US028565

ĸ Pitti Marsters SA,

382/24.

※公司等用等用等所需要的等等。

Je 36; 74pp; English

P; 10 A; 18 C; 13 G; 9 T; 0 U; 0 Other;

0; Gaps CCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGG 576 Score 50; DB 2; Length 50; Pred. No. 7.7e-13; 0; Indels 100.0%; Pred. wv. 3.6%; onservative arity

(first entry)

99US-0134287P. 99US-0144758P. 99US-0145698P. 99WO-US021090. 99WO-US021547. 99WO-US005028. 99US-0130232P. 99US-0131445P. 38US-0113296P

(GETH ) GENENTECH INC.

Gurney AL, Marsters SA; Godowski PJ, J, Goddard A, Godo
Pitti RM, Wood WI; Ashkenazi AJ, Napier MA, P

WPI; 2000-442668/38.

Novel composition to inhibit neoplastic cell growth or for treati in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or PRO866.

Example 3; Page 98; 172pp; English.

The present sequence is that of a DNA probe based on an isolated expressed sequence tag showing homology to human Apo-2 ligand. The was used to screen a human foetal kidney cDNA library to identify clone DNA30879-115.2 (see AAA49717), which encodes human artitumou protein PRO207 (see AAA95138). A claimed method for inhibiting the for a tumour cell comprises exposing the tumor cell to PRO179, PRO PRO30, PRO21, PRO21, PRO24, PRO388, PRO31, PRO509 or PRO866 (see AAY55337-49). The tumour is especially brea ovarian, renal, colorectal, uternie, prostate, lung, bladder or nervous system cancer, melanoma or leukaemia. Nucleic acids encod PRO179 etc. are used in the recombinant production of antitumour polypeptides

Sequence 50 BP; 10 A; 18 C; 13 G; 9 T; 0 U; 0 Other;

Ö . 0 3.6%; Score 50; DB 3; Length 50; 100.0%; Pred. No. 7.7e-13; iive 0; Mismatches 0; Indels Local Similarity 100. nes 50; Conservative Query Match Matches

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RESULT 24

ABK40292 standard; DNA; 50 BP. ABK40292

ABK40292;

15-JUL-2002 (first entry)

Oligonucleotide probe for human PRO207 DNA.

Human, PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disciplammatory disorder; immune disorder; angiogenic disorder; cytc neuroprotective; probe; ss.

Homo sapiens.

26-JUL-2001.

WO200153486-A1

2000WO-US003565 11-FEB-2000; 99WO-US005028

08-MAR-1999;

990S-0123972P. 990S-0133459P. 99WO-US012252. 99US-0140650P. 99US-0140653P. 11-MAR-1999 11-MAY-1999 22-JUN-1999 22-JUN-1999 20-JUL-1999 02-JUN-1999

99US-0145698P, 99US-0146222P, 99US-0149395P, 99US-0151689P. 26-JUL-1999 28-JUL-1999 31-AUG-1999 

99WO-US020111 99WO-US021090 01-SEP-1999; 15-SEP-1999;

Hillan KJ;

Stone DM;

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.nvention relates to the isolation of novel human PRO (AAU86128-AAU86162) and the polynucleotide sequences or The PRO polypeptides, agonists, antagonists or anti-PRO re useful for treating benign or malignant tumours (e.g. ', bladder, breast, etc), leukaemias and lymphoid other disorders such as neuronal, glial, astrocytal, glandular, macrophagal, stromal and blastocoelic disorders, immune and angiogenic disorders. The polynucleotide immune and angiogenic disorders. The present sequence probe useful in gene therapy. The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    egne expression profiling, allograft rejection,
sie, congestive heart failure, systemic lupus erythematosus,
cthritis, osteoarthritis, cytomegalovirus, infection, probe,
                                                                                                                                                                                                                                                                                                                                                                      ucleic acids encoding PRO polypeptides, useful for treating .ignant tumors, leukemias and lymphoid malignancies, angiogenic and immunologic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGG 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  te gene expression profiling probe SEQ ID NO 2558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.6%; Score 50; DB 6; Length 50; 00.0%; Pred. No. 7.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P; 10 A; 18 C; 13 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                     AL,
V,
                                                                                                                                                                                                     Gurney A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arity 100.0%; Pred. ....
                                                                                                                                                                                                     d A, Godowski PJ,
Pitti RM, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ge 109; 302pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-US047856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0241994P
2001US-0296764P
99WO-US028313.
99WO-US028301.
                                                           99WO-US028634.
                                                                                      2000WO-US000219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dard; DNA; 50
                                                                                                                                                                                                  Goddard A,
                                                                                                                                                                                                                                   Pan J, E
Wood WI;
                                                                                                                                            TECH INC.
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Gaps

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Phillips J;

Prentice J,

K, Matcuk G, Altman P, P) Quertermous T, Johnson F;

6525/68

ARDIA INC. , Fry K, ard R, On

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The invention relates to a system for detecting gene expression, comprises one or two isolated DNA molecules that detect expressic gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disea predicting therapeutic outcome, determining prognosis for a patic predicting disease complications in an individual or monitoring it treatment in an individual. The diseases include cardiac allogation, kidney allografit rejection, liver allogatic rejection, atherosclerosis, congestive heart failure, systemic lupus erythem rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour necrosis factor receptor; signal transducer molecule; TNF developmental abnormality; gestational abnormality; prostate G APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; cytoplasmic domain; immunogen; antibody preparation; breast carc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Tumor Necrosis Factor family receptor polypeptides and ligan useful for diagnosis and treatment of prostate cancer and develo or gestational abnormalities.
        New system for leukocyte expression profiling, diagnosing a disesmonitoring (the rate of) progression of a disease, e.g. atherosol or congestive heart failure, comprises diagnostic oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                1196 TTCAGGCACTAAGAGGGCCTGGACCTGGCGGCAGGAAGCCAAAGAGACTG 1245
                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTG 50
                                                                                                                                                                                                                                                                                                                                                               Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                               Sequence 50 BP; 14 A; 11 C; 19 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                               DB 6; Le:
. 7.7e-13;
                                                                                                                                                                                                                                                                                                                                                   3.6%; Scor. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "TNRL3"
                                                                             Claim 1; Page 408; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX23425 standard; DNA; 701 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US018393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00924634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ø
                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis; mouse; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-205191/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW93591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse TNRL3 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaudhary PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9911791-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX23425;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX23425
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Fig 13B; 156pp; English.
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n describes isolated Tumor Necrosis Factor (TNF) family peptides: APO4, APO6, APO8 and APO9 or their active disolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or fragments. APO4 is useful for diagnosing prostate cancer by evels of APO4 in an individual. Prostate cancer can also be APO4 selective binding agents linked to a therapeutic polypeptides are also useful for identifying selectives, useful in diagnosis/treatment of disease by binding of polypeptide/active fragment which is extracellular, or the cell surface. The binding is preferably performed in lypeptides/active fragments are also useful for screening and antagonists by binding and observing the changer in APO4 disease are also identified using APO4 polypeptides/active APO4 signal transducer molecules that specifically interact asmic domain of APO4 and detecting a change in level of APO4 method is performed in vivo or in vitro. APO polypeptides method is performed in vivo or in vitro. APO polypeptides agnosis/treatment of developmental or gestational duced apoptosis

BP; 139 A; 210 C; 203 G; 149 T; 0 U; 0 Other;

Gaps . 0 3.4%; Score 46; DB 2; Length 701; 100.0%; Pred. No. 5e-11; ive 0; Mismatches 0; Indels onservative

0;

TGGGCTCTACTACCTGTACTGTCAGGTGCACTTTGATGAGGG 620 resecteractacerstratersecretactricalsases 401

dard; cDNA; 1168 BP.

(first entry)

tumour necrosis factor related ligand (TRELL) gene.

necrosis factor related ligand; tnf; treatment; cancer; sease; immune system; stimulation; suppression; on; ds.

/note= "tumour necrosis factor related ligand" Location/Qualifiers 619. \*tag=

96US-0023541P. 96US-0028515P. 97WO-US013945 97US-0040820P GENEVA FACULTY MEDICINE.

e Y, Browning JL;

619/13

Tumour necrosis factor related ligand - useful for, e.g. treating auto-immune disease and immune responses to tissue grafts.

Claim 2; Page 45-46; 69pp; English.

The sequence is that encoding mouse tumour necrosis factor relate (TRELL). TRELL or active fragments can be included with a carrier pharmaceutical compositions to treat cancer, autoimmune diseases immune responses to tissue grafts, or to stimulate or suppress the system. It is useful to screen for TRELL receptors, by labelling detectable label and screening compositions for binding. Agents interfering with TRELL receptor binding can also be screened for, then be administered, optionally with interferon-gamma, to induct death or treat, suppress or alter immune responses (especially in human adenocarcinoma cells) involving a signal pathway between TR its receptor. The DNA sequence can be used in gene therapy for TR related disorders in mammals (especially humans), e.g. tumours, autoimmune and inflammatory diseases or inherited genetic disorder introducing into cells, and expressing, therapeutically effective of a vector, e.g. a virus comprising a gene encoding TRELL. It me be of use in the preparation of prepare probes for screening therapeutically synthetic DNAs for TRELL-encoding sequences and for antist the preparation of prepare probes for screening cherapy 

Sequence 1168 BP; 242 A; 360 C; 298 G; 268 T; 0 U; 0 Other;

.; 0 3.4%; Score 46; DB 2; Length 1168; 100.0%; Pred. No. 4.9e-11; ative 0; Mismatches 0; Indels Query Match
Best Local Similarity luv...
Local Similarity luv...
Local Similarity

399 GGCCTGGCCTCTACTACCTGTCAGGTGCACTTTGATGAGGG 444 ð g

RESULT 28

ABX37032 standard; cDNA; 408 BP ABX37032

20-FEB-2003 (first entry)

gene analysis; cattle breeding.

Bos Taurus.

US2002137139-A1.

HALL SEE STANDER STAND

Tao N, Byatt JC, Mathialagan N,

WPI; 2003-110599/10.

New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and ar cattle breeding, or for genetically improving cattle.

575 GGCTGGGCTCTACTACTGTACTGTCAGGTGCACTTTGATGAGGG 620

ABX37032;

Bovine EST associated with lactation/muscle/fat deposition #2197

Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identific

26-SEP-2002.

12-JAN-1999; 99US-0115707P. 11-JAN-2000; 2000US-00480902. (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N. (TAON/) TAO N.

24-SEP-2001; 2001US-00960352.

Warren WC;

WARREN W C.

(WARR/)

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muscle and fat deposition (designated LMFD), derived from the LMFD nucleic acid can specifically hybridise to a second molecule comprising any of 15112 nucleotide sequences, ABX34836-ABX49947, or complements of them. Also included are sformed cell having a nucleic acid comprising an LMFD nucleic to a promoter and a 3' non- translated sequence that the cell to cause termination of transcription and addition lated ribonucleotides to a 3' end of the mRNA molecule; and ing a level or pattern of a molecule in a bovine cell or ising a level or pattern of a molecule in a bovine cell or ising a level or pattern of a molecule in a bovine cell or ising a level or pattern of a molecule in a bovine cell or ising a nucleic acid sequences or its complement or fragment) with a y nucleic acid sequences or its complement or fragment) with a public acid molecule obtained from the bovine cell or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y nucleic acid permits the detection of the molecule; and (b) e level or pattern of the complementary nucleic acid, where nof the complementary nucleic acid is predictive of the term of the molecule lands of the alevel or pattern of a molecule in a bovine cell or tissue. For genome mapping, gene identification and analysis, cattle paration of constructs for use in cattle gene expression, or lly improving cattle. The present sequence is one of the LMFD EST (expressed sequence tag) nucleic acids. Note: The ence was not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hybridisation between the marker nucleic acid and the nucleic acid permits the detection of the molecule; and (b) level or pattern of the complementary nucleic acid, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rmat from the USPTO web site:
.gov/sequence.html?DocID=20020137139
ID NO 2197; 245pp; English
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; 0 2.6%; Score 36; DB 7; Length 408; 0; Indels BP; 78 A; 136 C; 137 G; 57 T; 0 U; 0 Other; Pred. No. 2.3e-06; 100.0%; Pred. ... Conservative

GGCCTGCCTCGGCCTCCTGCTGGCCGTGGTCAG 233 GGCCTGCCTCGCCTCCTGCTGGCCGTGGTCAG 152

ndard; DNA; 412 BP

ated gene, SEQ ID 1352 (first entry)

expression profile; hepatotoxicity; liver; ng; toxicity assay; ds gene

2002US-00060087. 2002US-0364045P. 2002US-0364055P. 2003WO-US003194. 2002US-0436643P

LOGIC INC.

Elashoff M; Castle A, 'n Johnson K, Higgs Porter M, 9530/65.

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The present invention relates to a method for predicting a toxic of a compound. The method comprises preparing a gene expression of a tissue or cell sample exposed to the compound, and comparing gene expression profile to a database comprising SEQ ID 1-4925, differential expression of the gene indicates at least one toxic The method is useful for predicting at least one toxic effect of compound, predicting hepatotoxicity or the progression of a toxic of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathway compound modulates in a cell, and identifying an agent that module present invention using a database of genes having liver toxin-idefferential expression, are useful in identifying proxicity mark
Predicting a toxic effect of a compound, useful in identifying t markers in liver tissues or cells for drug screening and toxicit comprises preparing gene expression profile of tissue or cells e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               liver tissues or cells for drug screening and toxicity assays. ^{\rm N} sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification, but was obtained in electronic format directly fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                    Claim 1; SEQ ID NO 1352; 1156pp; English.
                                                                                     the compound.
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2.1%; Score 29; DB 9; Length 412; 100.0%; Pred. No. 0.0043; Live 0; Mismatches 0; Indels 29; Conservative Query Match Best Local Similarity Matches

Sequence 412 BP; 104 A; 87 C; 116 G; 105 T; 0 U; 0 Other;

ö

1336 TATTTTTTTTTTTTTTGTGACAAATGTT 1364 67 TATTTTTATTATTATTGTGACAAAATGTT 39 d ð

RESULT 30

· 0

ABK40356 standard; DNA; 26 BP. ABK40356,

ABK40356;

Reverse PCR primer for gene amplification analysis of human PROS 15-JUL-2002 (first entry)

Human; PRO; benign tumour; malignant tumour; lymphoid malignancy leukaemia, neuronal disorder; stromal disorder; blastocoelic disinflammatory disorder; immune disorder; angiogenic disorder; cyt neuroprotective; PCR; primer; ss.

WO200153486-A1.

26-JUL-2001.

11-FEB-2000; 2000WO-US003565

990S-0123972P. 99US-0133459P. 99WO-US012252. 99US-0140650P. 99US-0140653P. 99US-0146222P 99US-014569BP 11-MAR-1999; 11-MAY-1999; 02-JUN-1999; 22-JUN-1999; 22-JUN-1999; 20-JUL-1999; 26-JUL-1999 08-MAR-1999 17-AUG 

99WO-US020111. 99WO-US021090. 99WO-US028313. 99US-0149395P 01-SEP-1999; 15-SEP-1999; 30-NOV-1999;

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99WO-US028634.
99WO-US028634.
2000WO-US000219.
                                                                           Goddard A,
                                                   FECH INC
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Hillan KJ; Stone DM; Gurney AL, Smith V, l A, Godowski PJ, Pitti RM, Roy MA, Pan J, P Wood WI;

ucleic acids encoding PRO polypeptides, useful for treating ignant tumors, leukemias and lymphoid malignancies, angiogenic and immunologic disorders.

age 140; 302pp; English.

윘첉믡읡밁읩읩댬댬댬뜐씂뿂뚔큺둺뮵첉쒖푽믔믔믔잗뺚찞궦궦

nvention relates to the isolation of novel human PRO (AAU86128-AAU86162) and the polynucleotide sequences. The PRO polypeptides, agonists, antagonists or anti-PRO e useful for treating benign or malignant tumours (e.g., bladder, breast, etc), leukaemias and lymphoid other disorders such as neuronal, glial, astrocytal, glandular, macrophagal, stromal and blastocoelic disorders, immune and angiogenic disorders. The polynucleotide also useful in gene therapy. The present sequence PCR primer used in the methods of the present invention

P; 7 A; 1 C; 9 G; 9 T; 0 U; 0 Other;

Gaps 0; 1.9%; Score 26; DB 6; Length 26; 0; Indels Pred. No. 0.12; onservative

· 0

ICCCACATAAATACAGTATICC 1030 rccacaraaracagrafic 1

à

dard; DNA; 140 BP

(first entry)

ssion-related sequence, SEQ ID 542

irucide, apoptotic; gene therapy; tumour suppression; ion; apoptosis; virus resistance; viral infection; tumour; tive disease; ds.

2002WO-FR000543.

ULAR ENGINES LAB 2001FR-00001925.

Susini L; Tuijnder M, Атвоп К,

cid encoding a translationally controlled tumor protein, eating, preventing and diagnosing viral, tumor or diseases.

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The present invention relates to novel nucleic acid sequences (AE MEZ79313), which are involved in the molecular pathways of tumour suppression, tumour reversion, apoptosis and/or virus resistance. sequences are also useful for treatment or prevention of viral, the sed diseases, and also for diagnosis and prognotese are also useful for treatment or prevention of viral, the secuence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tumour suppressor; virucide; cytostatic; nootropic; neuroprotective; neuroleptic; gene therapy; tumour suppression; tumour reversion; apoptosis; viral resistance; viral infection; cell degeneration; Alzheimer's disease; schizophrenia; cancer; o
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0
                                                                                                                                                                                             1.9%; Score 26; DB 7; Length 140; 100.0%; Pred. No. 0.11; ative 0; Mismatches 0; Indels
                                                                                                                                                                 Sequence 140 BP; 43 A; 23 C; 28 G; 46 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                      67 ATGTCATTGTTAGACTTTGAAATTTC 42
                                                                                                                                                                                                                                                     1 ATGTCATTGTTAGACTTTGAAATTTC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human oligonucleotide SEQ ID 542.
             Disclosure; Page; 45pp; French.
                                                                                                                                                                                                                                                                                                                                                      ABZ09382 standard; DNA; 140
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                         26; Conservative
                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                ABZ09382;
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                          RESULT 32
                                                                                                                                                                                                                                                                                                                                       ABZ09382/
X X X C C C C C C C X X X
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The present invention relates to human oligonucleotides (Ab208841 AB209860). The expression of the oligonucleotides is implicated is suppression or reversion, apoptosis and/or viral resistance. The oligonucleotides are useful for preventing and/or treating viral infection, tumour development and cell degeneration (e.g. Alzheim New human nucleic acid, useful for diagnosis, prognosis and treat e.g. of tumors, also related vectors, transformed cell, polypepti antibodies. disease and schizophrenia), especially cancer Susini L; Disclosure; Page 120; 189pp; French. Tuijnder M, Amson R, WPI; 2003-032204/03. Telerman A,

(MOLE-) MOLECULAR ENGINES LAB 13-FEB-2001; 2031FR-00001925. 20-MAR-2002; 2032FR-00003459

FR2822475-A1. Homo sapiens

27-SEP-2002

Ö 0 Query Match 1.9%; Score 26; DB 7; Length 140; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 26; Conservative 0; Mismatches 0; Indels Sequence 140 BP; 43 A; 23 C; 28 G; 46 T; 0 U; 0 Other;

56 CATTGTTAGACTTTGAAATTTC

ndard; DNA; 145 BP

(first entry)

ession-related sequence, SEQ ID 15.

virucide; apoptotic; gene therapy; tumour suppression; sion; apoptosis; virus resistance; viral infection; tumour; ative disease; ds.

52

2002WO-FR000543.

2001FR-00001925.

CULAR ENGINES LAB

Susini L; Tuijnder M, Amson R,

acid encoding a translationally controlled tumor protein, reating, preventing and diagnosing viral, tumor or diseases.

Page; 45pp; French.

invention relates to novel nucleic acid sequences (ABZ78294-hich are involved in the molecular pathways of tumour tumour reversion, apoptosis and/or virus resistance. The e also useful for treatment or prevention of viral, tumour enerative diseases, and also for diagnosis and prognosis of so. Note: The sequence data for this patent is not in the printed specification but is based on sequence supplied by the European Patent Office

BP; 51 A; 28 C; 23 G; 43 T; 0 U; 0 Other;

ö Score 26; DB 7; Length 145; 0; Indels 0.11; 100 0%; Prec. ... 1.9%; Conservative larity

0

Gaps

TCATTGTTAGACTTTGAAATTTC 26 rearretragactrigaaarric 99

ndard; DNA; 145 BP.

(first entry)

ession-related seguence, SEQ ID 135.

virucide; apoptotic; gene therapy; tumour suppression; sion; apoptosis; virus resistance; viral infection; tumour;

suppression, tumour reversion, apoptosis and/or virus resistance sequences are also useful for treatment or prevention of viral, and cell degenerative diseases, and also for diagnosis and progn these diseases. Note: The sequence data for this patent is not represented in the printed specification but is based on sequencinformation supplied by the European Patent Office New nucleic acid encoding a translationally controlled tumor prouseful for treating, preventing and diagnosing viral, tumor or degenerative diseases. The present invention relates to novel nucleic acid sequences (A ABZ79313), which are involved in the molecular pathways of tumou Sequence 145 BP; 51 A; 28 C; 23 G; 43 T; 0 U; 0 Other; Susini L; Tuijnder M, Disclosure; Page; 45pp; French. cell degenerative disease; ds. (MOLE-) MOLECULAR ENGINES LAB. 13-FEB-2002; 2002WO-FR000543. 13-FEB-2001; 2001FR-00001925. Telerman A, Amson R, WPI; 2003-058286/05. WO200264731-A2 Unidentified. 22-AUG-2002 

1 ATGTCATTGTTAGACTTTGAAATTTC 26 74 AIGICALIGITAGACTITGAAATITC 99 à 셤

.. o

1.9%; Score 26; DB 7; Length 145; 100.0%; Pred. No. 0.11; ive 0; Mismatches 0; Indels

Best Local Similarity 100.0%; Pr Matches 26; Conservative 0;

Query Match

RESULT 35 ABZ08855

ABZ08855 standard; DNA; 145 BP.

ABZ08855;

(first entry) 16-JAN-2003

Human oligonucleotide SEQ ID 15.

cell degeneration; Alzheimer's disease; schizophrenia; cancer; d Human, tumour suppressor, virucide, cytostatic, nootropic, neuroprotective, neuroleptic, gene therapy, tumour suppression, tumour reversion, apoptosis, viral resistance, viral infection, 

Homo sapiens.

FR2822475-A1

27-SEP-2002.

20-MAR-2002; 2002FR-00003459.

13-FEB-2001; 2001FR-00001925.

MOLE-) MOLECULAR ENGINES LAB SA

Susini L; Telerman A, Amson R, Tuijnder M,

RAFRARNRARKK

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204/03

leic acid, useful for diagnosis, prognosis and treatment,  $_{\rm 3},$  also related vectors, transformed cell, polypeptides and

ige 40; 189pp; French.

땅놈보보통적없첧음음음음음음성였

nvention relates to human oligonucleotides (ABZ08841-e expression of the oligonucleotides is implicated in tumour r reversion, apoptosis and/or viral resistance. The des are useful for preventing and/or treating viral mour development and cell degeneration (e.g. Alzheimer's chizophrenia), especially cancer

BP; 51 A; 28 C; 23 G; 43 T; 0 U; 0 Other;

Gaps ó Score 26; DB 7; Length 145; 0; Indels Pred. No. 0.11; 1.9%; Scc. No. ... 100.0%; Pred. No. ... 0; Mismatches onservative

ò

SATIGITAGACTITGAAATTIC 99 CATTGTTAGACTTTGAAATTTC 26

Ż

dard; DNA; 145 BP

(first entry)

cleotide SEQ ID 135.

suppressor; virucide; cytostatic; nootropic; ve; neuroleptic; gene therapy; tumour suppression; ion; apoptosis; viral resistance; viral infection; tion; Alzheimer's disease; schizophrenia; cancer; ds.

2002FR-00003459.

2001FR-00001925.

##BCXP#F#B#E@@@@axd#a#a#a#a#a#a##FEa##BBBBB##

JLAR ENGINES LAB SA.

Susini L; Tuijnder M, Amson R,

204/03

leic acid, useful for diagnosis, prognosis and treatment, 3, also related vectors, transformed cell, polypeptides and

age 58; 189pp; French.

nvention relates to human oligonucleotides (ABZ08841-e expression of the oligonucleotides is implicated in tumour r reversion, apoptosis and/or viral resistance. The des are useful for preventing and/or treating viral mour development and cell degeneration (e.g. Alzheimer's chizophrenia), especially cancer

BP; 51 A; 28 C; 23 G; 43 T; 0 U; 0 Other;

1.9%; Score 26; DB 7; Length 145;

AA169032/c

RESULT 38

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stranded DNA (or its complementary strand or the corresp stranded DNA) which comprises one of the 7837 "GS" sequences giv AAT19001-T28837 and which is able to hybridise to part of human g DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences we obtained from 3'-directed CDNA libraries prepared from various human g DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences we obtained from 3'-directed CDNA libraries prepared from various human g DNA, CDNA or mRNA is claimed. Since the 3'- untranslated sequence i to a particular mRNA species, almost all the 3'-oriented cONNAs hy with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular mRNA library can be determined (esp. using primers and probe in a cDNA library can be determined (esp. using primers and probe detrived from the GS sequences) as a means of diagnosing abnormal
                                                                                                                                                                                                                                                                                                              Gene signature; messenger RNA; mRNA; relative abundance; frequenc human; cloning; mapping; non-biased library; diagnosis; detection cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single-stranded DNA for identifying gene signatures - isolated fr directed human cDNA library that reflects relative abundance of c
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100.0%; Prec. No.
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                                                                                                                                                                           AAT19717 standard; cDNA to mRNA; 147 BP.
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                                                                                       74 Argreatretragactricaaartre 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 456; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                Human gene signature HUMGS00791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA in specific human tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94WO-JP001916.
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                                                                                                                                                                                                                                              05-JUL-1996 (first entry)
       Best Local Similarity 100.
Matches 26; Conservative
                                                         1 ATGTCATTGTTAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.99
Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsubara K, Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                    WO9514772-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1995.
                                                                                                                                                                                                             AAT19717;
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                                                                                                                                           RESULT 37
                                                                                                                                                             AAT1971
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TITLE JOURNAL REFERENCE

TITLE JOURNAL AUTHORS

3

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CGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCCTTCCTCACCTACTTCGGACTC 37039 CAGCTCTCTGGGCACCCCGGTCCCCTCTGCCCCACCCTCAGCCGCTCTTTGCTCCAGA 36919 STGCACTITGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGT 37219 CTGGCCCTGCGCTGCCTGGAGGAATTCTCAGCCACTGCGGGCGAGTTCCCTCGGGCCC 37159 CAGGITCACTGAGGGGCCCTGGTCTCCCCGCAGTCCTCCCAGGCTGCCGGCTCCCCT 36979 GCCCCTCCTCTAGAGGCTGCCTGGCCTGTTCACGTGTTTTCCATCCCACATAAAT 36859 STATTCCCACTOTTAICTTACAACTCCCCCACCCCACTCCTCCACCTCACTAGCTC 36799 AATCCCTGACCCTTTGAGGCCCCCAGTGATCTCGACTCCCCCCTGGCCACAGACCCC 36739 CCAPATGTGAGGGGGGAGAAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGAT 36559 SCCCTCCCTCTAGAGGCTGCCTGGCCTGTTCACGTGTTTTCCATCCCACATAAAT 1020 STATTCCCACTCTTATCTTACAACTCCCCCACGCCCACTCTCCACCTCACTAGCTC 1080 AATCCCTGACCCTTTGAGGCCCCCAGTGATCTCGACTCCCCCCTGGCCACAGACCCC 1140 SECATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCCACTTCAG 1200 CTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGGCTAGGCCAGGAG 1260 CCAAATGTGAGGGGGGAAAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGAT 1320 780 900 CGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCTTCCTCACCTACTTCGGACTC 840 CAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCACCCTCAGCCGCTCTTTGCTCCAGA 960 CTCCGCCTCTGCCAGGTGTCTGGGCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGG CAGGITCACTGAGGGCCCTGGTCTCCCCACAGTCGTCCCAGGCTGCCGGCTCCCCT CTGGCCCTGCGTGGAGGAATTCTCAGCCACTGCGGCCCAGTTCCCTCGGGCCC IAAAACAGATATTTTTTTTTTTTTTTTTGTGACAAATGTTGTTATTGTG IAAAACAGATATTTTTTTTTTTTTTTTGTGACAAATGTTGATAAATGG 1373

> $\leq$ 6

ases 1 to 218485)
ellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
ellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
elly,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K.,
Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X.,
J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P.,
B., Idol,J.R., Karlins,B., Kwong,P., Laric,P., Lee-Lin,S.-Q.,
pi,R., Maduro,Q.L., Maduro,V.B., Margulies,B.H., Masiello,C.,
ri,B., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E.,
j.A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K.,
C., Stantripop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V., HTG 05-JUN-2003 yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; lia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 470 218485 bp DNA linear HTG 05-JU roglodytes clone RP43-145D13, WORKING DRAFT SEQUENCE, 17 470 470.4 GI:31415893 roglodytes (chimpanzee) roglodytes pieces.

88313

**452**22

Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green, NISC Comparative Sequencing Initiative Unpublished Grovemont Circle, Gaithersburg, MD 20877, USA On Jun 5, 2003 this sequence version replaced gi:26449071 Direct Submission Submitted (05-JUN-2003) NIH Intramural Sequencing Center, Sequencing Center, Submitted (17-JUL-2002) NIH Intramural Sequenc Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 218485) Center: NIH Intramural Sequencing Center Center code: NISC Web site: http://www.nisc.nih.gov Contact: nisc\_zoo@nhgri.nih.gov ----- Project Information Center project name: cms Center clone name: 145D13 ---- Genome Center (bases 1 to 218485) Direct Submission Green, E.D. Green, E.D

AUTHORS TITLE JOURNAL

COMMENT

REFERENCE

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indica order and orientation of each sequence contrig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g. human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associat with a Phrap-derived quality score.

Quality coverage: 12.65x in Q20 bases; agarose-fp Quality coverage: 11.08x in Q20 bases; sum-of-contig Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 215255 bases at least Q30 Consensus quality: 215255 bases at least Q30 Insert size: 190000; agarose-fp Insert size: 216885; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that har provided by the submittor.

\* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

\* 7549 7648: gap of unknown length 7549 31917: contig of 7548 bp in length 7649 31917: contig of 24269 bp in length 7649 31917: contig of 24269 bp in length 7649 31917: contig of 18416 bp in length 7649 35018 50434 50531 gap of unknown length 7649 55375 95374: contig of 44741 bp in length 76598 100088: gap of unknown length 769989 100088 unknown length of 7646 bp in length of 10906 bp in unknown length unknown length 117719: gap of u 128625: contig o 128725: gap of u 143521: contig o gap of contig 117619: 0 109973: 117620 117720 128626 109874 109974

of 14796 bp in length

128726

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murin:
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Submitted (14-OCT-1997) Cell Biology, Biogen, 12 Cambridge Cambridge, MA 02142, USA
3 (bases 1 to 1239)
Chicheportiche, Y., Bixler, S., Tizard, R. and Browning, J.
           52645 GIGCIGGCCTGCGTGCCTGGAGGAATICICAGCCACTGCGGCGAGIICCCTCGG
                                                                                                      52885 CGACAGCTCTCTGGGCACCCGGTCTCTTTGCCCCCACCCTCAGCTGCTCTTTGCTC
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Chicheporitche, Y., Bourdon, P.R., Xu, H., HBu, Y.M., Scott, H. Hession, C., Garcia, I. and Browning, J.L.
TWEAK, a new secreted ligand in the tumor necrosis factor that weakly induces apoptosis
J. Biol. Chem. 272 (51), 32401-32410 (1997)
                                                                                                                                                                                                                                                                                                                                     52825 Trccadgricacrdadgedccrdgrcrccccecadrogrcccaddcrdcccgccrc
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1352 143621: gap of unknown length 150822 contrig of 7211 bp in length 150932: gap of unknown length 150932: gap of unknown length 150932: gap of unknown length 156173: gap of unknown length 187450: contrig of 31277 bp in length 1551 191571: gap of unknown length 1551 191571: contrig of 31277 bp in length 1552 207263: contrig of 15692 bp in length 1572 207263: contrig of 15692 bp in length 2064 207363: gap of unknown length 2064 207363: gap of unknown length 2014 207363: gap of unknown length 2014 20757: contrig of 1680 bp in length 2014 20757: contrig of 8424 bp in length 201667: gap of unknown length 201668 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201668 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap of unknown length 201667: gap 
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/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 683.4; DB 10; Length 1239;
Pred. No. 3.8e-115;
0; Mismatches 221; Indels 70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="ligand in the TNF family; secreted protein"
                                                                   .dge, MA 02142, USA
ne update by submitter
130, 2003 this sequence version replaced gi:2707220.
Location/Qualifiers
                                        12
                           ted (30-JUL-2003) Cell Biology, Biogen,
                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:10090"
/cell_type="peritoneal macrophages"
1.750
                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="TWEAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon start=1
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGACGGAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 CGAGCTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422 retreagrecactrigatgaggaaaggcigictaccigaagcregactrectegi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGTGCTGGCCTGCCTGGAAGAATTCTCAGCCACAGCAGCAGCTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 GACCAGGACCCGTCGGAACTGAATCCCCAGACAGAAGAAAGCCAGGATCCTGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCCGGGAGCCCCCTGAACTGAATCCCCAGACAGAGAAAGCCAGGATGTGGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTGTGGACGGGACAGTGAGTGGCTGGGAAGGCCAGAATCAACAGCTCCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 GGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTACTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCTACGACCGCCAGATTGGGGGAATTTACAGTCATCAGGGCTGGGCTCTACTACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          718 CCCCAGCTCCGCCTCTGCCAGGTGTCTGGGCTGTTGGCCCCTGCGGGCCAGGGTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 614.6; DB 6;
Pred. No. 1.5e-102;
0; Mismatches 219;
                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                    2. .676.
Location/Qualifiers
                                                                                                                                                                                    Strandedness: Double;
Topology: Linear;
Key Locati
CDS 2. 67
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ilarity 75.8%;
Conservative (
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1072
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CCAGACCTGCCCCTCTCGCAGGCTGCCTGGGCCTGTTCACGTGTTTTCCATCCC 1012
                                                                                                                                                                                                                                   1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGAACCTGGGACTAG 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGGAGTTCCCAAATGTGAGGGGCGAGA-AACAAGACAAGCTCCTCCCTTGAGAATTC 1311
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SRASLSAGBPAQERAGEDOPPSELAPQTESCOPPAPETNRIVRPRASAPKRRKTR
ARRALAHYEVHPRFGODGAGAVDGTVSGREBARINSSSPLRYNRQIGEFIVTRAGI
YYLYCQSSDALEAWENGERSRKRRAVLTQKQKKKQHSVLHLVPINATSKDDSDVTEVMM
                                                                                                                                                                                                                                                                                                                                             ACCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCC 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRI 12-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
!ia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="expressed in primary I lymphocytes and monocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ted (21-FEB-2002) DIO, CNB, ctra de Colmenar Viejo, MADRID,
                                                                                                             PAATACAGTATTCCCACTCTTATCTTACAACTCCCCCACCGCCCACTCTCCACCTC
                                                                                                                                                                   -- ACAGACGTATCCTTGCTCTTTAACATCCCATCCCACCACAACTATCCACCTC
                                                                                                                                                                                                                                AGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGATCTCGACTCCCCCTGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGTTCCCAACTGTGAGGGGGAAGAGCTGGGGACAAGCTCCTCCCTGGA----tC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      logenous hybrid mRNA encodes TWE-PRIL, a functional cell: e TWEAK-APRIL fusion protein
1. 21 (21), 5711-5720 (2002)
189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -Balade, B., Medema, J.P., Lopez-Fraga, M., Lozano, J.C., shoten, G.M., Picard, A., Martinez-A, C., Garcia-Sanz, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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:-Balade,B., Garcia-Sanz,J.A. and Hahne,M.
: Submission
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAL90443.1"
/db_xref="GI:24934974"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28049, Spain
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        )51.1 GI:24934973
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QPALRRGRGLQAQCYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG
IRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSPHGTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AGAGGAGCAGGACCCGTCGGAACTGAATCCCCAGACAGAAGAAAAAAGCCAGGAT
                                                                                                                                          51 ATCCCTCGGGTCCCGGGATGGGGGGGCGGTGAGGCAGGCCACAGCCCCCCGCCCCCC
                                                                                                                                                                  111 CGCCCGTCGGAGCCAGAGGCGGAGGGGGCGCCGGGGGAGCCGGGCACCGCCTG
                                                                                                                                                                                                                                               121 cccecrcecerresecrresecrresecrresecrreserreserresecr
                                                                                                                                                                                                                                                                                                                                                          231 CAGITIGGGGAGCCGGGCAICGCIGICCGCCCAGGAGCCIGCCCAGGAGGAGCTG
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                                                                                                        ·,
                                                                       Length 1816;
                                                                                                      0; Indels
                                                                   40.3%; Score 553; DB 9; I
100.0%; Pred. No. 2.8e-91;
iive 0; Mismatches 0;
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                                                                                                      Matches 553; Conservative
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                                                                                       Similarity
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GenCore version 5.1.6 Copyright (c) 1993 - 2004. Compugen Ltd.	.c search, using sw model	cil 7, 2004, 17:30:19 ; Search time 524.669 Seconds (without alignments) 1117.066 Million cell updates/sec	.09-245-198A-3 )3 itgtcattgttagactttgagacaaaatgttgataaatgg 1373	SNTITY NUC OOP 10.0 , Gapext 1.0	73863 segs, 2124099041 residues	s satisfying chosen parameters: 6747726	jth: 0 jth: 200000000	.nimum Match 0% uximum Match 100% sting first 45 summaries

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the number of results predicted by chance to have a than or equal to the score of the result being printed, if by analysis of the total score distribution. geneseqn2003as:\*
geneseqn2003bs:\*
geneseqn2003cs:\*
geneseqn2004s:\*

genesequ1980s:\* genesequ1990s:\* genesequ2000s:\* genesequ2001as:\* genesequ2001bs:\*

Geneseq 29Jan04:\*

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#### SUMMARIES

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0 1373	7	AAV18600	Aav18600 Homo sapi
0 1364	9	ABK34881	Abk34881 Human cDN
7	0	AAX56000	Aax56000 Human tum
7	e	AAA49717	Aaa49717 Human PRO
Н	9	ABK40255	Abk40255 cDNA enco
6 1306	7	ACC57587	Acc57587 Polynucle
130	7	ACC57901	Acc57901 Human TWE
130	σι	ADC35205	2
123	7	AAV47613	m
7	4	AAD04350	Aad04350 Human TRE
7 1030	7	AAX23424	Aax23424 Human INR
12	σ	ADC97713	Adc97713 Murine FL
868 8.		AAS03964	Aas03964 Expressio
11		AAV18599	Aav18599 Mus muscu
8 701	7	AAX23425	Aax23425 Mouse INR
4		ACH34013	Ach34013 Human end
5 408		ABX37032	Abx37032 Bovine ES
9 282	7	AAT22190	Aat22190 Human gen
1 195		ABK29540	Abk29540 Colon ade
1 412		ADB56326	Adb56326 Toxicity-
7 264	7	ABX52254	Abx52254 Bovine ES
1 114955	7	AAX53491	Aax53491 Human ade
3163	6	ADC87060	Adc87060 Human GPC

The sequence is that encoding human tumour necrosis factor relatew (TRELL). TRELL or active fragments can be included with a carrier

Claim 2; Page 48-50; 69pp; English.

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Abt09678	Adc86736	Abk98631	Acd13882	Abk98592	Acd13843	Adc86688	Aaz17263	Aaa02484	Abn58848	Abn41049	Abn58593	Abn58591	Abn58849	Adc86738	Aaa10594	Aaa02488	Abt 09682	Aad36876	Ada71938	Aad36874	Abq52497	٠.,
ABT09678	ADC86736	ABK98631	ACD13882	ABK98592	ACD13843	ADC86688	AAZ17263	AAA02484	ABN58848	ABN41049	ABN58593	ABN58591	ABN58849	ADC86738	AAA10594	AAA02488	ABT09682	AAD36876	ADA71938	AAD36874	ABQ52497	
9	σ	9	œ	9	8	σ	~	m	9	9	ø	9	9	9	m	ო	9	7	7	7	9	
1064	5452	12733	12733	12739	273	1117	1337	1000	9	9	9	09	9	3133	10732	1218	1065	1017	2000	29870	009	
4.8	4.6	4.5	4.5	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.3	4.3	4.2	4.1	4.0	4.0	4.0	4.0	
65.4				62.2	62.2	61.4	61	9.09	09	9	09	9	09	9.	59.2	58		54.8		4.	54.4	
24	7	~	N	7	c 29	e	31	c 32	33	34	35	36	37	m	39	c 40	41	42	43	C 44	45	

## ALIGNMENTS

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TRELL; tumour necrosis factor related ligand; tnf; treatment; can autoimmune disease; immune system; stimulation; suppression; graft rejection; ds.
                                                                                                                                                                                                                                                                                                                                                                                               Tumour necrosis factor related ligand - useful for, e.g. treating auto-immune disease and immune responses to tissue grafts.
                                                                               Homo sapiens tumour necrosis factor related ligand (TRELL) gene.
                                                                                                                                                                        1. .852
/*tag= a
/note= "tumour necrosis factor related ligand"
                                                                                                                                                                                                                                                                                                                 (BIOJ ) BIOGEN INC. (UYGE-) UNIV GENEVA FACULTY MEDICINE.
                                                                                                                                                               Location/Qualifiers
                     AAV18600 standard; cDNA; 1373 BP.
                                                                                                                                                                                                                                                                                                                                               Chicheportiche Y, Browning JL;
                                                                                                                                                                                                                                                                         96US-0023541P.
96US-0028515P.
97US-0040820P.
                                                                                                                                                                                                                                                       97WO-US013945.
                                                           21-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-145619/13.
P-PSDB; AAW47525.
                                                                                                                                                                                                                                                                         07-AUG-1996;
18-OCT-1996;
18-MAR-1997;
                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                      07-AUG-1997;
                                                                                                                                                                                                                WO9805783-A1
                                                                                                                                                                                                                                   12-FEB-1998.
                                         AAV18600;
RESULT 1
AAV18600
                                                                                                                                                               Key
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ö suseful to screen for TRELL receptors, by labelling with a bell and screening compositions for building to screening compositions for building a bell in with a with TRELL-receptor binding can also be screened for, can nistered, optionally with interferon-gamma, to induce cell at, suppress or alter immune responses (especially involving a racinoma cells) involving a signal pathway between TRELL and The DNA sequence can be used in gene therapy for TRELL and redright in mammals (especially humans), e.g. tumours, by into cells, and expressing, therapeutically effective amounts 120 360 120 180 180 240 240 300 360 420 420 480 540 540 099 300 480 600 900 999 720 720 780 9 9 e.g. a virus comprising a gene encoding TRELL. It may also the preparation of prepare probes for screening letic DNAs for TRELL-encoding sequences and for antisense | CATTGTTAGACTTTGAAATTTCCGCCCGCCGGCTCCCCCTCCCCCGATCCCTCGGG rcarrenagacriricaaaarricceccecceccecceccecceccecearecereses .AGAGGCGGGGCGCCCGGGGGAGCCGGGCACCCCCTGCTGGTCCCCGCCTCGC secondecondecondeconoconoconde de la secondecidad d GGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGCTGGTGGCAGAGGAGCAC BACCCGTCGGAACTGAATCCCCAGACAGAAGAAAGCCAGGATCCTGCGCCTTTCCTG PACCCGTCGGAACTGAATCCCCAGACAGAAGAAAGCCAGGATCCTGCGCCTTTCCTG BACGGGACAGTGAGTGGCTGGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGC ACCECCAGATCGGGGAGTTTATAGTCACCCGGCTGGGCTCTACTACTGTACTGT TGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGT TCCGCCTCTGCCAGGTGTCTGGGCTGTTGGCCCTGCGGGCCAGGGTCCTCCCTGCGG sacchédedende de la contraction de la contractio GGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGGAGCTGGTGGCAGAGGAGGAC GACTAGTTCGGCCTCGCAGAAGTGCACCTAAAAGGCCCGGAAAACACGGGCTCGAAGA GACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGA TCGCAGCCCATTATGAAGTTCATCCACGACTGGACAGGACGGAGCGCAGGCT BACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGC ACCGCCAGATCGGGGGAGTTTATAGTCACCCGGGCTGGGCTCTACTACTGTACTGT TIGGCCCTGCCTGCAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGGGCCC redeceraceraceradadarrencadecacracadecadriceredadece 0; Gaps compositions to treat cancer, autoimmune diseases or Length 1373; BP; 247 A; 462 C; 394 G; 270 T; 0 U; 0 Other; 0, Indels ; Score 1373; DB 2; ; Pred. No. 1.9e-282; 0; Mismatches 0; 100.0%; larity 100.0%; Conservative 0

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06-APR-2000; 2000US-0195582P. 29-MAR-2001; 2001WO-US010224

WO200177288-A2. Homo sapiens.

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出 Ö 18-OCT-2001

(GEMY ) GENETICS INST INC

Human, secreted protein, gene, ss; nutritional supplement, haemoy viral infection; bacterial infection; fungal infection; diabetes autoimmune disorder; rheumatoid arthritis; multiple sclerosis; trautoimmune thyroiditis; allergic reaction; neurodegenerative dis Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer coagulation disorder; inflammatory disorder; Crohn's disease; tissue regeneration; wound healing; burn; haematopoiesis; myeloid cell deficiency; lymphoid cell deficiency. 1081 CCCAATCCCTGACCCTTTGAGGCCCCCAGTGATCTCGACTCCCCCCTGGCCACAG. 721 CAGCTCCGCCTCTGCCAGGTGTCTGGGCTGTTGGCCCTGCGGCCCAGGGTCCTCCC ATCCGCACCCTCCCTGGGCCCATCTCAAGGCTGCCCCCTTCCTCACCTACTTCG ccreccccrccrcrasassecreccresecrerrerecererrerecererre ACAGTATTCCCACTCTTATCTTACAACTCCCCCACCGCCCACTCTCCACCT CCCAATCCCTGACCCTTTGAGGCCCCCGAGTGATCTCGACTCCCCCCTGGCCACAG 1141 CAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCCAC TTCCCAAATGTGAGGGGGGAGAACAAGACAAGCTCCTCCTTCCCTTGAGAATTCCCTG Treceaatergaeeeegaaaacaaeacaaecreercereerrgaeaarreerre Arccecaccereceraseccearereassersececerrecreaceraceres 901 caacagererendedecacedegreeerrendececacereacedererreer CCTGCCCCTCCCTCTAGAGGCTGCCTGGGCCTGTTCACGTGTTTTCCACACA ACAGIATITCCCACTCTTATCTTACAACTCCCCCACGCCCACTCTCCACCTGACT 1141 CAGGGCATTGTGTTCACTGTACTCTGTGGCCAAGGATGGGTCCAGAAGACCCCCAC 1201 GCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGGCC TTCCAGGTTCACTGAGGGCCCTGGTCTCCCCACAGTCGTCCCCAGGCTGCCGGCT Trecaderreacreaceceresrerececacacacereceasecreeces GCACTAAGAGGGGTTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGGC TITIAAAACAGAIAITATITITIATIATITATIGIGACAAAAIGITGATAAAIGG 1321 TITITAAAACAGATATTATTTTTATTATTGTGACAAAATGTTGATAAATGG CGACAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCCACCCTCAGCCGCTC Human cDNA encoding secreted protein #19. BP ABK34881 standard; cDNA; 1364 (first entry) 08-MAY-2002 781 781 841 196 961 1021 1021 1081 1201 1261 1261 1321 ABK34881; 841 901 ABK34881 ð g ò qq ò a ò d ò g ð 셤 ò q ò g ð d à d 

셤 βp g ð 셤 셤 g g g g П ઠે ò ò ð õ ð à ò ð qq à ð q à 셤 relates to 592 polynucleotides which have been derived from unman tissue sources and which encode novel secreted polynucleotides can be used as probes for the and isolation of full length cDNA and genomic DNA. The sand proteins can also be used as nutritional supplements. It useful in the treatment of various immune deficiencies such as viral infections, bacterial infections, fungal troimmune disorders (e.g. rheumatoid arthritis, multiple oimmune thyroiditis and diabetes) and allergic reactions (e.g. asthma). They are also useful for treating ive diseases (e.g. Alzheimer's disease, Parkinson's if fibrosis, coagulation disorders (e.g. heemophilia), isorders (e.g. crohn's disease) and tumours. They are also seue regeneration, for wound healing and in the treatment of ms and ulcers. The proteins are also useful for regulating and in the treatment of and for treating myeloid or lymphoid cell deficiencies. 244 204 264 564 ACAGCCCCCCCCCCATGGCCGCCCCTCGGAGCCAGAGGCGGAGGGGGCGCCGG 144 124 184 324 304 AGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGA 384 364 444 424 504 484 and ninety two polynucleotides derived from a variety of cources which encode secreted proteins, useful for treating ancies and disorders such as autoimmune disorders. 84 64 CGGCCTCCTGCTGGCCGTGGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAG CCGCCGGCTCCCCTCCCCGATCCCTCGGGTCCCGGGATGGGGGCGGTGAGG coccescroccorrectedarecricesareceressares ACAGCCCCCCCCCCCCATGGCCGCCCCTCGGAGCCCAGAGGCGGAGGGGCGCCGG GCCGGGCACCGCCCTGCTGGTCCCGCTCGCGCTGGGCCTGGGCCTGGGCCTGGCC CGGCCTCCTGCTGGCCGTGGTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAG TGCCCAGGAGGAGCTGGTGGCAGAGGAGCCAGGACCCGTCGGAACTGAATCCC TGCCCAGGAGGAGCTGGTGGTGGTAGAGGACCAGGACCGTCGGAACTGAATCCC AGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGA ACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTT ACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTT AGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTTT Æ; Gaps Resnick 0, DB 6; Length 1364; BP; 246 A; 461 C; 394 G; 263 T; 0 U; 0 Other; 2; Indels ninety two polynucleotides derived from SH, Howes Score 1345.8; DB 6. Pred. No. 1.2e-276; 0; Mismatches 2; Agostino MJ, 82; 372pp; English. Fechtel K, 98.0%; 99.9%; nservative HF, 21/23.

544

CACCCGGGCTGGGCTCTACTACTGTACTGTCAGGTGCACTTTGATGAGGGGAAG 624

AGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTTT

Human; tumour necrosis factor; Apo-3 ligand; lymphotoxin; apoptos: NF-kappaB-dependent transcription; JNK/SAPK-dependent response; ca GAATICICAGCCACTGCGGCCAGTTCCCTCGGGCCCCCAGCTCCGGCTCTGCCAGGT GAATTCTCAGCCACTGCGGCGAGTTCCCTCGGGCCCCAGCTCCGCCTCTGCCAGGT GGGCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGGATCCGCACCCTCCCCTGGGC CTCAAGGCTGCCCCTTCCTCACCTACTTCGGACTCTTCCAGGTTCACTGAGGGGC creaksecriseccerrecreaceracinesaacrerrecasserreacreacers GTCTCCCCACAGGCTGCCGGCTCCCCTCGACAGCTCTGGGCACCC Grerecededagrecendecrecederrecerreceredadaderereradadaece CTGGGCCTGTTCACGTGTTTTCCATCCCACATAAATACAGTATTCCCACTCTTATC CTGGGCCTGTTCCACGTGTTTTCCATCCCACATAAATACAGTATTCCCACTCTTATC 1045 AACTCCCCCACCGCCCACTCTCCACCTCACTAGCTCCCCAATCCCTGACCCTTTGA 1025 AACTCCCCCACCGCCCACTCTCCACTAGCTCCCCAATCCCTGACCCTTTGA CCCAGTGATCTCGACTCCCCCTGGCCACAGACCCCCAGGGCATTGTGTTCACTGT CCCAGTGATCTCGACTCCCCCTGGCCACAGACCCCCAGGGCATTGTGTTCACTGT TGTGGGCAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGGTGGACC TGTGGGCAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGGCTGGACC GGCAGGAAGCCAAAGAGACTGGCCCTAGGCCAGGAGTTCCCCAAATGTGAGGGGCGA 1205 GGCAGGAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGCGA GCTGTCTACCTGAAGCTGGACTTGCTGGTGATGGTGTGTGCTGGCCCTGCGCTGCCT CAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAACAGATATTATTT 1265 CAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAACAGATATTATTT Human tumour necrosis factor Apo-3 ligand polynucleotide sequence TATTATTGTGACAAAATGTTGATAAATGG 1373 TATTATTGTGACAAAATGTTGATAAATGG 1353 Location/Qualifiers BP AAX56000 standard; DNA; 1421 (first entry) Homo sapiens. 15-JUL-1999 605 685 805 785 845 905 965 1105 1085 1225 1345 545 1165 1145 1285 AAX56000; 625 665 745 725 865 925 985 Key AAX56000 엄

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PRO207; human; antitumour; tumour; therapy; cytostatic; breast carovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; central nervous system cancer; melanoma; leukaemia; neoplasm; ss.
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                                                                                                 AGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGGCCCT
                                                                                                                                     603 AGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGTGCTGGCCCT
                                                                                                                                                                                                                          GCCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGGGGCCCCCAGCTCCGCCT
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                                                                                                                                                                                                                                                                                                                                                737 AGGTGTCTGGGCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGGATCCGCACCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence encodes a human tumour necrosis factor (TNF) and nomologue designated Apo-3 ligand. Apo-3 ligand has trivity. Apo-3 ligand can be used to induce apoptosis in icer cells, to induce NF-kappaB-dependent transcription as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sarccirca creacer care con contra contra con contra contra con contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGCCAGATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 281 A; 464 C; 404 G; 272 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03- ligand (a tumor necrosis factor) homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   </sapk-dependent responses in mammalian cells</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1325; DB 2; Length 1-
Pred. No. 3.1e-272;
0; Mismatches 20; Indels
92. .841
/*tag= a
/product= "Apo-3 ligand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В,
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97US-0069862P.
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98.5%;
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Jonservative
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squence is that of cDNA clone DNA30879-1152 (ATCC 209358)
1 PRO207 (see AAY95338), which shows homology to several
2 tumour necrosis factor family, especially human
13.4%). The cDNA was identified in a foetal kidney cDNA
1 ing identification of an expressed sequence tag with
1 man Apo-2 ligand. A claimed method for inhibiting the
1 mour cell comprises exposing the tumor cell to PRO19,
2 PRO219, PRO224, PRO228, PRO310, PRO566, SPRO362,
3 or PRO866 (see AAY95337-49), their agonists or chimeric
1 noorporating them. The tumour is especially a cancer
2 breast, ovarian, renal, colorectal, uterine, prostate,
and central nervous system cancer, melanoma and leukaemia. ion to inhibit neoplastic cell growth or for treating tumor prises polypeptides PRO179, PRO207, PRO320, PRO219, PRO221, PRO301, PRO526, PRO509 or PRO866. CCGTCGGAGCCAGAGGGGGGGGGGCCGGGGGAGCCGGGCACCGCCTGCTG 120 STITGGGGAGCCGGGCAICGCIGICCGCCCAGGAGCCTGCCCAGGAGGAGCTGGTG 288 CCGTCGGAGCCAAAGGCGGAGGGGGCCCCGGGGAAGCCGGGCACCGCCTGCTG 168 257 A; 443 C; 389 G; 264 T; 0 U; 0 Other; 96.2%; Score 1320.2; DB 3 99.8%; Pred. No. 3.3e-271; 0; Mismatches Godowski PJ, | WI; 3; 172pp; English. our polypeptides 99US-0144758P. 99US-0145698P. 99WO-US021090. 99US-0131445P. 99US-0134287P. 99WO-US005028 99US-0130232P 99WO-US028565 98US-0113296P 99WO-US021547 /\*tag= b 178. .804 /\*tag= a 58. .177 nservative . .807 Goddard A /\*tag= ECH INC. 368/38.

27

2.

ndard; cDNA; 1353 BP

(first entry)

human PRO207 polypeptide.

benign tumour; malignant tumour; lymphoid malignancy; euronal disorder; stromal disorder; blastoccelic disorder; disorder; immune disorder; angiogenic disorder; ; cytostatic; neuroprotective; gene; ss.

2000WO-US003565

99WO-USO05028. 99US-0133972P. 99US-013459P. 99WO-US012252. 99US-0140650P. 99US-0144653P. 99US-014569BP. 99US-014569BP. 99US-014569BP. 99WO-US020111. 99WO-US021090. 99WO-US028313. 99WO-US028634 2000WO-US000219

믶珠무슨목요료요료요요요요요요요요점점점문중요중품표표품품교표표표표표표표표표표표표점점급료표중요점점료표표중요점

TECH INC.

Hillan KJ; Stone DM; Gurney AL, Smith V, Godowski PJ, i RM, Roy MA, Pan J, Pitti RM, Wood WI; Goddard A,

567/26.

ucleic acids encoding PRO polypeptides, useful for treating ignant tumors, leukemias and lymphoid malignancies, anglogenic and immunologic disorders.

13; 302pp; English.

and the polymucleotide sequences encoding them. The PRO agonists, antagonists or anti-PRO antibodies are useful for agonists, antagonists or anti-PRO antibodies are useful for pro malignant tumours (e.g. renal, kidney, bladder, leukaemias and lymphoid malignancies, other disorders such glial, astrocytal, hypothalamic, glandular, macrophagal, Jastocoelic disorders, inflammatory, immune and angiogenic e polymucleotide sequences are also useful in gene therapy.

257 A; 443 C; 389 G; 264 T; 0 U; 0 Other; BP;

CTGGTGGATGGTGTGTGGCCCTGCGCTGCTGGAAGTTCTCAGCCCCTGCGG 121 GTCCGGCTCGCGCTGGGCCTGGGCCTGGCGTGGCCTGCCTCGTGCTGG GECAGTITGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGC 349 GCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGA 301 GCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGA CGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGG 361 CGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGG GCGCAGGCAGGTGTGGACGGACAGTGACTGGCTGGGAGGAAGCCAGAATCAACA 421 GCGCAGGCAGGTGTGGACGGGACAGTGAGTGGCTGGGAGGAGGAAGCCAGAATCAACA 589 TACCIGIACTGICAGGIGCACTITGAIGAGGGAAGGCIGICIACCIGAAGCIGG 541 TACCTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGG CTGGTGGATGGTGTGCTGGCCTGCGCTGCGAGGAATTCTCAGCCACTGCGG 709 TCCCTCGGGCCCCAGCTCCGCCTCTGCCAGGTGTCTGGGCTGTTGGCCCTGCGGC 661 recercedececeaderecedereraceagrareragemerrageceraceae TCCTCCCTGCGGATCCGCACCCTCGGCCCCATCTCAAGGCTGCCCCTTCCT 721 recreecredegareegeacecreeceregeceearereaggereegeceerree CTTTGCTCCCAGACCTGCCCCCCCCTCTAGAGGCTGCCTGGTCTCACGTGTTT 109 GCCGCCCGTCGGAGCCAGAGGCGGAGGGGCCCCGGGGGGAGCCGGGCACCGCCC GTCAGTTTGGGGAGCCGGCCTGTCGCCCCAGGAGCCTGCCCAGGAGGAGGAG 529 AGCCCTCTGCGCTACAACGGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGC 481 AGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGC TACTICGGACTCTTCCAGGTTCACTGAGGGGCCCTGGTCTCCCCCACAGTCGTCCC raciricadacriciriccadarreacridadedececinedrerecededagreereed GCCGGCTCCCCTCGACAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCACCCTCAG GCCGCTCCCTCGACACTCTCTGGGCACCCGGTCCCCTCTGCCCCACCTCAGC TCCCACATAAATACAGTATTCCCACTCTTATCTTACAACTCCCCCACGCCCACTC CTTTGCTCCAGACCTGCCCCTCCTAGAGGCTGCCTGGGCCTGTTCACGTGTT 6; Length 1353; · 0 3; Indels Score 1320.2; DB 6 Pred. No. 3.3e-271; 0; Mismatches 3; 96.2%; Query Match
Best Local Similarity 99.8
Matches 1322; Conservative 169 229 181 289 469 409 694 841 649 601 829 781 949 1009 889 901 196 쉽 ò a ò g à 원 ò 셤 ð g ð 셤 à g ਨੇ g ò pp ò g g g à ਨੇ à 엄 à g ð g ð d

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lard; DNA; 1306 BP.

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(first entry)

encoding tumour necrosis factor superfamily member. tumour necrosis factor; osteopathic; bone; gene; ds.

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:002WO-US033022.

:001US-0329393P.

3-JEWISH HOSPITAL.

F, Teitelbaum SL;

46/40.

c comprising a core, and at least one external loop, useful processes of bone formation or inhibiting bone resorption, treatments for disease or condition characterized by loss

ige 66-67; 78pp; English.

equence is that of a polynucleotide encoding a non-RANKL tumour necrosis factor (TNF) superfamily. The invention naturally-occurring proteins that contain one or more of the ice loops of RANKL (see ABR42066-70) in combination with a protein core obtained from a non-RANKL member of the TNF iso provided are polynucleotides encoding such proteins. Ind to RANK, acting as mimics of RANKL. They can be used to imma providing treatment for diseases or conditions by loss of bone mass

BP; 247 A; 434 C; 368 G; 257 T; 0 U; 0 Other;

A B A B A B A B A B A B A B A B A B A B	93.6%; Score 1285; DB 7; Length 1306; Press 1285; DB 7; Length 1306; Description of the press 20; March 1300.0%; Press 20; Mismatches 0; O 1 Indels 0; O 2 1 Indels 0; O 2 Indels 1300.0%; Press 20; Mismatches 0; O 1 Indels 0; O 2 Indels 1300.0%; Press 20; Mismatches 0; O 1 Indels 0; O 2 Indels 0; O 2 Indels 0; O 3 Indels 0;
oy ob	01 GCTGTTCACGTGTTTTCCACCCACATAAAAAAAAATATATAT
qa X	ciccacigeccactrificaectractractracidearteccaatractractraraege tgatctrgactrcccccctggccacagacccccagggcattgtgttcactgtact

ă 8 S

0

Indels

ö 7;

Score 1285; DB 7; Pred. No. 1e-263; Mismatches

Length 1306;

481 TCACCCGGGCTGGGCTCTACTACCTGTACTGTCAGGTGCACTTTGATGAGGGGAA 1 cacadecececececeardacececeredaagecaagageagagagagageeeeg ACCGGGCCCCGCCCTGCTCCCGCTCGCGCTGGGCCTGGGCCTGGGCCTGGCCTGGC 209 TCGGCCTCCTGCTGGCCGTGGTCTTGGGGAGCCGGGCATCGCTGTCCGCCCA 121 TCGGCCTCCTGCTGGCCGTGGTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCA CTGCCCAGGAGGAGCTGGTGGCAGAGGAGGACCAGGACCCGTCGGAACTGAATCC CAGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAG 241 CAGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAG TCACCCGGGCTGGGCTCTACTACTGTCAGGTGCACTTTGATGAGGGGAA TCTACCTGAAGCTGGACTTGCTGGTGGTGTGTGCTGGCCCTGCGCTGCCTGGA 541 reracerdaageregaerreergeregargereregeeergeeregeeregeer TCTCAGCCACTGCGGCCAGTTCCCTCGGGCCCCCAGCTCCGCCTCTGCCAGGTGTC 601 Tereagearergegecagnicerregagececagereegecreagergre 809 AGGCTGCCCCCTTCCTCACCTACTTCGGACTCTTCCAGGTTCACTGAGGGCCCCT 721 AGGCTGCCCCTTCCTCACTTCGGACTCTTCCAGGTTCACTGAGGGCCCT CCCCACAGTCGTCCCAGGCTGCCGGCTCCCCTCGACACTCTCTGGGCACCCGGT 989 GCCTGTTCACGTGTTTTCCATCCACATAAATACAGTATTCCCACTCTTATCTTA GCCTGTTCACGTGTTTTCCATCCCACATAAATACAGTATTCCCACTCTTATCCTTA 1049 CCCCCACCGCCCACTCTCCACTAGCTCCCCAATCCTGACCCTTTGAGGCC 89 CACAGCCCCCCCCCCCCCATGGCCGCCCGTCGGAGCCAGAGGCGGAGGGGGGCGCCG AGCCGGGCACCGCCTGCTGGTCCCGCTCGCGCTGGGCCTTGGGCCTTGGCGCTTGGC 181 CTGCCCAGGAGGAGCTGGTGGCAGAGGAGGACCAGGACCCGTCGGAACTGAATCC CACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGT 301 CACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGT 509 AAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTT 421 AAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTT TGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGGATCCGCACCCTCCCCTGGGCCCCA CCCCACAGTCGTCCCAGGCTGCCGGCTCCCCTCGACAGCTCTCTGGGGCACCCGGT Sequence 1306 BP; 247 A; 434 C; 368 G; 257 T; 0 U; 0 Other; 93.6%; Scc... 100.0%; Pred 0; h Matches 1285; Conservative Query Match Best Local Similarity 149 61 269 329 389 449 569 629 689 749 661 698 781 929 ( 841 901 X S g ð d à д à qq à q ò g à g à g ð g ð d à qq à 음 ò g G  $\delta$ g à g à 셤 à 1228 AGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGGGGAAAAAAA 1288 AGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGGGGAGAAAAGA 1200 AGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAACAGATATTATTTTTATT 1348 sequence is that of a polymucleotide encoding human TWEAK.

I relates to compositions comprising heterotrimeric complexes prosis factor (TNF) ligand family members, and their use in ), prevention and treatment of disease. In one embodiment, [meric complex comprises full-length or extracellular [WEAK and full-length or extracellular portions of other TNF members, preferably VEGI or VEGI-SV. The heterotrimeric the invention are useful for treating an autoimmune disease, seoporosis, and particularly for inhibiting cancer cell, increasing B cell proliferation, or inducing apoptosis of Itimeric complex having a first polypeptide member of the is factor (TNF) ligand family, and a second different member family, useful for treating cancer, osteoporosis or an AAGGATGGGTCCAGAAGACCCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCA ; tumour necrosis factor; ligand; cytostatic; cor; osteopathic; gene; ss. age 367-368; 388pp; English. STGACAAATGTTGATAAATGG 1373 STGACAAATGTTGATAAATGG 1285 /product= "Human TWEAK" Location/Qualifiers 18. .767 ndard; cDNA; 1306 4 GENOME SCI INC. 2002WO-US023782 2001US-0307838P coding sequence. (first entry) ಹ

/\*tag=

Rosen CA; 659/40.

뿧긂믔몆몆섫봕찞뫢찞흕몆솭섫첉첉짫맖멅쒖첉몆빏몆쳁첉첉첉첉첉찞첉쁔첉똮눖찞맖찞캶쒖쌇쒖읁읁읁읁읁

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Indels

Length 1306;

ВР

dard; cDNA; 1306

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E.

(first entry)

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Nardelli

Rosen CA, 72/66.

C A.

2001US-0312542P. 2001US-0330761P. 2002US-00218547

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CCCCACTTCAGGCACTAAGAGGGGCTGGACTTGCGGGGAGGAAGCCAAAGAACTG 1140 TAGGCCAGGAGTTCCCAAATGTGAGGGGGGAGAAACAAGACAAGCTCCTTCGTTGA 1305 CACAGACCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAG CCCACATAAATACAGTATTCCCACTCTTATCTTACAACTCCCCCACCGCCCACTCT CTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGATCTCGACTCCCCC CCACAGACCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAG CCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTG TTTGCTCCAGACCTGCCCTCCTCTAGAGGCTGCCTGGGCCTGTTCACGTGTTTT TCCCTGTGGATTTTTAAAACAGATATTTTT 1341 rcccreredarrirraaaacagararrrr

dard; cDNA; 1236

2.

INF related endothelium proliferative agent) cDNA.

necrosis factor; TNF; angiogenesis; wound healing; TREPA; ndothelium proliferative agent; tumour; metastasis;

Location/Qualifiers 1. .750

98US-00105343.

<u>ଳୁଷ୍ଟର୍ଷ୍ଟର୍ଗ୍ରେପ୍ରକ୍ତିପ୍ରପ୍ରପ୍ରସ୍ଥରେ ଅନ୍ତର୍ଗ୍ରମ୍ବର୍ଦ୍ୟ ନଳ୍ପର୍ଗ୍ରମ୍</u>

97US-0079B692, 98US-00021706.

LAB.

60/29

genesis in mammal at desired sites for promoting wound uninistering soluble fragment of extracellular domain of factor related endothelium proliferative agent protein.

53pp; English 73-74;

CCCACATAAATACAGTATTCCCACTCTTATCTTACAACTCCCCCACCGCCCACTCT 1065 1125 1020 1185 1080 1245 1305 1140 960 CCCCACATAAATACAGTATTCCCACTCTTATCTTACAACAACCCCACCGCCCACTCT CTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGATCTCGACTCCCCC crcactagerececarecergacerrieaggeeececagrarereaggaceeee SCCACAGACCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAG ACCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTG TCCCTGTGGATTTTTAAAACAGATATTATTT 1341 rcccrerecarrirraaacacararrarrir 1236

ä

造 25 63 á dard; DNA; 1030

(first entry)

NA.

sis factor receptor, signal transducer molecule; TNF; APO4; abnormality; gestational abnormalitity; prostate cancer; NPO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease; lomain; immunogen; antibody preparation; breast carcinoma; SB.

Location/Qualifiers /product= "TNRL3" ø 1. .627 /\*tag=

ERICKUKEKUMENTAN BANGKALUBUKEN KAN KAN BANGKAN DILIKAN KONU PROMENUMENTAN BANGKAN KAN DERIKAN KAN BANGKAN BANGKAN BANGKAN BANGKAN KONU

98WO-US018393.

97US-00924634.

WASHINGTON

191/17.

rosis Factor family receptor polypeptides and ligands - agnosis and treatment of prostate cancer and developmental abnormalities.

Fig 13A; 156pp; English.

on describes isolated Tumor Necrosis Factor (TNF) family peptides: APO4, APO6, APO8 and APO9 or their active id isolated TNF related ligands 1 and 3 (TNFL1 and TNFL3) or

their active fragments. APO4 is useful for diagnosing prostate cace determining levels of APO4 in an individual. Prostate cancer can treated using APO4 selective binding agents linked to a therapeu moiety. APO4 polypeptides are also useful for identifying select binding agents, useful in diagnosis/treatment of disease by bind agents to the polypeptide/active fragment which is extracellular expressed on the cell surface. The binding is preferably perform vivo. APO4 polypeptides/ active fragments are also useful for sc for agonists and antagonists by binding and observing the change activity. Effective pharmacological agents useful in diagnosis of treatment of disease are also identified using APO4 polypeptides fragments and APO4 signal transducer molecules that specifically with a cytoplasmic domain of APO4 and detecting a change in leve activity. The method is performed in vivo or in vitro. APO polyper activity. The method is performed in vivo or in vitro. APO polyper activity are all useful as immunogens for preparing antibodies. APO8 was transfected to human breast carcinoma ce abnormalizines. 1 GTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGC GCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGA 121 GCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAGTGCACCTAAAGGCCGGAA CGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGG 181 c\u00e3\u00e3c\u00e3a\u00e3\u 241 GCGCAGGCAGGTGTGGACGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAC AGCCCTCTGCGCTACTACCGCCAGATCGGGGGGTTTATAGTCACCCGGGCTGGGC 589 TACCIGIACTGICAGGIGCACTITGAIGAGGGGAAGGCIGICIACCIGAAGCIGG TACCTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGG CTGGTGGATGGTGTGTGGTGCCTGCGTGCCTGGAGGAATTCTCAGCCACTGCGG TCCTCGGGCCCCAGCTCCGCCTCTGCCAGGTGTCTGGGGCTGTTGGCCCTGCGGCC recercesecentesecretesecassistes TCCTCCCTGCGGATCCGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCCTTCCT TACTICGGACICTICCAGGITCACTGAGGGGCCCTGGTCTCCCCACAGICGTCCC 229 GICAGITIGGGGAGCCGGCAICGCIGICCGCCCAGGAGCCIGCCCAGGAGGAGG GCGCAGGCAGGTGTGGACGGGACAGTGAGTGGCTGGGAAGGCCAGAATCAACA 529 AGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCCGGGCTGGGC CTGGTGGATGGTGTGCTTGCCTTGCGCTTGCAGGAATTCTCAGCCACTGCGG TACTTCGGACTCTTCCAGGTTCACTGAGGGGCCCTGGTCTCCCCACAGTCGTCCC GCCGGCTCCCCTCGACAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCCACCTCAG GCCGGCTCCCCTCGACAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCTCAGC TCCTCCCTGCGGATCCGCACCCTCCCCTGGGCCCCATCTCAAGGCTGCCCCCTTCC ٥; 60.7%; Score 833.4; DB 2; Length 1030; 99.9%; Pred. No. 1.1e-167; Sequence 1030 BP; 223 A; 317 C; 279 G; 211 T; 0 U; 0 Other; 1; Indels Pred. No. 1.1e-167; 0; Mismatches 1; induced apoptosis Matches 834; Conservative Similarity 289 409 ( 349 Query Match 469 301 709 481 541 361 649 421 694 829 601 889 661 Local ਨੇ g à g g g q g à g g g ò Š à ò ਨੇ ð g 셤 ð ò à 셤

GCTCCAGACCTGCCCCTCCTAGAGGCTGCCTGGGCCTGTTCACGTGTTTTCCA 1008 GCTCCAGACCTGCCCTCCTCTAGAGGCTGCCTGGGCCTGTTCACGTGTTTTCCA ACATAAATACAGTATICCCACTCTTATCTTACAACTCCCCCACCGCCCACT 1063 

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ВР CDNA; 1239 dard;

(first entry)

AK coding sequence.

cell death; organ disease; neural disease; cartilace disease; connective tissue disease; cellular death; hepatotropic; l; gastrointestinal; osteopathic; gene; ss. EAK; TNF relatedness and weak ability to induce cerosis Factor; TWEAK; fibrosis, cardiac disease; lung disease; kidney disease; skin disease; ; lung disease; kidney disease; skin di le disease; adipose tissue disease; nal tract disease; pancreatic disease;

/\*tag= a /product= "FL-TWEAK" Location/Qualifiers .750

2003WO-US011350

3002US-0371611P

Hahm Ŀ, Zheng Ą, ubowski

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kidney, 'AK-related condition, e.g. liver, gastrointestinal, kic. ic, cartilage or neural tissue condition in a subject nistering to the subject a TWEAK agonist or antagonist.

ID NO 2; 120pp; English

quence is the coding sequence for murine transmembrane FL-atedness and weak ability to induce cell death, where TNF osis Factor). TWEAK is a member of the TWF family. TWEAK tagonists are useful for treating a TWEAK-related fibrosis; cardiac disease; liver disease; lung disease; sthin disease; skeletal muscle disease; adipose tissue ointestinal tract disease; pancreatic disease; reproductive neural disease; cartilage disease; bone disease; sue disease; callular death; and a pathological condition pressing a TWEAK receptor

BP; 249 A; 386 C; 331 G; 273 T; 0 U; 0 Other;

9, Gaps 70; 49.8%; Score 683.4; DB 9; Length 1239; rity 77.0%; Pred. No. 9.7e-136; nservative 0; Mismatches 221; Indels 70;

ATGGCCGCCCGTCGGAGCCAGAGGCGGAGGGGCGCCGGGGGGAGCCGGGCACCG 1 ATGGCCGCCCGTCGGAGCCCAGAGGCGGGCGCCCCGCCGGGGGAGCCGGCCCCC GTGGTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGG Gredricadecrideseaecrideseaacecricaciccadeaeccricacaeaeae 181 ACAGCAGAGGACCGCCGGGAGCCCCTGAACTGAATCCCCAGACAGGAAAGCCA 346 CCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCC 241 GTGGTACCTTTCTTGGAACAACTAGTCCGGCCTCGAAGAAGTGCTCCTAAAGGCCG ACACGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACA 301 GCGCGGCCTCGCCGAGCTATTGCAGCCCATTATGAGGTTCATCCTCGCCGAGGACA GGAGCGCAGGTGTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAA TCCAGCCCTCTGCGCTACAACCGCCAGATCGGGGGGGTTTATAGTCACCCGGGCTGG 421 rccasccrcrscscracsccsccasarresssarriacasrcarcarcasscres TACTACCTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCT TIGCTGGTGGATGGTGCTGGCCCTGCGTGCCTGGAGGAATTCTCAGCCACTGC Adcricrocrosoccicoscrocorrigios de actividades de ac GGGTCTTCCCTTCGGATCCGCACCCTCCCTGGGCTCATCTTAAGGCTGCCCCTT ACCTACTTCGGACTCTTCCAGGTTCACTGAGGGGCCCTGGTCTCCCCACAGTCGTC Accracitirdeacicitirdaadirdacidadadadcicitidciccoagarrocria ----CCTCGACAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCA 781 TTCCCTGGCTCCAGGAGCATCACCACCTCCCTACCCCCACCCCCACTCCTCCACC CAGCCGCTCTTTGCTCCAGACCTGCCCCTCTCTAGAGGCTGCCTGGGCTGTTC ACTCTCCACCTCACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGATCTCG CCCCCTGGCCACAGACCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGAT 1181 TCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAA TACTACCTGTACTGTCAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCT Tridchidaracadridridchidacacardacaracaradaadaarhachadacaacada GGGTCCTCCCTGCGGATCCGCACCCTCCCCTGGGCCCCATCTCAAGGCTGCCCCCTT ccccccccccccccccccccccccccccccc---ACTATCCACCTCACTAGCTCCCAAAGCCCCTAC------AGTICCCICGGGCCCCAGCICCGCCTCTGCCAGGIGICTGGGCT GCTGCCGGCTCC 166 61 226 286 406 586 481 646 541 466 661 721 904 994 951 826 886 841 1001 1001 898 1121 966 g 8 DD 8 원 ð ద à Ω PP 임 ð ò ð d ò 쉽 ઠે 셤 ö d ò 셤 g ò à g ð g ð g à 셤 ò

1299 IGAGAATICCCIGIGGATTITIAAAACAGATATIATTITITATTATIATIGIGACAAA 1359 3GA----TCCCTGTGGGATTTTGAAA--AGATACTATTTTTTATTATTATTGTGACAAA 1196 

> Ä

TTGA 1366 FTAA 1203 BP. ndard; DNA; 898

(first entry)

ector pDC409-LZ-TWEAK fusion protein-encoding DNA.

silular domain, tumour necrosis factor; TNF; angiogenesis; scularisation; diabetic retinopathy; necvascular glaucoma; as; retinopathy of prematurity; retrolental fibroplasia; sitis; macular degeneration; arthritis; rheumatism; ds; neovascularisation; psoriasis; metastatic condition; nour; sarcoma; carcinoma; benign tumour; haemophilic joint; condition; myocardial angiogenesis; wound granulation; vascular adhesion; telangiectasia; ischaemia; human; ic plaque neovascularisation; coronary atherosclerosis; herosclerosis; TWEAKR; TWEAKR; TWEAKR;

/product= "Fusion protein comprising a growth hormone leader, a leucine zipper multimerisation domain, and human TWEAK extracellular domain" Location/Qualifiers .873 /\*tag=

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2000WO-US034755.

2000US-0203347P. 99US-0172878P

EX CORP.

975/44.

igiogenesis in a mammal for treating diseases mediated by e.g. solid tumors and vascular deficiencies of cardiac or ssue, by administering antagonist or agonist of TWEAK

ge 39-40; 46pp; English.

represents a DNA from the expression vector pDC409-LZ-TWEAK, a fusion protein comprising a growth hormone leader, a

AAV18599 standard; cDNA; 1168

RESULT 14
AAV18599
ID AAV18

leucine zipper multimerisation domain, and the extracellular dom human TWEAK. The fusion protein was used in the isolation of hum receptor (TWEAKR) expressing clones from a COS cell human cDNA learners and induces angiogenesis. TWEAKR may therefore be used to screen and induces angiogenesis. TWEAKR may therefore be used to screen develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human contactorised by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retineovascular glaucoma, retinoblastoma, retinopathy of prematurity retrolental fibroplasia, rubeosis, uveitis, macular degeneration corneal graft neovascularisation, and inflammatory diseases such malignant and metastatic conditions such as sarcomas and carcino malignant and metastatic conditions such as sarcomas and carcino benign tumours and preneoplastic conditions, myocardial angiogen haemophilic joints, scleroderma, vascular adhesions, atheroscler plague neovascularisation, telangiectasia, wound granulation, co atherosclerosis, peripheral atherosclerosis and ischaemia 250 AGITTGGGGAGCCGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGCTGG CCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAA 370 CCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAGTGCACCTAAAGGCCGGAAAA 412 GCTCGAAGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGACG 430 GCTCGAAGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGACG CAGGCAGGTGTGGACGGGACAGTGGCTGGGAGGAAGCCAGAATCAACAGCT GTGGATGGTGTGCTGGCCTGCGTGCCTGGAGAATTCTCAGCCACTGCGGCCAC CTCGGGCCCCAGCTCCGCCTCTGCCAGGTGTCTGGGGCTGTTGGCCCTGCGGGCCAGC 232 AGTITIGGGGAGCCGGGCATCTCCGCCCAGGAGCCTGCCCAGGAGGAGCTGG 490 CAGGCAGGTGTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACACT CCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGGCTGGGCTCT 550 CCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCT 592 CIGIACTGICAGGIGCACTITGAIGAGGGAAGGCIGICIACCIGAAGCIGGACI Cristractica de caratra de la casa de caractra de cara GTGGATGGTGTGCTGCCCTGCCTGCAGGAATTCTCAGCCACTGCGGCCA CICGGGCCCCAGCTCCGCCTCTGCCAGGTGTCTGGGCTGTTGGCCCCTGCGGCCAGG recerecedareceracereceresecentereasecreecerecere TCCCTGCGGATCCGCACCCTCCCTGGGCCCATCTCAAGGCTGCCCCCTTCCTCA . 0 DB 4; Length 898; Sequence 898 BP; 187 A; 266 C; 267 G; 178 T; 0 U; 0 Other; 3; Indels Score 629.2; DB 4; Pred. No. 3.1e-124; 0; Mismatches 3; TICGGACTCTTCCAGGTTCACTGAGGGGCCCTGG 865 TTCGGACTCTTCCAGGTTCACTGAGCGGCCGCGG 45.8%; 99.5%; Query Match Best Local Similarity 99.59 Matches 631; Conservative 292 352 472 532 730 610 652 670 712 772 790 832 850 ð g ð d à g à d qq ద ð g ð à à à 셤 d ठ g à

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tnf; treatment; cancer; tumour necrosis factor related ligand (TRELL) gene. necrosis factor related ligand; tnf; treatment sease; immune system; stimulation; suppression; on; ds. (first entry)

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> /\*tag= a /note= "tumour necrosis factor related ligand" Location/Qualifiers 2. .679 \*tag=

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> 96US-0023541P. 96US-0028515P. 97US-0040820P. 97WO-US013945.

GENEVA FACULTY MEDICINE.

e Y, Browning JL; 619/13 is factor related ligand - useful for, e.g. treating cancer, isease and immune responses to tissue grafts.

45-46; 69pp; English.

or active fragments can be included with a carrier in a compositions to treat cancer, autoimmune diseases or see to tissue grafts, or to stimmlate or suppress the immune useful to screen for TRELL receptors, by labelling with a bel and screening compositions for binding. Agents ith TRELL-receptor binding can also be screened for, can istered, optionally with interferon-gamma, to induce cell; suppress or alter immune responses (especially involving richnoma cells) involving a signal pathway between TRELL and The DNA sequence can be used in gene therapy for TRELL-fers in mammals (especially humans), e.g. tumours, it inflammatory diseases or inherited genetic disorders, by the cells, and expressing, therapeutically effective amounts or cells, and expressing, therapeutically effective amounts. Gravius comprising a gene encoding TRELL. It may also the preparation of prepare probes for screening that encoding mouse tumour necrosis factor related ligand

BP; 242 A; 360 C; 298 G; 268 T; 0 U; 0 Other;

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3CCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGGAGCTGGTGGCAGAGGAG 297 Gaps 70; Score 614.6; DB 2; Length 1168; 0; Mismatches 219; Indels Pred. No. 4.2e-121; 44.8%; nservative arity

ceccessascecercasacressarececasacasasasasasecassareraserae Treganchactregecerceangangreerectanangecegeage 418 AGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGACGGAGCGC 362 cectaceacceccaeatresesaartracaercarcaesescresecreracra GGTGTGCTGGCCTGCCTGGAAATTCTCAGCCACAGAAGCTCTCC 542 ccccadcrccarrioraccaagrarcragacrarraccacracaaccaaagrarra 602 CGGATCCGCACCCTCCCCTGGGCTCATCTTAAGGCTGCCCCTTCCTAAGCTAACCTACTT CICITCCAGGIICACTGAGGGGCCCTGGICICCCCAACAGICGICCCAGGCIGCCGG 662 crcirrcaagricacigagggccrigcriciccagarrccriaaacrrrccrigg ----CCTCGACAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCACCCTCAGCCGCT 953 GCTCCAGACCTGCCCCCCCTCTAGAGGCTGCCTGGGCCTGTTCACGTGTTTTCCA 781 dercchárcerererece--reaaksecasecasaserrererer 1073 ACTAGCTCCCCAATCCCTGACCCTTTGAGGCCCCCCAGTGATCTCGACTCCCCCTG 892 ACTAGCTCCCAAAGCCCCTAC------Trarcccrdacrccccaco 1133 CAGACCCCCAGGGCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAG 1193 CACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGC ----CAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAGAGACCTGGGA( GCCAGGAGTTCCCAAATGTGAGGGGGGGAA-AACAAGACAAAGCTCCTCCCTTGAGA 298 GACCAGGACCCGTCGGAACTGAATCCCCAGACAGAAGAAAGCCAGGATCCTGCGC CTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGG 242 cGAGCTATTGCAGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCAC GGTGTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCC 302 GGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCC TGTCAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGG 658 GGTGTGCTGCCCTGCCTGCCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCCC 722 AGGAGCATCACCACCTCCCTACCCCACCCCCACTCCTCCACCCCCTC-GCTGCT 1013 ACATAAATACAGTATTCCCACTCTTATCTTACAACTCCCCCACCGCCCACTCTCCA 838 -----ACAGACGTATCCTTGCTCTTAACATCCCATCCCACCACAACTATCCA GCCAGAAGTTCCCAACTGTGAGGGGAAAGAGCTGGGGACAAGCTCCTCCCTGGA--TGTCAGGTGCACTTTGATGAGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGG CCCCAGCTCCGCCTCTGCCAGGTGTCTGGGCTGTTGGGCCCTGCGGCCAAGGGTCCT CCTGTGGATTTTTAAAACAGATATTTTTTTTTTTTTTTGTGACAAATGTTGA CCTGTGGATTTTGAAA--AGATACTATTTTTATTATTATTGTGACAAAATGTTAA 778 CGGAICCGCACCTICCCCIGGGCCCAICTCAAGGCIGCCCCCIICCTCACCIACI 937 CACCCGACCACGTGTTATTGACTTTGTGCAC--------182 838 868 358 478 538 598 422 482 718 696 1253 1024 1312 1080

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ndard; DNA; 701 BP.

(first entry)

sis factor receptor; signal transducer molecule; TNF; APO4; l abnormality; gestational abnormalitity; prostate cancer; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease; domain; immunogen; antibody preparation; breast carcinoma;

Location/Qualifiers /product= "TNRL3" æ 1. .636 /\*tag=

98WO-US018393.

97US-00924634.

WASHINGTON

3191/17.

unosis Factor family receptor polypeptides and ligands - agnosis and treatment of prostate cancer and developmental abnormalities.

Fig 13B; 156pp; English.

on describes isolated Tumor Necrosis Factor (TNF) family peptides: APO4, APO6, APO8 and APO9 or their active of isolated Tumof APO9 or their active of isolated Tumof Indands 1 and 3 (TNRL1 and TNRL3) or fragments. APO4 is useful for diagnosing prostate cancer by evels of APO4 in an individual. Prostate cancer can also be APO4 selective binding agents linked to a therapeutic polypeptides are also useful for identifying selective is, useful in diagnosis/treatment of disease by binding of the cell surface. The binding is preferably performed in Typeptides/active fragment which is extracellular, or the cell surface. The binding as preferably performed in Typeptides/active fragments are also useful for screening and antagonists by binding and observing the changer in APO4 ective pharmacological agents useful in diagnosis or disease are also identified using APO4 polypeptides/active ammic domain of APO4 and detecting a change in level of APO4 method is performed in vivo or in vitro. APO polypeptides agnosis/treatment of developmental or gestational duced apoptosis

BP; 139 A; 210 C; 203 G; 149 T; 0 U; 0 Other;

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                                      Gaps
                                      ·,
37.8%; Score 519.2; DB 2; Length 701;
87.3%; Pred. No. 7.3e-101;
tive 0; Mismatches 83; Indels 0;
                                 onservative
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/ cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
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#### SUMMARIES

Length DB ID  1364 9 US-09-822-849A-19 1353 14 US-10-210-951-3 1356 12 US-10-211-884-3 1306 14 US-10-22-411-16 1306 14 US-10-272-411-16 1306 14 US-10-272-328A-16 1306 14 US-10-272-328A-16 1306 14 US-10-10-793-29 1306 14 US-10-10-793-29 1306 14 US-10-10-793-29 1306 14 US-10-10-793-29 1306 14 US-10-10-793-29 1306 14 US-10-10-793-29 1306 14 US-10-10-793-29 1306 14 US-10-10-793-29 1306 14 US-10-10-793-29 1306 14 US-10-10-793-29 1306 14 US-09-883-777-1 1493 10 US-09-883-777-1 1493 10 US-09-983-777-1 1408 9 US-09-883-777-1 1408 9 US-09-883-777-1 1408 9 US-09-860-35-21225 1408 9 US-09-950-35-21225 1408 9 US-09-950-35-21225 1408 9 US-09-95-35-35-35-36-35-376 1408 9 US-09-95-35-35-35-37-36-35-37-36-35-37-36-37-37-37-37-37-37-37-37-37-37-37-37-37-				1	. –			. –	. –			d			٠.,	
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	DB	σ	14	14	12	14	14	14	14	σ	σ	10	9	12	15	6
74 0000000000000 B4	Length	1364	1353	1353	1306	1306	1306	1306	1306	868	868	493	408	213	213	264
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wong, Gordon G.

LALCANT: Clark, Hilary
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Resninck, Richard J.
APPLICANT: Rensinck, Richard J.
APPLICANT: Graham, James R.
APPLICANT: Graham
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Pred. No. 0;
0; Mismatches 2; Indels 0;
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99.9%;
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Matches 1347; Conservative
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Qy         1225 GGCAGGAAGCCAAAGAACCTAGGCCTAGGCCAGGAGTTCCCAAATGTCAGGGCCC           Db         1205 GGCAGGAAGCCAAAGAACTGCGCCTAGGCCAAGAGTTCCCAAATGTCAGGGCCCC           Qy         1285 CAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAACAGATATTATT           Db         1265 CAAGACAAGCTCCTCCTTGAGAATTCCTGTGGATTTTTAAAACAGATATTATT           Qy         1345 TATTATTGTGACAAAATGTTGATAAATGG           Db         135 TATTATTGTGACAAAATGTTGATAAATGG           Db         135 TATTATTGTGACAAAATGTTGATAAATGG	RESULT 2 US-10-210-951-3 ; Sequence 3, Application US/10210951 ; Publication No. US203030170228A1 ; GENERAL INFORMATION: ; APPLICANT: Ashkenazi, Avi J. ; APPLICANT: Goddard, Audrey ; APPLICANT: Goddard, Audrey ; APPLICANT: Godwaki, Paul J. ; APPLICANT: Godwaki, Paul J. ; APPLICANT: Hillan, Kenneth J.	APPLICANT: Path, James APPLICANT: Pitti, Robert M. APPLICANT: Pitti, Robert M. APPLICANT: Stone, John M. APPLICANT: Stone, Donna M. APPLICANT: Watanabe, Colin K. APPLICANT: Watanabe, Colin K. APPLICANT: Watanabe, Colin K. APPLICANT: Watanabe, Colin K. APPLICANT: Wood, William I. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF CURRENT APPLICATION NUMBER: US/10/210,951	PRIOR FILING DATE: 1996-04-01  PRIOR PELICATION NUMBER: 60/026943  PRIOR PELICATION NUMBER: 60/026943  PRIOR PELICATION NUMBER: 60/029121  PRIOR PELING DATE: 1997-07-17  PRIOR PELING DATE: 1997-07-17  PRIOR FILING DATE: 1997-09-19  PRIOR FILING DATE: 1997-09-19  PRIOR PELICATION NUMBER: 60/062037  PRIOR APPLICATION NUMBER: 60/063755  PRIOR PELING DATE: 1997-10-10  PRIOR PELING DATE: 1997-10-17	125:20.4   125:20.5
GCACAGCCCCCCGTCGCCCGTCGGAGCCAGAGGGGGGGCCCGG			GCCTCTGCCAGGTGTCT GCCTCTGCCAGGTGTCT GCCTCCCCTGGGCCCAT CCCTCCCCTGGGCCCAT CCCTCCCCTGGGCCCAT CCTCCCCTGGGCCCAT CCTCCCCTGGGCCCTGT	

Db 1141 ACCCCACTTCAGGCACTAAGAGGGCTGGACCTGGCGGCAGGAAGCCAAAGACTC Qy 1249 CTAGGCCAGGAGTTCCCAAATGTGAGGGGGAGAAACAAGACAAGACAAGCCAAAGACTTC Db 1201 CTAGGCCAGGAGTTCCCAAATGTGAGGGGGAGAAACAAGACAAGACACCTCCCTTC Qy 1309 TTCCCTGTGGATTTTTAAAACAGATATTTTTATTATTATTATTGTGACAAAATGTT Db 1261 TTCCCTGTGGATTTTTAAAACAGATATTTTTATTATTATTGTGACAAAATGTT Qy 1369 AATGG 1373 Db 1321 AATGG 1373	RESULT 3 US-10-211-884-3 Sequence 3, Application US/10211884 Publication No. US20030175900A1 GENERAL INFORMATION: APPLICANT: Abkenazi, Avi J. APPLICANT: Goddard, Audrey APPLICANT: Godwski, Paul J. APPLICANT: Gurney, Austin L. APPLICANT: Marsters, Scot A. APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pan, James APPLICANT: Pan, James	APPLICANT: Smith, Victoria APPLICANT: Stone, Donna M. APPLICANT: Stone, Donna M. APPLICANT: Stone, Donna M. APPLICANT: Watanabo, Colin K. APPLICANT: Wood, Walliam I. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF T FILE REPERENCE: P2931R1C1 CURRENT APPLICATION NUMBER: 60/104699 PRIOR FILING DATE: 1996-04-01 PRIOR PRILING DATE: 1996-04-01 PRIOR PRILING DATE: 1996-09-03 PRIOR PRILING DATE: 1996-09-13 PRIOR PRILING DATE: 1996-09-13 PRIOR PRILING DATE: 1996-09-17	PRIOR APPLICATION NUMBER: 60/059352  PRIOR FILING DATE: 1997-09-19  PRIOR FILING DATE: 1997-03-19  PRIOR FILING DATE: 1997-10-10  PRIOR FILING DATE: 1997-10-17  PRIOR APPLICATION NUMBER: 60/063045  PRIOR PILING DATE: 1997-10-24  PRIOR FILING DATE: 1997-11-24  PRIOR FILING DATE: 1997-11-24  PRIOR FILING DATE: 1997-11-24	RAION FILIN ROMBER OF S ROWBER OF S ROW 10 3 LENGTH: 13 TYPE: DNA ORCANISM: -10-211-884- Ouery Match Best Local S Matches 1322	Db 1 CGATCCCTCGGGATGGGGGGGGGGGGGGGGAGGCACACACCCCCCCC
	CTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACA 408  CTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACA 360  CTTTCCTGAACAGCTTCGCAGCCTGCTGCAGAGTGCACCTGAACGCCCGGAAAACA 360  CTCGAACAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGACGA 468	TCTGCGCTACAACCGCCAGATCGGGGACTTTATAGTCACCCGGGCTGGGCTTACAACCGCCAGATCGGGGAACTCTATATAGTCACCCGGGCTGGGCTTACACCGGGCTCTACCTAC	CCTGCGGATCCGCTGGGCCCATCTCAAGGCTGCCCCTTCCTCACC 828  CCTGCGGATCCGCTCCTCGCTGGGCCCATCTCAAGGCTGCCCCTTCCTCACC 828  CCTGCGGATCCTTCCAGCTTCACTGAGGGCCCTTCCTCAGGCTTCCTCACC  CGGACTCTTCCAGGTTCACTGAGGGCCCTGGTCCCCCCCAGTCCTCCCAGGCT 840  CCTCCCCTCGACAGCTCTCTGGGCACCCGGTCCCCCCCCC		The state of the s

	RESULT 4 US-10-202-062-23  Sequence 23, Application US/10202062  Publication No. US20040038349A1  GENERAL INFORMATION:  APPLICANT: Human Genome Sciences, Inc.,  TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members  FILE REPERENCE: PF559  CURRENT APPLICATION NUMBER: US/10/202,062  CURRENT FILING DATE: 2002-07-25  PRIOR FILING DATE: 2001-07-27  NUMBER OF SEQ ID NOS: 42  SOFTWARE: PatentIn version 3.0  SEQ ID NO 23  LENGTH: 1306  TYPE: DNA  CORANISM: human  US-10-202-062-23	Query Match         93.6%;         Score 1285;         DB 12;         Length 1306;           Best Local Similarity 100.0%;         No. 0;         Indels 0;           Matches 1285;         Conservative 0;         Mismatches 0;         Indels 0;           Qy         89 CACAGCCCCCGCCCCATGGCCCGTCGGAGCCGAGAGGCGGCGCCG	Qy         149 AGCCGGGCACCGCCTGGTGGTCCCGCTCGGGCTGGGCCTGGGCCTGGGCCTGGGCCTGGCGCTGGC           Db         6.1 AGCCGGCACCGCCTGGTGGTCCCGCTCGGCTGGGCCTGGGCCTGGCGTGGC           Qy         2.09 TCGGCCTCTGCTGGTGGTCAGTTTGGGGAGCCGGGCATCGCTCCGCCCA           Db         121 TCGGCCTCTGCTGGTGGTCAGTTTGGGGAGCCGGGCATCGCTGCCCCA	Qy         269         CTGCCCAGGAGGAGCTGGTGGCAGAGGACGACCCGTCGGAACTGAATCC           b         181         CTGCCCAGGAGCTGGTGGCAGAGGAGGACCCGTCGGACTCGGAACTGAATCC           Qy         329         CAGAAGAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAG           Db         241         CAGAAGAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAG	Qy         389         CACCTAAAGGCCGGAAAACACGGGCTCGAAGGCGATCGCAGCCCATTATGAAGT           Db         301         CACCTAAAGGCCGGAAAACACGGGCTCGAAGGCGATCGCCACTTATGAAGT           Qy         449         CACGACCTGGACGGAGGCGCAGGCGGGACGGGACAGTGAGTG
3CCCGTCGGAGCCAGAGGGGGCGCCGGGGGAGCCGGCCCCTGCTG 168 3CCCGTCGGAGCCAGAGGGGGCGCCGGGGGAGCCGGCCCTGCTG 168 3CCCGTCGGAGCCAGAGGGGGCGCCGGGGGGAGCCGGCCCTGCTG 120 5CGCTCGCGCTGGGCCTGGGCCTGGCCTGGCCTCCTGCTGC					

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ORGANISM: DUNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/AF030099.1
DATABASE ACCESSION NUMBER: NCBI/AF030099.1
DATABASE BUTRY DATE: 1997-12-20
RELEVANT RESIDUES: (1). (1306)
PUBLICATION INFORMATION:
DATABASE BUTRY DATE: 2002-10-07
RELEVANT RESIDUES: (1). (1306)
PUBLICATION INFORMATION:
DATABASE BUTRY DATE: 1998-05-04
RELEVANT RESIDUES: (1). (1306)
PUBLICATION INFORMATION:
DATABASE ROTES (1). (1306)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/BC019047.1
RELEVANT RESIDUES: (1). (1306)
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RELEVANT RESIDUES: (1). (1306)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: ACBI/BC019047.1
RELEVANT RESIDUES: (1). (1306)
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CCTGAAGCTGGACTTGCTGGTGGTGGTGTGCTGGCCCTGGGCTGCCTGGAGGAAT
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                                                                                                                                                                                                              149 AGCCGGGCACCGCCCTGCTGGTCCCGCTCGCGCTGGGCCTGGGCCTGGCGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 CACCTAAAGGCCGGAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTT
                                                                                                                     .,
                                                                                    Length 1306;
                                                                                                                    Indels
                                                                               Query Match 93.6%; Score 1285; DB 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1285; Conservative 0; Mismatches 0;
DATABASE ACCESSION NUMBER: NCBI/AF030100.1
DATABASE ENTRY DATE: 1997-12-20
RELEVANT RESIDUES: (1)..(1306)
                                                 US-10-272-411-16
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Jewish Hospital IS20030100068A1

Jonathan

3, F. Patrick
clbaum, Steven
con: RANKL MIMICS AND USES THEREOF
6019620-0202
TON NUMBER: US/10/272,411
NATE: 2002-10-15
N WIMBER: 60/329,393
E: 2001-10-15
NOS: 52

In version 3.1

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3666CCTC	ςλ Dp	149 AGCCGGGCACCGCCTGGTGCTCCGCTCGGGCTGGGCCTGGGCCTGGCGCTGCCTGCTG
CACCCGGTCCCCT 92	Qy Db	209 TCGGCCTCCTGCTGGCCGTGGTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCC7
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FTATCTTACAACT 10                 FTATCTTACAACT 96	. da	329 CAGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACGACTAGTTCGGCCTCGCAC 
TTTGAGGCCCCCA 11	Š d	389 CACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGT 
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plication US/10218547 US20030100074A1	λo q	809 AGGCTGCCCCTTCCTCACCTACTTCGGACTCTTCCAGGTTCACTGAGGGGCCCTTCACTTCACTGAGGGGCCCTTTCTTCACTTCACTTTCACACTTTCACACTTTCACACTTTCACACACTTTCA
Au Genome Sciences, inc. TION: Methods And Compositions For Treating Metabolic Bone Diseases Rel TION: Human Endokine Alpha : PF561	δ	σ
ATTON NUMBER: US/10/218,547 DATE: 2002-08-15 [ON NUMBER: 60/312,542 ATE: 2001-08-16	8 8 7	CTGCCCACCTCAGCCTTTGCTCCAGACTCCCTCTGGCCTCTCTTGGCCTCTCTTGTCTTGTTGTTG
ON NUMBER: 60/330,761  TYPE: 2001-10-30  ID NOS: 57  ILI Version 3.1	8 & 1	841 CIGCCCACCCICAGCCGCTCTTTGCTCCAGACCTGCCCTCCCTCTAGAGGCTGG 989 GCCTGTTCACGTGTTTTCCATCCCACATAAATACAGTATTCCCACTCTTATCTTAG
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9	δδ	COTGGCCACAGACCCCCAGGGCATTGTGTTC
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	QY	1169 GGCAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGC

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Sequence 29, Application US/10310793
Publication No. US20030198640A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Shosen, Craig A
APPLICANT: Zhang, Jun
APPLICANT: Abng, Jun
APPLICANT: Rei, Ping
TITLE OF INVENTION: Methods And Compositions For Treating Inflammatoritle OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma |
FILE REFERENCE: PF573
CURRENT APPLICATION NUMBER: US/10/310, 793
          421 AAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTT
                                             TCACCCGGGCTGGGCTCTACCTGTACTGTCAGGTGCACTTTGATGAGGGGAA
                                                                            481 TCACCCGGGCTGTGCTTACTGTACTGTACTGCACTTTGATGAGGGGAA
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TION NUMBER: US/10/272,328A
DATE: 2003-01-24
ON NUMBER: 60/329,393
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyeaq, Inc.
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/315,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PLING DATE: 1999-01-20
                                                                                                                                                                                            DB 9;
                                                                    FEATURE:
COTHER INFORMATION: TWEAK fusion protein construct
NAME/KEY: CDS
COCATION: (52)..(873)
OTHER INFORMATION:
US-09-883-777-1
                                                                                                                                                                                          45.8%; Score 629.2; DB 9; 99.5%; Pred. No. 1.1e-162;
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                                                                                                                                                                                                                             0; Mismatches
                                   TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                       Query Match
Best Local Similarity 99.59
Matches 631, Conservative
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US-09-918-995-21225
                        LENGTH: 898
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                                                                                                      0; Gaps
1ON: Description of Artificial Sequence: human TWEAK 1ON: fusion protein construct
                                                                    Length 898;
                                                                                                  3; Indels
                                                             45.8%; Score 629.2; DB 9; 99.5%; Pred. No. 1.1e-162; 1ve 0; Mismatches 3;
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NN NUMBER: US 60/172,878
E: 1999-12-20
NN UMBER: US 60/203,347
E: 2000-05-10
NN WUMBER: PCT/US00/34755
E: 2000-12-19
NN WUMBER: US 99/742,454
E: 2000-12-19
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0110853A1
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2968-C
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NOS: 16
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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoart.
FILE OF INVENTION: Compositions and Methods Relatiing to Osteoart.
CURRENT APPLICATION NUMBER: US/10/085,783A
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 58994
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                                                                                                                                                                                                                        143 GGGGGAGCCGGGCACCGCCTGCTGGTCCCGCTCGCGCTGGGCCTGGGCCTGGG
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Best Local Similarity 99.5%; Pred. No. 1.1e-41;
Matches 189; Conservative 0; Mismatches 1; Indels 0;
                           45; Indels
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                           0; Mismatches
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; Sequence 55176
; Publication No. US20040037841A1
; GENERAL INFORMATION:
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) LOCATION: (212)...(213)
) OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-55176
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SEQ ID NO 55176
LENGTH: 213
                    Matches 346; Conservative
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tt, John C.

Ahalagan, Nagappan

TION: NUCLEIC AND THER MOLECULES ASSOCIATED WITH LACTATION AND

ION: NUCLEIC AND FAT DEPOSITION

16511.006/37-21(10298)C

TION: VUMBER: US/09/960,352

DATE: 2001-09-24
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'ION: Clone ID: 10-LIB3057-025-Q1-K1-C5
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Pred. No. 4.9e-67;
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ID NOS: 38054
SEQ for Windows Version 3.0
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ON: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
ON: MUSCLE AND FAT DEPOSITION
37-21(10297)C
ION NUMBER: US/09/983,965
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CTAGGCCAGGAGTTCCCAAATGTGAGGGCCCAGAACAAGACAAGCTCCTCCCTT 120
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ION: Compositions and Methods Relatiing to Osteoarthritis
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Pred. No. 1.1e-41;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                            FION NUMBER: US/10/242,535A
DATE: 2002-09-12
                                                                                                                                                                                                                                                                     N NUMBER: US 10/085, 783

TE: 2002-02-28

N NUMBER: US 60/305, 340

TE: 2001-07-13

NN NUMBER: US 60/275, 017

TE: 2001-03-12

NN NUMBER: US 60/271, 955

TE: 2001-02-28
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99.5%;
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                                             AAATGG 1373
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6.7%; Score 91.4; DB 9; Length 264;
Best Local Similarity 66.5%; Pred. No. 5.9e-15;
Matches 147; Conservative 0; Mismatches 71; Indels
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                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: 42-LIB3057-025-Q1-K1-C6 US-09-983-965-2183
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR PILLING DATE: 1999-12-15
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; LENGTH: 264
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GenCore version 5.1.6 Jopyright (c) 1993 - 2004 Compugen Ltd.	n search, using sw model	<pre>il 7, 2004, 17:41:57; Search time 15.6228 Seconds    (without alignments)    1748.625 Million cell updates/sec</pre>	9-2 LLD	)SUM62 )Op 10.0 , Gapext 0.5	1366 segs, 96191526 residues	s satisfying chosen parameters: 283366	.h.: 0 .h.: 200000000	nimum Match 0% ximum Match 100% sting first 45 summaries	<pre>% 78:* pir1:* pir2:* pir3:* pir3:*</pre>
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### SUMMARIES

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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	<b>4</b> .

# ALIGNMENTS

RESULT 2

S27224
N-methyl-D-aspartate receptor epsilon-4 chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence\_revision 01-Sep-1995 #text\_change 17-Mar-C;Date: 25-Feb-1994 #sequence\_revision 01-Sep-1995 #text\_change 17-Mar-C;Date: 25-Feb-1994 #sequence\_revision 01-Sep-1995 #text\_change 17-Mar-C;Date: 313, 34-38, 1992
FEBS Lett. 313, 34-38, 1992
FEBS Lett. 313, 34-38, 1992
A;Title: Cloning and expression of the epsilon-4 subunit of the NMDA recall and a state of the second and state of the second and second

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PGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEBAQEBLVAEBDODPSEL 106	QY  25 GAVEQAQPPAPMAARRSORRRGRRGEPGTALLUVPLALGLGLALA( Db  19 GAIKQKSMAVEKKNRRALGDIGNUVTUVGUEGKALPQUSRTITRGF( QY  74LAUVELGSRASLSAQEPAQEELUAEEDQDPSELNPQI Db  70 ANAEAAAAENNKNSLAUNAKGADGALPIKRAUARVPUÇKKTVKSKPQEIIEISPDI QY  115 DPAPPLNRLURPRRSAPKGRKTRARRAIAAHYEVHPRGQDGAQAGU Db  130APVLEKEITGEKSLKKKAPTLISTLIARSKAASV-VRIKFKEQIVDIDAADUNN	RGRRGEPGTALLVPLALGLGLALA(
	QY 166 SGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGR	CQVHFDEGK     : .VQVHYKFELSPE
protein - Streptomyces coelicolor myces coelicolor 9 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999	QY 213 KLDILVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGS :: :       : :     :     :	LLALREGS 257
Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. 4BL Data Library, August 1999	RESULT 8 T36946	3
ary; translated from GB/EMBL/DDBJ WA SAU> :SAU> : EMBL:AL109663; PIDN:CAB52000.1; GSPDB:GN00070; SCOEDB:SC4Al0.24c ce: strain A3(2)	probable cation-transporting ATPase - Streptomyces coelic C, Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_ C;Accession: 136946 R;Seeger, K.J.; Harris, D.; Thomson, N.R.; Parkhill, J.;	colorchange 18-Aug Baxrell, B.G.
110.24c 6.8%; Score 98; DB 2; Length 206; nrity 27.3%; Pred. No. 1.2;	September 1999 om GB/EMBL/DDBJ	
DISSETVATIVE 18; Mismatches 64; Indels 46; Gaps 7; 3GAVRQAOPPAPMAARRSQRRRGR	A.Crosstances: EMBL:AL109962; PIDN:CAB53131.1; GSPDB:GA:Bxperimental Bource: strain A3(2) C.Genetics: Acceptance: Strain A3(2) A:Genetics: SCORDB:SCJ1.13 C:Superfamily: ATPase nucleotide-binding domain homology	GSPDB:GN00070; SCO
ACLGLILAVVSLGSRASLSAQEPAQEELVAEEDODPSELAPQTEESQDPAPFLARL 123	inding domain homore re 93.5; DB 2; I.d. No. 12; Mismatches 103;	logy <atn> ength 776; Indels 65; G,</atn>
: :	Oy 47 RRGEPGTALLVPLALGLGLALACLGLLLA-VVSLGSRASLSAQEPAQEELVAEE:	DEPAQEELVAEE: 
clin 2 - garden snapdragon num majus (garden snapdragon) #Sequence revision 13-In-1305 #Favt chance 16 T.1 1000	104 SELNPQTEESQDPAPFLNRLVRPRRSAPK     :	WPRPGODGAQA(     WP
0 -1 11	OY 164 TVSGMEBARINSSSPLRYNRQIGEFIVTRAGLYXLYCQVHFDEGKAVYLI 	VHFDEGKAVYL) :
T Cell division revealed by transcriptional regulation of genes durin S41709; MUID:94148008; PMID:8313906 cid sequence not shown	QY 217 LVDGVIALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLR- 	-VSGLLALRPGSSLR- :
	Qy 261 -IRTLPWAHLKAAPFLTYFGL 280                   Db 275 LVVATPCPLLLAAPVAVVSGL 295	
in cle control; cell division control; mitosis 6.7%; Score 97; DB 2; Length 441; rity 24.0%; Pred. No. 3.4; nservative 44; Mismatches 104; Indels 74; Gaps 15;	RESULT 9 T15838 hypothetical protein C54D2.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_C;Accession: T15838 R;Minx, P.	change 17-Mar-

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an c. A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Retures prealiminary A;Reture prealiminary A;Reture prealiminary	A;Residues: 1-664 <sto> A;Residues: 1-664 <sto> A;Cross-references: GB:AE004753; GB:AE004091; NID:g9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE004091; NID:g9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE004091; NID:g9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE004091; NID:G9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE004091; NID:G9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE004091; NID:G9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE004091; NID:G9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE004091; NID:G9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE004091; NID:G9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE004091; NID:G9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE004091; NID:G9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE004091; NID:G9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE004091; NID:G9949433; PIDN:AAG06 A;Cross-references: GB:AE004753; GB:AE04753; GB:AE004753; GB:AE004753; GB:AE004753; GB:AE04753; GB:AE004753; GB:AE004753; GB:AE004753; GB:AE004753; GB:AE004753; GB:AE04</sto></sto>	Atches 77; Conservative 28; MISHGLOHES 11; 2003-201-201-201-201-201-201-201-201-201-201	246 129 300 187		dH2 PA4814 [imported] - Pseudo inosa e_revision 15-Sep-2000 #text_c	Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warreher, Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warreher, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, i. Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Retus: preliminary	A; Molecule type: DNA A; Rolecule type: DNA A; Residues: 1-681 <sto> A; Residues: 1-681 <sto> A; Cross-references: GB:AE004894; GB:AE004091; NID:g9951076; PIDN:AAG A; Cross-references: grain PAO1 C; Genetics: A; Gene: fadH2; PA4814 C; Superfamily: Methylophilus methylotrophus W3Al trimethylamine dehy</sto></sto>		Db 442 FRVRLERLGVDLRLGHRVRQGELDGQFDDVVALGIGEAGARAINE
arity 24.5%; Pred. No. 11;  onservative 24; Mismatches 99; Indels 80; Gaps 14;  MAARRSORREGREGEPGTALLVPLALGLGIALACLGLLLAVVSLGS 81  RIVMAMSSTPPVRRLEGIPRRVFSQVLLMQLAIAAGVAVLATGLFIAPLGDQL 59 RASISAOEPBAGEELVAREDQDPSELNPQTEESQDPAPFLNRLVRPRRAPKGRK 135	MRRALAIAQTTAQQPQVVRD	 PLRDGDGEIVGAVSVGIAYDSVRARLIHAIPÖLFAYAGGALAVGALASWIISRR 216 FSATAASSLGPQLRLCQVSGLLALR 254 FRDLAFSDIAGLAER 236	<pre>sin Rv1219c - Mycobacterium tuberculosis (strain H37RV) sterium tuberculosis 98 #sequence_revision 17-Ju1-1998 #text_change 22-Oct-1999 11 sch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. ies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. ies, R.; Devlin, K.; Schuel, T.; Skelton, S.; Squares, S.</pre>	A4, 1998 , R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. , R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. ing the biology of Mycobacterium tuberculosis from the complete genome r: A70500; MUID:98295997; PMID:9634230 11 11 11 11 11 11 11 11 11 11 11 11 11	DINA <col/> s: GB:293777; GB:AL123456; NID:G3261726; PIDN:CAB07841.1; PID:e1299832; urce: strain H37Rv	6.3%; Score 91.5; DB 2; Length 212; Larity 24.5%; Pred. No. 4.1; Conservative 26; Mismatches 78; Indels 59; Gaps 9; REPGTALLVPLALGIGLALACLGLILAVVSLGSRASLSAQEPAQEELVAEE 99	CADALKSNDPTTWLAQMAEIESQDPAPFLMRLVRPRRSAPKGRKTRARRAIAAHYEVHPR 151  (AAAALKSNDPTTWLAQMAEIESYAPLMAYLVRSMQSGGELAKMLWQKWI 117  2DGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEI-VTRAGLYYLYCQVHFD 205  CHARACT CONTAGRACT	LKI  -  PSI	tein PA3305 [imported] - Pseudomonas aeruginosa (strain PAO1) lomonas aeruginosa (secudinosa

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GenCore version 5.1.6 opyright (c) 1993 - 2004 Compugen Ltd.	<pre>il 7, 2004, 17:41:27 ; Search time 39.6149 Seconds</pre>	09-245-198A-4 4 SLLDFEISARRLPLPRSLGPWAHLKAAPFLTYFGLFQVH 284	0.0 , Gapext 0.5	/041 begs, 3155102/02 residues s satisfying chosen parameters: 1017041	th: 0 th: 200000000	nimum Match 0% ximum Match 100% sting first 45 summaries	TREMBL 25:* sp_archea:* sp_bacteria:*	<pre>sp_tung1:* sp_human:* sp_invertebrate:* sp_invertebrate:*</pre>	sp_mhc:* sp_organelle:*	<pre>sp_phage:* sp_plant:* sp_rodent:* sp_vodent:* sp_vodent:*</pre>	<pre>sp_vartebrate:* sp_vartebrate:* sp_vrivas: sp_vrivas:* sp_bracteriap:*</pre>	· · · · · · · · · · · · · · · · · · ·	the number of results predicted by chance to have a than or equal to the score of the result being printed, d by analysis of the total score distribution.	SUMMARIES	ry ch Length DB ID Description	410 11 Q8BXS2 330 4 Q8IZK7 261 5 O8MRW2	325 409 509 509 509 509	409 5 QBIGD3 398 6 QBMK49 532 16 QB2HP6	Q9ky66 Q84t85 Q7x114 Q9x17	375 16 Q9RRH5 893. 16 Q81ZX0 611 11 Q8KOM8

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                                      SDRREPPELNPQTEESQDVVPFLEQLVRPRRSAPKGRKARPRAIAAHYEVHPRPGQ
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RSQRRRGRRGEPGTALLAPLVLSLGLALACLGLLLVVVSLGSWATLSAQQEPSQEE
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                                                                           )AGVDGTVSGWEEARINSSSPLRYNROIGEFIVTRAGLYYLYCOVHFDEGKAVYLKL
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711.5720(2002).
71.5450443.1;
70. C:membrane, IEA.
73. F:tumor necrosis factor receptor binding; IEA.
75. P:immor response; IEA.
7066952; TNF family.
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Picard A., Martinez-A C., Garcia-Sanz J.A.,
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Last annotation update)
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100.0%; Pred. No. ...
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(Human)

269 243 1 N.A.

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261 AA

PRELIMINARY;

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STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Cellniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherr S.E., Li P.W., Hoskins R.A., Galle R.F.
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.]
                                                                                                                                                                                                                                                                                                                   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C., Nunco J., Pacleb J., Paragas V., Park F. Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 LIVINIGLYYVYAQICYNNSHDQNGFIVF-----QGDTPFLQCLN----TVPTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKES--PAPLHHRRRMHSRHRHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 RSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIVTRAGLYYLYCQV----HFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Figure (20) 600.0016020; C:membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.

GO; GO:000555; F:immune response; IEA.

InterPro; IPR006952; INF family.

InterPro; IPR069983; INF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2005
CG12919 protein.
BIGER OR CG12919.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
T-wdroidea; Drosophilidae; Drosophila.
                                                                                                                                                            Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.0%; Score 116; DB 5; Length 261; 25.4%; Pred. No. 0.048; ative 32; Mismatches 97; Indels
                                                                                                                           Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygot
Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 RLCQVSGLLALRPGSSLRIRTL---PWAHLKAAPFLTYFGLFQV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 HTCHTSGLIHLERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RASLSAQEPAQEELVAE----EDQDPSELNPQTEESQDPAPFLNR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29780 MW; 13B6D5A04EC9122C CRC64;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY119233; AAM51093.1; -. FlyBase; FBgn0033483; eiger.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 261 AA; 29780 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Signan J.R., Yandell M.D., Zhang Q., Chen L.X., Aggers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., acyani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., asu A., Baxendale J., Bayraktaroglu L., Beasley E.M., ends P.V., Berman B.P., Bhandari D., Bolshakov S., tchan M.R., Bouck J., Brokstein P., Bolshakov S., awis P.V., Berman B.P., Cadieu E., Center A., Chandra I., awiey S., Dahlke C., Davengort L.B., Davies P., Dietz S.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Di.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., vangelista C.C., Ferriera S., Fleischmann W., rielian A.B., Garry N.S., Gelbart W.M., Glasser K., g F., Gorrell J.H., Gu Z., Gana P., Harris M., arvey D., Hehman T.J., Hernandez J.R., Heuck J., Stonk K.A., Howland T.J., Wei M.-H., Ibeyam C., ush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., odiac C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., B., McIntosh T.C., McLeod M.P., McPherson D., Ishina N.V., Mobarry C., Morris J., Moshrefi A., Shith T., elson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., mington K.A., Naxon K., Nusskern D.R., Pacleb J.M., Pittman G.S., Pan S., Pollard J., Puri V., Santh T., elson C., Stapleton M., Skupski M.P., Smith T., dalling A.C., Stapleton M., Skupski M.P., Smith T., Modger T., Worley K.C., Wu D., Yang S., Yao Q.A., F., Zaveri J.S., Zhan M., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., ers BW., Rubin G.M., Venter T., Singen M., Zhong W., Zhou S., Zho S., Shith H.O., ers BW., Rubin G.M., Venter J.C., Spith H.O., Spith G., Stapleton C., Stableton C., Stapleton M., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., ers BW., Rubin G.M., Venter J.C., Stapleton C., Stap AGLYYLYCQV-----HFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQL 242 AQEPAQEELVAE----EDQDPSELNPQTEESQDPAPFLNR------LVRPR 127 JADVRNEEONIOGNHTELOEKSSNEATSKES--PAPLHHRRRMHSRHRHLLVRKG 175 GERKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGE 187 ARSEDSRP--AAHFHLSSRRRHQGSM-GYHGDMYIGNDNERNSYQG-HFQTRDGV 231 TTGLYYVYAQICYNNSHDQNGFIVP-----QGDTPFLQCLN----TVPTNMPHKV 281 Gaps 38; ; Filmor necrosis factor receptor binding; IEA.; P:immune response; IEA.
06052; TNF family.
19983; TNF-like. ; DB 5; Length 325; 0.063; ches 97; Indels ; 'SGLLALRPGSSLRIRTL---PWAHLKAAPFLTYFGLFQV 283 36862 MW; 6ESCCB69694F1A3A CRC64; 32; Mismatches 8.0%; Score 116; 55.4%; Pred. No. 0 C:membrane; IEA. AAF58848.1; -. 25.4%; 033483; eiger 51; TNF 1; 1. nservative rity

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-ocT-2002 (TrEMBLrel. 22, Last sequence update)
-ocT-2003 (TrEMBLrel. 25, Last annotation update)
F superfamily ligand, Eiger (Tumor necrosis factor family member
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 RASLSAQEPAQEELVAE----EDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 RAGLYYLYCQV----HFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQL
                                                                                                                                                                               MEDLINE=22060500; PubMed=12065414;
Igaki T., Kanda H., Yamamoto-Goto Y., Kanuka H., Kuranaga E.,
Aigaki T., Miura M.;
"Biger, a TNF superfamily ligand that triggers the Drosophila JNK
pathway.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 RKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKES--PAPLHHR----RRMHSRHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 ARRA-----IAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 VRKARSEDSRPAAHFHLSSRRRHQGSM-GYHGDMYIGNDNERNSYQG-HFQTRDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 NTGLYÝVYAQICYNNSHDQNGFIVF-----QGDTPFLQCLN----TVPTNMPHKV
                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidaa; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                       Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 409;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Inohara N., Nunez G.;
"DT1, a Drosophila tumor necrosis factor family member.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBU databases.
EMBL; AB073865; BAC00950.1;
EMBL; AF142799; AA015310.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.0%; Score 116; DB 5; Length 40
25.5%; Pred. No. 0.084;
ive 33; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 VSGLLALRPGSSLRIRTL---PWAHLKAAPFLTYFGLFQV 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 AA.
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01-0CT-2002 (TrEMBLrel. 22, Last seqn
01-0CT-2003 (TrEMBLrel. 25, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 25.5
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                              EIGER OR DT1 OR CG12919.
                                 INF superfamily ligand,
                                                                                                                                                                       SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                   01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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409 AA. (rEMBLrel. 22, Created) RELIMINARY;

88869E

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923; PubMed=12176339;

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Sorex cinereus (Masked shrew).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Insectivora, Soricidae, Soricinae, Sorex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=21608557; PubMed=11743200;
Murphy W.J., Elzirik E., O'Brien S.J., Madsen O., Scally M.,
Douady C.J., Teeling E., Ryder O.A., Stanhope M.J., de Jong W.W.,
Springer M.S.;
"Resolution of the early placental mammal radiation using Bayesia"
                                                                                                                                                                                                                                                                                                                                                                        84 SLSAQEPAQEEL-----VAEEDQDPSELNPQTEE-----SQDPAPFLNRLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 APKGRKTRARRA-----LAAHYEVHPRPGODGAQAGVDGTVSGWEEARINSSSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 HSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSM-GYHGDMYIGNDNERNSYQG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 QIGEFIVTRAGLYYLYCQV----HFDEGKAVYLKLDLLVDGVLALRCLEBFSATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 RDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVF-----QGDTPFLQCLN----TV
                                                                                                                                                                                                                                                                                                                                                                                                                         198 SYNAHKKKOERKSRSIADVRNEEONIOGNHTELOEKSSNEATSKERPAPLHHR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 294:2346-2351(2001).

EMBL; AJ315936; CAC87000.1; -

EMBL; AJ315936; CAC87000.1; -

EO; GO:001601; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin.

InterPro; IPR00027; GPCR_Rhodopsn.

PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                         Indels 44;
               GO; GO:0016164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
GO; GO:0006515; F:tumor necrosis factor receptor binding; IEA.
InterPro; IPR006502; TNF family.
InterPro; IPR006983; TNF like.
SMART; SM00207; TNF; 1.
PROSITE; PS500251; TNF; 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 409 AA; 46401 MW; FCZE9BD9E012D257 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 PHKVHTCHTSGLIHLERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 GPQLRLCQVSGLLALRPGSSLRIRTL---PWAHLKAAPFLTYFGLFQV 283
                                                                                                                                                                                                                                                                    / Match 7.8%; Score 113; DB 5; Length 409; Local Similarity 23.7%; Pred. No. 0.15; hes 54; Conservative 36; Mismatches 94; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.2%; Score 104; DB 6; Length 398; Best Local Similarity 25.2%; Pred. No. 0.91; Matches 55; Conservative 23; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398 AA; 43576 MW; D57E67B689535E27 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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PROSITE; PS00237, G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha 2B adrenergic receptor (Fragment).
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FlyBase; FBgn0064801; BcDNA:RH51659
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398
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NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SARSEDSRP--AAHFHLSSRRRHQGSM-GYHGDMYIGNDNERNSYQG-HFQTRDGV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAGLYYLYCQV----HFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTGLYYVYAQICYNNSHDQNGFIVF-----QGDTPFLQCLN----TVPTNMPHKV 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38; Gaps
                            n M., Basler K.;
TNF Signaling Mechanisms. JNK-Dependent Apoptosis
Eiger, the Drosophila Homolog of the TNF Superfamily.";
2:1263-1268(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brokstein P., Hong L., Agbayani A., Carlson J., navez C., Dorsett V., Dresnek D., Farfan D., Frise B., nazalez M., Guarin H., Kronmiller B., Li P., Liao G., Hungall C.J., Nunco J., Paceleb J., Paragas V., Park S., wanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                            938; PubMed=12894227;
Maaty W.S., Chen P., Tomar R.S., Eby M.T., Chapo J.,
ore N., Zachariah S., Sinha S.K., Abrams J.M.,
                                                                                                                                                                                                                                                                            receptor, Wengen, comprise a TNF-like system in
                                                                                                                                                                                                                                                                                                                                                                                                                              0; C:membrane; IEA.
4; F:tumor necrosis factor receptor binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
lopterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%; Score 116; DB 5; Length 415; 25.4%; Pred. No. 0.086; ive 32; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAQEPAQEELVAE----EDQDPSELNPQTEESQDPAPFLNR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | | | : | : : : : : | | | : | : | 15GLIHLERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSGLLALRPGSSLRIRTL---PWAHLKAAPFLTYFGLFQV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46918 MW; E087A26DE222D2BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TrEMBLrel. 23, Created)
TrEMBLrel. 23, Last sequence update)
TrEMBLrel. 25, Last annotation update)
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5; P:immune response; IEA. 006052; TNF family. 008983; TNF\_like.

251; TNF 1; 1. 049; TNF 2; 1.

AA;

7; TNF; 1

onservative

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6; AAM76710.1; -. 1; AAM66763.1; -. 860-4867 (2003).

0033483; eiger.

409 AA

PRT;

RELIMINARY;

lanogaster (Fruit fly).

1 N.A.

@ # COLUMN TO THE TO TH

64;

W-2002) to the EMBL/GenBank/DDBJ databases. (8; AAN71595.1; -.

OY 159AGVDGTV-SGWEEARINSSPLRYNRQIGEFIVTRAGLYYLY.  Db 428 TGIDFPVSYGTTVLATDGTVRTGWNSACRMAITAKDGTETWY.  OY 204 FDECKAVYLKLDLIVDGVLALRCLEEFSATAASGLGPQLRLCQVSGLLALRPGSSLI  Db 475 LSTYKVASGTTVKAGDPIAFSGNSGNSTGPHLHFEVRPAGGS;  OY 264 LPW 266  Db 521 LPW 523	TO SOLL	OC Streptomycineae; Streptomycetaceae; Streptomyces. OX NCBI_TaxID=1902; RN [1] RP SEQUENCE FROM N.A. RC STRAIN-A3 (2); RA Brown S.P., Harris D.; RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. BP SEQUENCE FROM N. A.		RA Kinashi H., Hopwood D.A.; RT "A set of ordered cosmids and a detailed genetic and physical map RT "A set of ordered cosmids and a detailed genetic and physical map RT HA 8 Mb Streptomyces coelicolor A3(2) chromosome."; RL Mol. Microbiol. 21:77-96(1996). RN [4] RN SEQUENCE FROM N.A. RC STRAIN-A3(2) / MA45; RX MEDLINE-21996410; PubMed=12000953;	Bentley S.D., Chater K.F., Cerdeno-Tarraga AM., Chatlis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth Huang CH., Kieser T., Larke L., Murphy L., Oliver K., O'Neil Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylo	Warren 1., Wletzoffek A., Woodward U., Baffell B.G., Hopwood D.A.; "Complete genome sequence of the model actinomycete coelicolor A3(2)."; EMBL, A1939121, CAB92661.1; EMBL, A2939121, CAB92661.1; GO; GO:0006508; P:metalloendopeptidase activity; IEA GO; GO:0006508; P:procelolysis and peptidolysis; IEA InterPro; IPR002886; Peptidase M37. Pfam; PF01551; Peptidase_M37; I. Complete proteome. SEQUENCE 565 A3, 58070 MW; 7D0418D480C6A284 CRC6 SEQUENCE 565 A3,	Duery Match Sest Local Similarity Matches 70; Conserva
SRDGGAVRQA-QPPAPMAAR	<pre>(RRAQLSREKRFTFVLAVVİĞVFVLCWFPFFSY 381 (ELIMINARY; PRT; 532 AA.</pre>	<pre>vermitilisnobacteria, Actinobacteridae, Actinomycetales, .e, Streptomycetaceae, Streptomyces03, N.A N.A D.bbAad=11572948.</pre>	la H., Ishikawa J., Hanamoto A., Takahashi C., ikahashi Y., Horikawa H., Nakazawa H., Osonoe T., iiba T., Sakaki Y., Hattori M.; ice of an industrial microorganism Streptomyces leducing the ability of producing secondary ad. Sci. U.S.A. 98:12215-12220(2001).	N.A.  / ATCC 31267 / NCIMB 12804 / NRRL 8165;  06; PubMed=12692562;  Kawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,  tori M., Omura S.;  me sequence and comparative analysis of the industrial  Streptomyces avermitilis.";  31. 21:526-531(2003).	); BAC71174.1; - ; F:metalloendopeptidase activity; IEA. }; P:proteolysis and peptidolysis; IEA. )02886; Peptidase_M37. Peptidase_M37; I. 3 AA; 55998 MW; 6E3FICEC6IE5A738 CRC64;	17.2%; Score 103.5; DB 16; Length 532;  Nastity 23.4%; Pred. No. 1.4;  Naservative 22; Mismatches 107; Indels 103; Gaps 14;  SLGSRDGGAVROAQPPAPMAARRSQRRRGEPGTALLVPLALGIGIALACIGIL 73	

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Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H. Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Fu Y.F., Wang S.Y., Chen J., Kang H., Chen X.Y., Shao C.Y., Shan Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu R.H., Hong G.F.; submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 RSLGS------RDGGAVRQ-----AQPPAPMAARRSQRRRGEPGTALLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHVSELEARKAALAEIAREVEEERAAALISTTAMVEAQDTLRLQHASWEAELK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 LGLALACLGLLLA------VVSLGSRASLSAQEPAQEELVAEE---DQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 NPOTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457 ADRLREAEBAAREAAR-VRQAEBAAREBAARARQABEAAKEBADRARQABATA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     511 GAPWPRANTAVLDGFNAQVEALRAERAELEAAWTRV--EEGRR---SVDAMVEVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 -GVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPW-AHLK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 ---TEPCRGNLISPPRWSFNRPPRSDVPSHPSRHPKSGQSEAEDPAAAEERRRESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 GWEEARINSSSPLRYNROIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 RKLGGTPPPSPPRGGGAVRASSRRPEGAAPTSQPEGERKKKKLRKTGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.0%; Score 101.5; DB 10; Length 967; Best Local Similarity 23.9%; Pred. No. 4.6; Matches 70; Conservative 35; Mismatches 123; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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SEQUENCE 967 AA; 106012 MW; 3FA9D0CFE245B970 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
11-ORT-2003 (TrEMBLrel. 23, Last annotation update)
Hypotheital protein SC02220.
SC02220 OR SC10B7.15.
                                                                                                                                                                                                                                                                                                                              Last annotation update)
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                                                                                                                                                                                                                                                         Created)
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233 TIEAIRAKRQQLQQPRHAAP 252
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OSJNBA0094P09.13.
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SEQUENCE FROM N.A.
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84; Indels 107; DB 16; Length 375;

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25 GAVRQAQPPAPMAA-----RRSQRRRGRRGEPGT--ALLVPLALGLGLALACLGLLI
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                                                                                                                                                                                                                                                                                                                   78 SLGSRASLSAQE-PAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKC
                                                                                                                                                                                                                                                                                                                                                                                                            137 RARRAIAAHYEVHPR-PGQDGAQAG--VDGTVSGWEEARINSSSPLRYNRQIGE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 GRGHRCOPTPGRAATARRLRRPGRAPGRRGOPGSHPAARQRLRADLGAALA----
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EMBL, AP005041; BAC72718.1.
GO, GO:0005524; F:ATP binding; IEA.
GO, GO:0004674; F:Protein serine/threonine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-MA-4680 / ALCC 31267 / NCIMB 12804 / NRRL 8165;
STRAIN-MA-4680 / ALCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-2147403; PubMed=1127948;
MEDLINE-21477403; PubMed=1127948;
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T. Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermittils: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 ATAASSLGPQLRLCQVS------GLLALRPGSSLRIRT 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 ---PSATGEQTHLSLVAPGPGPRDPDWLPWQLALTALSGGSASRLFT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=33903;
                                                    ll protein; Complete proteome.
375 AA; 39596 MW; 197B397658ED30B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                59 DVVTRPTLPAGELPTLLDLAR------ODLESLDDSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 VVADADAQEVYELVAGLFADWQPGEDRPMPAHFQPGLRLHL--
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                              24.0%; Pred. No. 1.7; tive 27; Mismatches
                                                                                                                          7.0%; Score 100.5;
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Nat. Biotechnol. 21:526-531(2003).
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InterPro; IPR02290; Ser thr pkinase.
Pfam; PF00069; pkinase; 1.
SMART; SM0220; Frot kinase; 2.
SMART; SM0220; 3 TKC; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
InterPro, IPR007863; Peptidase M16_C. Pfam; PF05193; Peptidase M16_C; 1. Hypothetical protein; Complete proteon
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                                                                                                                                                                       69; Conservative
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                                                                                                                                                Similarity
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                                                                        SEQUENCE
                                                                                                                       Query Match
Best Local
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Q81ZX0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSARTDFSVWPARGGLTGDEELLRRALA----VWARPGESVGVSATPGTATG--- 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GP-----VLHDGLRVABEVDTARVV-----VLHDGLRLVRYAEPK 365
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96; PubMed=10567266;
n J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
(aft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
In H., Jiang L., Pamphile W., Crosby M., Shen M.,
I., Lam P., McDonald L., Utterback T., Zalewski C.,
Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Alavind L., Daly M.J., Minton K.W., Fleischmann R.D.,
M145;

10; PubMed=12000953;

Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Chater K.F., Cerdeno-Tarraga A.-M., Kieser H.,
eman A., Brown S., Chandra G., Chen C.W., Collins M.,
ser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
ieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
E., Rajandream M.A., Rutherford K., Rutter S.,
nders D., Sharp S., Squares R., Squares S., Taylor K.,
tzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                   me sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AALDFARTDGAGRAAATAVVLG----RADGNVRYLTAPWVTKAAA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ice of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSL------GPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Mismatches 122; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      1217A5C88E3CD419 CRC64;
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YERMBLrel. 13, Last sequence update)
YERMBLrel. 24, Last annotation update)
rotein DR2516.
                                                                                                                                                                                                                                                                                                                                                                                                                                        7.0%; Score 101; DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----LPRSLGSRD-GGAVRQAQ----
                                                                                                                                                                                                                                                                                                                                                             rotein; Complete proteome. AA; 66537 MW; 1217A5C86
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.; AAF12062.1; -.,75264.
                                                                                                                                                                                                                                                                                                                -147(2002).
; CAB90868.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELIMINARY;
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893 AA.

PRT;

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diodurans.

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7;
                                                                                                                                                                               ILLIAVVSL-----GSRA----SLSAQEPAQEELVAEEDQDPSELN 107
                                                                                                                                                                                                                                                                 ESODPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGODGAQAGVDGTVSG 167
                                                                                                                                                                                                                                                                                                                                                     RLPLPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALLVPLALGLGLAL 67
                                                                7.0%; Score 100.5; DB 16; Length 893; arity 22.7%; Pred. No. 5.1; onservative 29; Mismatches 83; Indels 45; Gaps
e/threonine-protein kinase; Complete proteome.
3 AA; 92763 MW; CC4DA95AFAFE2407 CRC64;
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April 7, 2004, 17:46:45 secs

RINSSSPLRYNROIGEFIV 190 

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11 7, 2004, 17:38:07 ; Search time 11.7171 Seconds
(without alignments)
1262.081 Million cell updates/sec SLIDFEISARRLPLPRSLG.........PWAHLKAAPFLTYFGLFQVH 284 141681 GenCore version 5.1.6 opyright (c) 1993 - 2004 Compugen Ltd. s satisfying chosen parameters: 681 seqs, 52070155 residues nimum Match 0% ximum Match 100% sting first 45 summaries a search, using sw model SUM62 op 10.0 , Gapext 0.5 th: 0 th: 2000000000 09-245-198A-4 issProt\_42:\*

1116

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the number of results predicted by chance to have a than or equal to the score of the result being printed, d by analysis of the total score distribution.

### SUMMARIES

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Description	3508 homo	gallu	canis		рошо								hom	mus		mus	P71422 klebsiella		rattu	homod	homo	рошо	oryct		P50592 mus musculu	Q9xt47 macropus eu		marm (	_	9aaw1	63 herpesv	471
ΩΙ	TN12_HUMAN	TNF5_CHICK	TNF5 CANFA	TNF9 HUMAN	HDA7 HUMAN	CG22_ANTMA	TNFB_MACEU		RHO MICLU	Y497 MYCTU	TN14 HUMAN	TNF6 CERTO	NFC4 HUMAN	MLH1 MOUSE	CADF HUMAN			-	INE	TNF	GFI	SEN				TNFC				METE_CAUCR	VGLB_H	VGLB_HSVBP
Length DB	249 1											280 1	902 1	760 1	814 1		280 1														933 1	28
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P12640 bovir 088609 mus m 060663 bomo	P95013 mycok 043763 homo Q9jm10 marmc		
VGLB_HSVBC LMXB_MOUSE LMXB_HUMAN	AROC_MYCTU TLX2_HUMAN TNFC_MARMO	MIS_PIG ZM15_HUMAN ICP0_HSV2H	RAGE BOVIN TUB MOUSE RTNZ_HUMAN
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85.5 85 85	84.5 84 84	8 8 4 8 4 4	83.5 83.5 5.5
3.4 3.5 3.5	37 39	4 4 4 0 L 2	4 4 4 6 4 8

## ALIGNMENTS

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Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y. Arakawa T., Hara A., Fukunishi Y., Korno H., Adachi J., Fukuda S. Arakawa T., Hara A., Fukunishi Y., Korno H., Adachi J., Fukuda S. Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I. Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R. Kadota K., Matsuda H.A., Babburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Ruchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbusl Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washic Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bustnoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sonoenbach C., Seya T., Shibata Y., Storch K. Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilmii Wynshaw-Bonish Y., Kawaji H., Kohtsuki S., Wanabari Y., Kawaji H., Kohtsuki S.
                                                                                                                                                                                                                                                                                                                                                                          TN12 MOUSE STANDARD, PRT, 225 AA.

O5497; O9CTP2;
28-FRB-2003 (Rel. 41, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
28-FRB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 12 (TNF-related winducer of apoptosis) (TWBAK) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicheportiche Y., Bourdon P.R., Xu H., Hsu Y.-M., Scott H., Hession C., Garcia I., Browning J.L.; "TWEAK, a new secreted ligand in the tumor necrosis factor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: Binds to FN14 and possibly also to TNRFSF12/AP03. Inducer of apoptosis in some cell types. Promotes angiogenes: the proliferation of endothelial cells. Mediates NF-KappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a col.
                            156 GAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVY
                                                                                                 LLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activation (By similarity).
-!- SUBUNIT: Homotrimer (Potential).
-!- SUBCELLULAR LOCATION: Type II membrane protein and secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- TISSUE SPECIFICITY: Widely expressed.
-:- PTM: The soluble form is produced from the membrane form by proteolytic processing (By similarity).
-:- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               weakly induces apoptosis.";
J. Biol. Chem. 272:32401-32410(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Retina;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Peritoneal macrophage; MEDLINE=98070415; PubMed=9405449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 83-225 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001)
                                                                                                                                                                                                     TYFGLFQVH 284
                                                                                                                                                                                                                                                    241 TYFGLFQVH 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity)
                                                                                                                                                                                                     276
                                                                                                      216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFSF12.
                                                                                                                                                                                                                                                                                                                                                           TN12 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation-Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            this statement is not removed. Usage by and for commercial dires a license agreement (See http://www.isb-sib.ch/announce/lail to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSORRRGERGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQD
                                                       061; PubMed=10085077; ang Y.-W., Leal J.A., Wiley S.R.; ang Y.C., Lund J.K., Chen Y.-W., Leal J.A., Wiley S.R.; s angiogenesis and proliferation of endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEMBER 12, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 12. SECRETED FORM.
CYTOPLASMIC (POTENVITAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REQRERGERGEPGTALL VPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                     TNRFSF12/APO3. Weak
                                                                                                                                                                                                                                                                              AR LOCATION: Type II membrane protein and secreted. ECIFICITY: Highly expressed in adult heart, pancreas, muscle, brain, colon, small intestine, lung, ovary, spleen, lymph node, appendix and peripheral blood es. Low expression in kidney, testis, liver, placenta, d bone marrow. Also detected in fetal kidney, liver,
                                                                                                                                                Binds to FN14 and possibly also to TNRFSF12/APO3. We apoptosis in some cell types. Mediates NF-KappaB n. May promote angiogenesis and the proliferation of all cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iogenesis; Apoptosis; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .lytic processing.

Y: Belongs to the tumor necrosis factor family.

Ref.3 sequence differs from that shown due to a t in position 125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1268; DB 1; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               soluble form derives from the membrane form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LINKED (GLCNAC. . .).
E660843361C28EBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; C:integral to plasma membrane; TAS.
2; F:receptor binding; TAS.
7; P:induction of apoptosis; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 4e-92; ive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; P:signal transduction, TAS. 006052; TNF family. 008983; TNF like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLEAVAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; AAH19047.1; ALT_FRAME.
1927; TNFSF12.
                                                                                                                                                                                                                                                         Homotrimer (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251; TNF 1; FALSE NEG. 049; TNF 2; 1.
                                                                                                                                274:8455-8459(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; AAC51923.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27216 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.8%;
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FUNCTION: Cytokine that binds to INFRSF5. Mediates B-cell

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wiss Institute of Bioinformatics and the BMBL outstaurous ioinformatics Institute. There are no restrictions on its rofit institutions as long as its content is in no way rofit institutions as long as its content.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tel: 43, Last annotation update)
s factor ligand superfamily member 5 (CD40 ligand) (CD40-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMBER 12, SECRETED FORM (BY SIMILARITY). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHILITITE THE PHILITITE PROBAÇAÇAĞYDĞTVSGWEETKINSSSPLR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEBFSATAASSPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 12, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .azoa; Chordata, Craniata; Vertebrata; Euteleostomi; vves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 N-LINKED (GLCNAC. . .) (POTENTIAL)
24781 MW; 90C412CC0480659B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            ogenesis; Apoptosis; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leghorn; TISSUB=Spleen;
,, Young J.R., Burnside J.;
putative chicken CD40 ligand.";
?-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1020; DB 1;
Pred. No. 8.5e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                               ; TNF; 1.
51; TNF_1; FALSE_NEG.
49; TNF_2; 1.
                                                                                                                                                                                                                                                                 06052; TNF_family.
08983; TNF_like.
                                                                                                                                                                                     ; AAC53517.1; -.
; BAB32249.1; -.
59; Tnfsf12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           el. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.6%;
88.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLG OR CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
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Probom; Plocestry TNF; 1.

SMART; SMO0207; TNF; 1.

PROSITE; PS00025; TNF_2; 1.

Cytokine; Transmembrane; Glycoprotein; Signal-anchor.

CHAIN

272

MENBER 5, MEMBRANE FORM
TUMOR NECROSIS FACTOR LIGAND SUPERFAI

TUMOR NECROSIS FACTOR LIGAND SUPERFAI

TUMOR NECROSIS FACTOR LIGAND SUPERFAI

TUMOR NECROSIS FACTOR LIGAND SUPERFAI

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TUMOR NECROSIS FACTOR LIGAND SUPERFAI

TOWN NECROSIS FORM (BY SIMILARITY

NEWBER 5, SOLUBLE FORM (BY SIMILARITY

NEWBER 5, SOLUBLE FORM (BY SIMILARITY

NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1, NEWBER 1,
                      proliferation in the absence of co-stimulus as well as IGE production in the presence of IL-4. Involved in immunoglobuliz class switching (By similarity).

-!- SUBCELULAR LOCATION: Type II membrane protein. Also exists as extracellular soluble form (By similarity).

-!- PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collebetween the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centities requires a license agreement (See http://www.isb-sib.ch/ē or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 RRAIAAHYEVHPRPGQDGAQAGVDGTVSGW-EEARINSSSPLRYNRQIGEFIVTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 RQPIATHLA-----GVKSNTTVRVLKWMTTSYAPTSSLISYHE--GKLKVEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 LYCQVHFDEGKA-----VYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.6%; Score 109.5; DB 1; Lengum 26.4%; Pred. No. 0.14; Lengum 26.4%; Pred. No. 0.14; Lindels 33;
                                                                                                                                                                                                                                                                                                                                     proteclytic processing (By similarity).
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 IYSQVSFCTKAAASAPFTLYIYLYLPMEEDRLL-MKGLDTHSTSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30832 MW; 8CD0338A924E044B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 ---SGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQV 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 IREGGVFELROGDMVFVNVTDSTAVNVNPGNTYFGMFKL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AJ243435, CAB95748.2; -. HSSP, P29955; IALY. GO; GO:0016021; Cintegral to membrane; ISS. GO; GO:0016021; Cintegral to ceeptor binding; ISS. GO; GO:00042100; P:B-cell proliferation; ISS. GO; GO:00042100; P:B-cell proliferation; ISS. GO; GO:0007159; P:Inflammatory response; ISS. GO; GO:0007159; P:leukocyte cell adhesion; ISS. GO; GO:0007159; P:leukocyte cell adhesion; ISS. InterPro; IPR003363; TWF 5.
InterPro; IPR006052; TWF_family.
InterPro; IPR006053; TWF_family.
InterPro; IPR003666; TWF_lamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00229; TNF; 1.
PRINTS; PR01702; CD40LIGAND.
ProDom; PD008600; TNF 5; 1.
ProDom; PD002012; TNF 8ubf; 1.
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124
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251
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110
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1251
272 AA;
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Best Local Similarity
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RESULT 4 TNF5\_CANFA

NEESERRESER \* \* > > > > \$ \$ \$ \$ \$ \$ \$ \$

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EMBL; U03398; AAA53134.1; -. PIR; 138427; I38427. Genew; HGNC:11939; TNFSF9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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01-FEB-1995
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Eur. J. I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TARKER BERNESSON OF THE STANKING STREET TO SOLUTION                                                                                                                                                                                                                                             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OT entry is copyright. It is produced through a collaboration Swiss Institute of Bloinformatics and the EMBL outstation. Bloinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial ires a license agreement (See http://www.isb-sib.ch/announce/ail to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unsmembrane; Glycoprotein; Signal-anchor.
1 260 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBER 5, MEMBRANE FORM.

WHORN RECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 5, SOLUBLE FORM (BY SIMILARITY).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                       perties of canine CD401.";
(G-198) to the BMEL/GenBank/DDBJ databases.
Cytokine that binds to TMPRSF5. Mediates B-cell
tion in the absence of co-stimulus as well as IgE
in in the presence of IL-4. Involved in immunoglobulin
Homotrimer (By similarity).
Homotrimer (By similarity).
AR LOCATION: Type II membrane protein. Also exists as
ular soluble form (By similarity).
                                                                                                                                                                                                                       tazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
heria; Carnivora; Fissipedia; Canidae; Canis.
                                                                   Rel. 40, Last sequence update)
Rel. 41, Last annotation update)
s factor ligand superfamily member 5 (CD40 ligand).
OLG OR CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ic processing (By similarity).
Y: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LINKED (GLCNAC. . .) (PC 604F69A19E98EB70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLEAVAGE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4, P.inflammatory response, ISS.
9, P.leukocyte cell adhesion, ISS.
8, P.platelet activation, ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11, C:integral to membrane; ISS. 4; F:CD40 receptor binding; ISS. 10; P:B-cell proliferation; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 0.16; 23; Mismatches
260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1003263; TNF 5.
1006052; TNP_family.
1008983; TNF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; AAD04375.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; 1.
subf; 1.
                                                  Rel. 40, Created)
Rel. 40, Last seq
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STANDARD;
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Interro, 125, 127, 1. SMART; SM0029; TNF; 1. SMART; SM00207; TNF; 1. PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1. Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Polymorphi: 28 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Cytokine that binds to TNFRSF9. Induces the proliferation of activated peripheral blood T cells. May have role in activation-induced cell death (AICD). May play a role cognate interactions between T cells and B cells/macrophages. -!- SUBGNIT: Homotrimer (Potential).
-!- SUBGRILULAR LOCATION: Type II membrane protein.
-!- IISSUE SPECTICITY: EXPRESSED IN BRAIN, PLACENTA, LUNG, SKEL! MUSCLE AND KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=94374434; PubMed=8088337; Adderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage F Falk B., Rows E., Baker E., Sutherland G.R., Din W.S., Goodwin R. Molecular and biological characterization of human 4-1BB and it:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collbetween the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction week by non-profit institutions as long as its content is impossible and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch, or send an email to license@isb-sib.ch).
103 EMKKEENIAMQKGDQDPRIAAHVISEASSNPASVL-----RWAPKGYYTISSNI
                                                                                                                                                                                                                                                                                                                                          178 SNRÅASSQAPF----VÅSLCLHSPSGTERVLLRAASSRGSSKPCGQQSIHLGGVF
                                                                                                                                                                                                         -----LAVKROGLYYVYAÇ
                                                                                                                                                                                                                                                                                       206 EGKAVYLKLDLLVDGVLALRCLEEFSAT-----AASSLGPQLRLCQVS----GLL
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                        146 YEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGBFIVTRAGLYYLYCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 9 (4-1BB ligand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 AA.
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GO; GO:0005102; F:receptor binding; TAS.

GO; GO:0006915; P:apoptosis; TAS.

GO; GO:0008283; P:cell proliferation; TAS.

GO; GO:0007267; P:cell-cell signaling; TAS.

GO; GO:0007165; P:signal transduction; TAS.

InterPro; IPR006993; TNF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|: : : | | | : : GASVFVNVTDPSQVSHGTGFTSFGLLKL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 GSSLRIRTLPWAHLKAAPFLTYFGLFQV 283
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REP SEQUENCE FROM N.A.  RAD Worley K.C.;  Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.  RI [5]  RP SEQUENCE OF 75-952 FROM N.A. (ISOFORM 1).  RC TISSUB-Uterus;  R. Koehrer K., Beyer A., Mewes HW., Gassenhuber J., Wiemann S.;  R. Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  R. Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.  R. Sterence OF 241-952 FROM N.A. (ISOFORM 1).  R. TISSUB-B-Cell, and Colon;  RX MEDLINE=22388257; PubMed=12477932;  RADLINE=22388257; PubMed=12477932;  RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  RA Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Heish F.,	RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T. RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S. RA Richards S.A., McEman P.J., McKernan K.J., Malek J.A., Ganzratne P.H. RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzwinski M.I., Skalska U., Smailus D.E., RA Butterfield Y.S.N., Krzwinski M.I., Skalska U., Smailus D.E., R. Generation and initial analysis of more than 15,000 full-length P. RT "Generation and initial analysis of more than 15,000 full-length P. RT proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	REP SUBCELLULAR LOCATION, AND INTERACTION WITH EDNRA.  REAL MEDINE—21264398; Pubmed=11262386;  RET "Tip60 and HDAC7 interact with the endothelin receptor a and may ker involved in downstream signaling.";  RT "Tip60 and HDAC7 interact with the endothelin receptor a and may ker involved in downstream signaling.";  RT J. Biol. Chem. 276:16597-16600(2001).  RE PIREACTION WITH HDAC7 LIDEN W., Hendzel M.J., Voelter W.,  RA MEDLINE—214447773; PubMed=11466315;  RA Fischle W., Dequiedt F., Fillion M., Hendzel M.J., Voelter W.,  RA Perdin B.;  RT "Human HDAC7 histone deacetylase activity is associated with HDAC2 vivo.";  RI U. Biol. Chem. 276:35826-35835(2001).  RE PUNCTION.  RR MEDLINE=2224741; PubMed=12239305;  R Bryant H., Farrell P.J.;  R Stynal transduction and transcription factor modification during	
E PROTEIN) R R R R R R R R R R R R R R R R R R R		STANDARD; PRT: 952 AA.  ; Q96K01; Q9BR73; Q9H7L0; Q9NWA9; Q9NYK9; PR el. 42, Last sequence update) el. 43, Last annotation update) el. 43, Last annotation update) 7. Human). Racoa; Chordata; Craniata; Vertebrata; Euteleostomi; PR eria; Primates; Catarrhini; Hominidae; Homo.  N.A. (ISOFORM 1). I carcafinoma; R N.A. (ISOFORM 1). I carcafinoma; R R N.A. (ISOFORM 1). R R N.A. (ISOFORM 1). R R N.A. (ISOFORM 1). R R R N.A. (ISOFORM 1). R R R R N.A. (ISOFORM 1). R R R R R R R R R R R R R R R R R R R	A. (ISOFORM ki Y., gawara M., iguchi S., ito K., Y., ariant 3.";

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Query Match
Best Local Similarity 24.2%
Matches 46; Conservative
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with the 14-3-3 protein YWHAE, MEF2A, MEF2B and MEF2C arity). Interacts with HTATIP and EDNRA.

*** LOCATION: Nuclear and cytoplasmic. In the nucleus, it is with distinct submuclear dot-like structures. Shuttles ne nucleus and the cytoplasm. Treatment with EDNI results ing from the nucleus to the perinoclear region. The cytoplasm depends on the interaction with the 14-3-3 WHAE and may be due to its phosphorylation.
                                                                                                                                                                                                                                                                                                                              experimental confirmation available; he shuttling between the nuclear export sequence mediates the shuttling between us and the cytoplasm [By similarity]. be phosphorylated by CaMKI (By similarity). Be phosphorylated by CaMKI (By similarity). Seconds: a cativity is inhibited by Trichostatin A (TSA), istone deacetylase inhibitor (By similarity). Y: Belongs to the histone deacetylase family. Subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         t in position 877.
Ref.2 (BAC56929) sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 regulation; Repressor; Repeat; Phosphorylation;
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7; F:histone deacetylase activity; TAS.
6; F:specific transcriptional repressor activit
44; F:transcription factor binding; TAS.
73; P:B-cell differentiation; TAS.
78; P:inflammatory response; TAS.
79; P:inflammatory response; TAS.
79; P:neurogenesis; TAS.
74; P:regulation of myogenesis; TAS.
75; P:regulation of call cycle; TAS.
76; P:regulation of call cycle; TAS.
77; P:regulation of deacetylee.
78; P:regulation of deacetylee.
79; Hist deacetylee.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ref.1 sequence differs from that shown due to
                                                                                                                                                                                                                          BWUI4-2; Sequence=VSP 007429, VSP 007431;
experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:cytoplasm; TAS.
C:histone deacetylase complex; TAS.
                                                                                                                                                         ernative splicing; Named isoforms=4;
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                                                                                                                                                                                                                                                                                8WUI4-4; Sequence=VSP_008772;
                                                                                                                                                                                                                                                                                                               8WUI4-3; Sequence=VSP_007430;
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                                                                                                                                                                                             8WUI4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; AAF63491.1; ALT_FRAME.
2; BAA91474.1; ALT_INIT.
0; BAA91545.1; ALT_INIT.
9; BAB15759.1; ALT_INIT.
1; BAB55363.1; ALT_INIT.
8; BAC56929.1; ALT_INIT.
8; BAC56929.1; ALT_SEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH06453.1; ALT INIT.
AAH20505.1; ALT_INIT.
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MEDLINE=94148008; PubMed=8313906; A Fobert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.; Fobert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.; Patterns of cell division revealed by transcriptional regulation of genes during the cell cycle in plants."; EMBO J. 13:616-624(1994).

L EMBO J. 13:616-624(1994).

-!- PUNCTION: Essential for the control of the cell cycle at the (mitosis) transition. G2/M cycline accumulate steadily during and are abruptly destroyed at mitosis.

-!- SUBUNIT: Interacts with the CDC2 and CDK2 protein kinases to a serine/threonine kinase holoenzyme complex. The cyclin submimparts substrate specificity to the complex.

-!- DEVELOPMENTAL STAGE: Accumulates steadily during G2 and is abruptly destroyed at mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
G2/mitcotic-specific cyclin 2.
Antirthinum majus (Garden snapdragon).
Antirthinum majus (Sredeophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asttlamiids; Lamiales; Antirthinaceae; Antirthinaceae; Antirthinum.
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                                                                                             NUCLEAR EXPORT (BY SIMILARITY).
INTERACTION WITH MEPZC (BY SIMILARII
INTERACTION WITH MEPZA (BY SIMILARII
INTERACTION WITH SINJA (BY SIMILARII
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FRANSCRIPTION REPRESSION 2 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 RRLPLPRSLGSRDGGAVR-------QAQPPAPMAAR---
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                                                                                                                                                                                                                                                                                                                                                                                                           (in isoform 3).
P_008772.
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Missing (In isoform 4).
/FTId=VSP_007430.
                                                         HISTONE DEACETYLASE.
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LAVVSLGSRASLS----AQEPAQEELVAEEDQDPSELNPQTEESQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAENNKNSLAVNAKGADGALPIKRAVARVPVQKKTVKSKPQEIIEISPDTEKKK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEKEITGEKSLKKKAPTLTSTLTARSKAASV-VRTKPKEQIVDIDAADVNNDLAV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ARINSSSPLRY---NRQIGEFIVTRAGLYYLYCQVHFD---EGKAVYL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DMYKFYKSAENDSRPHDYMDSQPEINEKM--RAILIDWLVQVHYKFELSPETLYL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JAQPPAPMAARRSQRR------RGRRGEPGTALLVPLALGLGLALACLGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KS-----MAVEKKNRRALGDIGNVVTVRGVEGKALPQVSRPITRGF-----CAQLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (el. 40, Last sequence update)
(el. 42, Last annotation update)
pha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            azoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDGVLALRC-----LEEFSATAASSLGPQLRLCQVSGLLALRPGS 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of lymphotoxin alpha (LT-alpha) from a marsupial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR LOCATION: Secreted (homotrimer) and membrane-
1 (heterotrimers) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.7%; Score 97; DB 1; Length 441;
24.0%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   92; CYCLINS; 1.

ycle; Cell division; Mitosis.

AA; 49205 MW; E6E4C037C98880A7 CRC64;
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il to license@isb-sib.ch).
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Cyclin_Cterm.
Cyclin_N.
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48; PubMed=10826697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ritro and in vivo.

(el. 40, Created)
(el. 40, Last sequ
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                                                                                                        CAA53729.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                       CYCLIN
                                                                                                                                                                                                                                                                                                                                              cyclin;
                                                                                                                                                                                                                                 06670;
                                                                                                                                                                                                                                                                  04367;
                                                                                                                                                                                                                                                                                                      06671;
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믔 Fragetemma호로단적공항성색당턴국용당당당당당당당당당당

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28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last aguence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 6 (FAS antigen li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca fascicularis (Grab eating macaque) (Cynomolgus monkey), an Macaca nemestrina (Pig-tailed macaque).

Bukaryota; Metazoa; Chordata; Carniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 ---W----RANTDHAFLRHGFSLSNNSLLVPTSGLYFVYSQVVFSGASCSEITPTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 DILVDG---VLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 NPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAI--AAHYEVHPRPGQDGAQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 NPDNSHSSSPAP-----PQTAQHLSQKSLKRETLKPAAHL-----VGDPSVQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 VSGWEEARINSSSP-LRYNRQI--GBFIVTRAGLYYLYCQVHFDEGKA-----V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 EVLLFSSKYQVHVPLLSAQKSVCSGTQGPWMRSVYQGAVFLLTQGDRLSTYTDGVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.; Mayne A.E., King C.L., Genain C.P., "Cloning, sequencing, and homology analysis of nonhuman primate Pas/Fas-ligand and co-stimulatory molecules."; Immunogenetics 53:315-328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.6%; Score 95.5; DB 1; Length 201;
23.2%; Pred. No. 1.2;
cive 27; Mismatches 84; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 AA; 21536 MW; 8C4C371CB5091627 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYMPHOTOXIN-ALPHA.
N-LINKED (GLCNAC.
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SPECIES=M.mulatta; TISSUE=Lymphocytes;
MEDLINE=21383618; PubMed=11491535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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TNFSF6 OR PASL OR CD95L.
Macaca mulatta (Rhesus macaque),
                                                                                                                                                                                                                                                                                                                                                  EMBL; AF119336; AAD41773.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae, Macaca.
NCBL_TaxID=9544, 9541, 9545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 23.2 tes 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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190 SPSSVFFGAF 199
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                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01374; 1TNR
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Db 79 GLCLLVMFFMVLVALVGLGLGMFQLFHLQXELAELRESTSQKHTAS	OY 122 RLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEBA-RINSS		Db 175 YKKGGLVINETGLYEVYSKVYF-RGQSCINLPLSHKVYMKNSKIFQDLVMMEGK Qy 226 CLEBFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLF	Db 232 CTTGQMWAHSSYLGAVFNLTSADHLYVNVSELSLVNFEESQTFFGLY	RESULT 10 RHO MICLU STANDARD; PRT; 690 AA.		Bacteria, Actinobacteria, Actinob Micrococcineae, Micrococcaceae, NCBI_TaxID=1270; [1]		RX MEDLINE=96.132802; PuDMed=855/881; RA Nowatzke W.L., Richardson J.P.; RT "Characterization of an unusual Rho factor from the high G + C gr RT positive bacterium Micrococcus luteus."; RL J. Biol. Chem. 271:742-747(1996).		<pre>RC STRAIN=EM; RX MEDLINE=94327472; PubMed=8051015; RA Opperman T., Richardson J.P.; RT "Phylogenetic analysis of sequences from diverse bacteria with RT homology to the Escherichia coli rho gene.";</pre>			CC -!- FUNCTION: FACILITATES TRANSCIPTION TERMINATION OF F CC TEAT INVOLVES RHO BINDING TO THE NASCENT RNA, ACTIVATION OF F CC RNA-DEPENDENT ATPASE ACTIVITY, AND RELEASE OF THE MRNA FROM :			CC This SWISS-PROT entry is copyright. It is produced through a coll CC between the Swiss Institute of Bioinformatics and the EMBL out CC the European Bioinformatics Institute. There are no restriction CC use by non-profit institutions as long as its content is in		EMBL; L27277; AAB1867 HSSP; P03002; 1A63. InterPro; IPR003593; InterPro; IPR00194;	InterPro; IPR002059; InterPro; IPR008994; InterPro; IPR004665;
	Alta, M.fascicularis, and M.nemestrina; T. Yoshino K. T. Toner and M.nemestrina;	uatanases. FAS, a receptor that s. May be involved in n T_cell development.	AS-mediated apoptosis may have a role in the induction of 1 tolerance, in the antigen-stimulated suicide of mature or both. Binding to the decoy receptor TNFRSF6B/DcR3	Homotrimer (Potential). AR LOCATION: Type II membrane protein and secreted (By	Soluble form derives from the membrane form by ic processing (By similarity).  Y: Belongs to the tumor necrosis factor family.	OT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation-Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial trans a license arreament (See http://www.ich.eib.ch/announce/itse		9; BAA90295.1; 0; BAA90296.1;	4TsV. 008064; Fas_ligand. 006052; TNF_abc. 006052; TNF_family. 008983; TNF_like.	003636; INF_subf.	81; FASLIGAND. 34; TNECROSISFCT. 012; TNF subf; 1. 7; TNF, 1. 251; TNF 1: 1.	049; TNF 2; 1. ptosis; Transmembrane; Glycoprotein; Signal-anchor.	1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, MEMBRANE FORM. 29 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6 SCHIFFLE FORM (BY STRILLED)	MEMBER 6, SOLUBLE FORM (BY SIMILARIII).  1 80 CYTOPLASMIC (POTENTIAL).  81 101 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  (POTENTIAL).	<b>-</b> -,-	129 CLEAVAGE (BY SIMILARITY) 232 POTENTIAL.	83 183 N-LINKED (GLCNAC) (POTENTIAL). 449 249 N-LINKED (GLCNAC) (POTENTIAL). 159 259 N-LINKED (GLCNAC) (POTENTIAL). 60 60 S -> P (IN REF. 1). 10 AA, 31367 NW, POB284D61A132EB4 CRC64;	6.5%; Score 94; DB 1; Length 280; larity 20.8%; Pred. No. 2.4; Conservative 45; Mismatches 117; Indels 74; Gaps 14;	PMAARRSQRRRGRGEBGTALLVVLAL             PPLPPPPSPLPPLPPLKKG	AQEELVAEEDQDPSE

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MEDLINE=22709107; PubMed=12788972;
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                                                                                                                                                                                                                                                EISARRLPIPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALLVPLAL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87; PubMed=9634230; sch R. Parkhill J., Garnier T., Churcher C., Harris D., iglmeier K., Gas S., Barry C.E. III, Tekaia F., sham D., Brown D., Chillingworth T., Connor R., lin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., gals K., Krogh A., McLean J., Moule S., Murphy L., orne J., Quail M.A., Radjandream M.A., Rogers J., orne Y., Skelton S., Squares S., Squares R., Taylor K., Whitehead S., Barrell B.G.; he biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                   63; Indels 41; Gaps
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                                                                                          (BY SIMILARITY)
(BY SIMILARITY)
                                                           cermination; Helicase; ATP-binding; RNA-binding.
                                                                                                                                        2; AA SEQUENCE).
                                                                                                                                                                                    DB 1; Length 690;
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3, 1765;
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                                                                                                                                                       75030 MW; F77C4C75EE1B8998 CRC64;
                                                                                          RNA-BINDING (RNP2) (RNP-BINDING (RNP1) (ATP (POTENTIAL).

G -> P (IN REF. 2; A
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el. 42, Last annotation update)
rotein Rv0497/MIO517/Mb0508.
                                                                                                                                                                                    6.5%; Score 93.5; DE
25.9%; Pred. No. 7.3;
ive 19; Mismatches
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tuberculosis, and
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    ATP-synt_ab; 1.
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Proof M., Biglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S. Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; Proc. Complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).

-! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a colla between the Swiss Institute of Bioinformatics and the EMBL outs the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centities requires a license agreement (See http://www.isb-sib.ch/a or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 -----EVHPRPGQDG-----PIAGADGTVSGWEEARINSSS---PI
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10-05357; 05476; 08WVF8; 096LD2;
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2103 (Rel. 42, Last annotation update)
10-Mumor necrosis factor ligand superfamily member 14 (Herpesvirus emediator-ligand) (HVEML.).

TNFSF14 OR LIGHT OR HVEML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.4%; Score 93; DB 1; Length 310;
44.4%; Pred. No. 3.2;
ve 25; Mismatches 103; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; Transmembrane; Complete proteome.
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306
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202
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D., Alland D., Eisen J.A., Carpenter L., White O., HeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., terback T., Weidman J., Khouri H., Gill J., Mikula A., obe W.R. Jr., Venter J.C., Fraser C.M.; comparison of Mycobacterium tuberculosis clinical and

s; STRAIN=AF2122/97;

184:5479-5490(2002)

rculosis; STRAIN=CDC 1551 / Oshkosh;

94; PubMed=12218036;

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197 YLYCQV 202
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Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Colling B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Gram P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Kuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
ton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
ton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
i., Touchman J.W., Green E.D., Dickson M.C.,
Crimwood J., Schmutz J., Myers R.M.,
S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schein J.E., Jones S.J.M., Marra M.A.,
ind initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        )43557-1; Sequence=Displayed;
Synonyms=LIGHT delta-TM;
)54557-2; Sequence=VSP 006452;
SECIFICITY: PREDOMINANTY EXPRESSED IN THE SPLEEN BUT ALSO
THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
ND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
(PRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR
                                                                                                   bner R., Montgomery R.I., Kochel K.D., Cheung T.C., en S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
                                                                                                                                                             member of the TNF superfamily, and lymphotoxin alpha are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 N.A. (ISOFORM 2), AND PROCESSING.

1948; PubMed=1167323;

Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;

acterization of LIGHT reveals linkage to an immune
is on circomcsome 19p13.3 and distinct isoforms generated
splicing or proteolysis.";
67:5122-5128-62081(2001).
                                                                                                                                                                                                                                                                                                                                                                                        entry mediator ligand (HVEM-L), a novel ligand for mulates proliferation of T cells and inhibits HT29 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine that binds to TNFRSF3/LTBR. Binding to the sptor TNFRSFB modulates its effects. Activates NFRB, is the proliferation of T cells, and inhibits growth of actionem HT-29. Acts as a receptor for Herpes simples.
                                                                                                                                                                                                                                                                                                          McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J., le K., Spampanato J., Silverman C., Hensley P., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .AR LOCATION: Type II membrane protein and secreted 1); Cytoplasmic (isoform 2). (VE PRODUCTS:
heria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .cad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                       erpesvirus entry mediator.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257; PubMed=12477932;
                                                          N.A. (ISOFORM 1).
340; PubMed=9462508;
                                                                                                                                                                                                                                                                                        532; PubMed=9765287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUMOR NECROSIS FACTOR LIGAND SUPERFY
MEMBER 14, MEMBRADE PORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFY
MEMBER 14, SOLUBLE FORM.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 QAQPPAPMAARRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 HPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQI-------GEFIVTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SGGPLLWETQLGLAFLRGLSYHDGALVVTI
NONHEMATOPOIETIC TUMOR LINES.
-!- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
-!- PTM: N-glycosylated
-!- PTM: The solublated form of isoform 1 derives from the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TRLPDGPAGSWEQLIQERRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 99
                                                                                                 by proteolytic processing.
--- SIMILARITY: Belongs to the tumor necrosis factor family.
--- CAUTION: Ref. 4 sequence differs from that shown due to a frameshift in position 178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.4%; Score 92; DB 1; Length 240;
llarity 23.7%; Pred. No. 2.8;
Conservative 19; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. ..).
Missing (in isoform 2).
/FTIGHVSP 006452.
L - V (IN REF. 2).
E -> K (IN REF. 2).
N; 49D0BF67E1390B39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL) CLEAVAGE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF_subf; 1.
SMART; SM0207; TNF; 1.
PR0SITE; PS00251; TNF 1; FALSE_NEG.
PROSITE; PS50049; TNF 2; 1.
Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO, GO:0005102; F:receptor binding; TAS.
GO, GO:0006917; P:induction of apoptosis; TAS.
GO; GO:00015; P:induction of apoptosis; TAS.
InterPro; IPR006053; TNF_abc.
InterPro; IPR006052; TNF_Emmily.
InterPro; IPR008983; TNF_like.
InterPro; IPR008983; TNF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AY022261; AAK2616011; -.
EMBL; BC018058; AAH1805811; ALT_FRAME.
HSSP; P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF036581; AAC39563.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 E
26351 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF064090; AAC25169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:11930; TNFSF14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 NPAMHLTGANSSLTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 ----EMV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
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58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187
102
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 2
240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38
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82
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102
38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 604520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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calcineurin, and NP-AT.";

Cell 96:611-614(1999).

-!- FUNCTION: Plays a role in the inducible expression of cytokine genes in T cells, especially in the induction of the IL-2 and 4 (By similarity).

-!- SUBUNIT: Member of the multicomponent NFATC transcription computate consists of at least two components, a pre-existing cytoplasmic component NFATC2 and an inducible nuclear component NFATC1. Other members such as NFATC4, NFATC3 or members of the activating protein-1 family, MAP, GATA4 and Cbp/p300 can also the complex. NFATC proteins bind to DNA as monomers.

-!- SUBCELLULAR LOCATION: Cytoplasmic for the phosphorylated form
                                                                                                                                                                                                                                                                                                                                                                     79 GLCLLVWFFWVLVALVGLG--LGMFQLFHLQKEL-----AELRESTSQKHTASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoey T., Sun Y.-L., Williamson K., Xu X.; "Isolation of two new members of the NF-AT gene family and functic characterization of the NF-AT proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 LPCPTSVPRRPGQRRPPPPPPPPPPPPPP-----PPPPPPLPPLPPLKKRGN
                                                                                                                                                                                                                                                                                                                                           GLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAF
                                                                                                                                                                                                                                                                                                                                                                                                                         122 RLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEA-RINSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 QIGHP---SPPPEKKEQRK--VAHLTGKPNSRSMPLE-------WEDTYGİVLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 YNRQIGEFIVTRAGLYYLYCQVHFDEGKA------VYLKLD-----LLVDGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 CLEBFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLF(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 CTTGQMWAHSSYLGAVFNLTSTDHLY------VNVSELSLVNFEESQ--TFFGLYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                    POTENTIAL.

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)

729EA60067B7D398 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99189746; PubMed=10089876;
Crabtree G.R.;
"Generic signals and specific outcomes: signaling through Ca2+,
                                                                                                                                                                                                                                                             13 LPLPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALLVPLAL----
                                                                                                                                                                         6.4%; Score 92; DB 1; Length 280; 20.8%; Pred. No. 3.4; Ive 44; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (T cell
                                      CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear factor of activated T-cells, cytoplasmic 4 transcription factor NFAT3) (NF-ATC4) (NF-AT3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 902 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95269130; PubMed=7749981;
                                                                                                                                       31407 MW;
                                                                                                                                                                                                20.8%;
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [mmunity 2:461-472(1995)
              64
232
183
249
259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
45
128
128
201
183
183
249
259
280 AA;
                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFATC4 OR NFAT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=T-cell;
                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NFC4 HUMAN
                                                                                                                                                                                                                                                                                                                                         62
                                                    DISULFID
                                                                                                                                                                             Query Match
                                                                            CARBOHYD
                                                                                                 CARBOHYD
                                                                                                                  CARBOHYD
                                                                                                                                         SEQUENCE
                                                                                                                                                                                                  Local
                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         014934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVIEW
                                                                                                                                                                                                                   Matches
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84444448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T entry is copyright. It is produced through a collaboration wiss Institute of Bioinformatics and the EMBL outstation-ioinformatics Institute. There are no restrictions on its roit institutions as long as its content is in no way his statement is not removed. Usage by and for commercial res a license agreement (See http://www.isb-sib.ch/announce/il to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ψ

    1. 41, Last sequence update)
    1. 41, Last annotation update)
    factor ligand superfamily member 6 (FAS antigen ligand)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, MEMBRANE FORM.
HUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the apoptotic signal into cells. May be involved in T cell mediated apoptosis and in T cell development. S-mediated apoptosis and where a role in the induction of tolerance, in the antigen-stimulated suicide of mature r both. Binding to the decoy receptor TNFRSF6B/DcR3 its effects (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                                                                            quatus atys (Red-crowned mangabey) (Sooty mangabey) azoa; Chordata, Craniata, Vertebrata, Euteleostomi; eria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytokine that binds to INFRSF6/FAS, a receptor that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encing, and homology analysis of nonhuman primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Glycoprotein; Signal-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bostik P., Mayne A.E., King C.L., Genain C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          processing (By similarity).
Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and co-stimulatory molecules.";
                                                                                                                    280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               18; PubMed=11491535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08064; Fas_ligand.
06053; TNF_abc.
06052; TNF_family.
08983; TNF_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; FASLIGAND.
4; TNECROSISFCT.
112; TNF subf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53:315-328(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK37606.1; -.
                                                                                                                                                            el. 41, Created)
                                                                                                                                                                                                                                                                                                                                             e; Cercocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; TNF 1; 1.
                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                             CD95L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sari A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tosis;
                V 147
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                                                                                                                                                                                                                                                    Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial ires a license agreement (See http://www.isb-sib.ch/announce/ail to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
fter activation that is controlled by calcineurin-
lephosphorylation. Rapid nuclear exit of NFATC is thought
mechanism by which cells distinguish between sustained
ient calcium signals. The subcellular localization of
y a key role in the gene transcription.
SCIFICITY: Highly expressed in placenta, lung, kidney,
a ovary. Weakly expressed in spleen and thymus. Not
in peripheral blood lymphocytes.
Is Similarity Domain (RSD) allows DNA-binding and
we interactions with API factors (By similarity).
phorylated by NFATC-kinase; dephosphorylated by
in (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRGPEDSWILLISAPGPTPASPRGRKRYSSSGTPSSA-----SPALSR 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SLGEEGS-----EPPPPPL-PLARDPGSPGPFDYVGAPPAES 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRKTRARRAIA----GTVSG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRRTSSEQAVALPRSEEPASCNGKLPLGAEESVAPPGGSRKEVAGMDYLAVPSPLA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLGSRDGGAVRQAQPPAPAPARRS-----QRRRGRRGEPGTALLVPLALGLGLALAC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #9. NUCFACTORATC.
9. IPT: 1.
204; BEL 1.
254; REL 2; 1.
regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                              3; F:transcription co-activator activity; TAS.
4; P:inflammatory response; TAS.
6; P:transcription from Pol II promoter; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.4%; Score 92; DB 1; Length 902; 25.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR LOCALIZATION SIGNAL.
DNA-BINDING.
NUCLEAR LOCALIZATION SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 APPROXIMATE SP REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E59F15F7647A47C6 CRC64;
                                                                                                                                                                                         Y: Belongs to the Rel/Dorsal family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALCINEURIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SP 2 (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          007110; IG-like.
002909; IPT TIG.
000451; NP Rel dor.
008366; P53-like.
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Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 LPAPAEAAAESENLERESLMETSDAAQKAAPTSSPGSSRKRHR--EDSDVEMVENP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kunaran M., Rao M.R.S.; "Cloning of the cDNA of the MutL homolog, MLH1 from mouse testis. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Edelmann W., Cohen P.E., Kane M., Lau K., Morrow B., Bennett S
Umar A., Kunkel T., Cattoretti G., Chaganti R., Pollard J.W.,
Kolodner R.D., Kucherlapati R.;
"Meiotic pachytene arrest in MLH1-deficient mice.";
Cell 85:1125-1134 (1996).
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EMBL; U60872; AAC52672.1; -.
EMBL; U59881; AAC52672.1; JOINED.
EMBL; U59882; AAC52672.1; JOINED.
EMBL; U59883; AAC52672.1; JOINED.
EMBL; U59884; AAC52672.1; JOINED.
EMBL; U59884; AAC52672.1; JOINED.
EMBL; U59884; AAC52672.1; JOINED.
EMBL; U59884; AAC52672.1; JOINED.
EMBL; U59884; AAC52672.1; JOINED.
EMBL; U59884; AAC52672.1; JOINED.
EMBL; U59884; AAC52672.1; JOINED.
EMBL; U59884; EMPL.
GO; GO:000093; C:condensed chromosome; IDA.
GO; GO:000099; P:male meiosis chromosome segregation; IMP.
                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA mismatch repair protein Mlh1 (Muth protein homolog 1).
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GO; GO:0007113; p:meiosis; IDA.
GO; GO:0007131; p:meiotic recombination; IMP.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003599; DNA mis repair.
PFEM: PF01119; DNA mis repair.
PFM: PF02518; HATPase_C; 1.
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TIGRPAMS; TIGR00585; mull; 1.
PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
            760 AA.
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MEDLINE=96270514; PubMed=8674118;
MIHI_MOUSE STANDARD; EQUIVOIT | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.000 | 100.
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Best Local Similarity 22./*,
Best Local Similarity 70;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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!LVRPRRSAPKGRKTRARRAIAAHYEV-------HPRPGQDGAQAGVDG 163 : | : | | | : | : | : | : | : | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | VEEDRINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDG--- 220 

TPW 266

--PW 716

April 7, 2004, 17:45:19 secs

GenCore version 5.1.6 >pyright (c) 1993 - 2004 Compugen Ltd.	n search, using sw model	<pre>il 7, 2004, 17:37:32 ; Search time 56.9116 Seconds</pre>	09-245-198A-4 4 SLIDFEISARRLPLPRSLGPWAHLKAAPFLIYFGLFQVH 284	SUM62 op 10.0 , Gapext 0.5	6107 segs, 282547505 residues	s satisfying chosen parameters: 1586107	ch: 0 ch: 2000000000	nimum Match 0% ximum Match 100% sting first 45 summaries	<pre>Jeneseq_29Jan04:*     geneseqp1980s:*     geneseqp290s:*     geneseqp200ts:*     geneseqp200ts:*</pre>

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ALIGNMENTS

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Abr42312 Adc35200 Add10300 Adv17030 Adv7717 Adv07417 Adv04527 Adv04537 Adv04537 Adv0657 Adv0657 Adv0657 Adv0657 Adv0657 Adv0657 Adv06687 Adv06687 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884 Adv066884

then number of results predicted by chance to have a than or equal to the score of the result being printed, by analysis of the total score distribution. geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* the

### SUMMARIES

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4.	ഹ	7	AAR64190	Aar64190	Human 4-1
4.	വ	7	AAW26657	2657	Human 4-1
4.	254	S	ABB75953	Abb75953	Human cyt

The sequence is that of human tumour necrosis factor related ligar (TRELL). TRELL or active fragments can be included with a carrier pharmaceutical compositions to treat cancer, autoimmune diseases cimmune responses to tissue grafts, or to stimulate or suppress the system. It is useful to screen for TRELL receptors, by labelling we detectable label and screening compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for then be administered, optionally with interferon-gamma, to induce death or treat, suppress or alter immune responses (especially inv

Claim 12; Page 50-51; 69pp; English.

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rcinoma cells) involving a signal pathway between TRELL and It's coding sequence can be used in gene therapy for TRELL-lers in mammals (especially humans), e.g. tumours, at inflammatory diseases or inherited genetic disorders, by nto cells, and expressing, therapeutically effective amounts e.g. a virus comprising a gene encoding TRELL. It may also the preparation of prepare probes for screening etic DNAs for TRELL-encoding sequences and for antisense
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                                                                                                                                                                                                                LALACIGILLAVVSIGSRASISAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL 120
                                                                                                                                                                                                                                                                    LALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL 120
                                                                                                                                                                                                                                                                                                                         RPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR 180
                                                                                                                                                                                                                                                                                                                                                       IGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGP 240
                                                                                                                                                               DFEISARRIPIPRSIGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALLVPLA 60
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                                                                                                             DFEISARRIPIPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALIVPLA
                                                            0; Gaps
Score 1444; DB 2; Length 284;
Pred. No. 2.4e-129;
Mismatches 0; Indels 0.
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(first entry)

necrosis factor Apo-3 ligand protein sequence.

necrosis factor; Apo-3 ligand; lymphotoxin; apoptosis; endent transcription; UNK/SAPK-dependent response; cancer.

98WO-US021407.

97US-0062037P. 97US-0069862P.

Marsters SA,

TECH INC

Pitti R;

7982/24.

33- ligand (a tumor necrosis factor) homologue

1; 74pp; English

sequence represents a human tumour necrosis factor (TNF) and

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lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has cytostatic activity. Apo-3 ligand can be used to induce apoptosis mammalian cancer cells, to induce NF-kappaB-dependent transcripti to induce JNK/SAPK-dependent responses in mammalian cells
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                                                                                                                                                                  1 MAARRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPA
                                                                                                                                           36 MAARRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPA
                                                                                                                                                                                              VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPR
                                                                                                                                                                                                                    61 VABEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRALAAHYEVHPR
                                                                                                                                                                                                                                                 156 GAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVY
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                                                                                                                                                                                                                                                                                                                  PRO207; human; antitumour; tumour; therapy; cytostatic; breast canvarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            central nervous system cancer; melanoma; leukaemia; neoplasm
                                                                                        Length 249;
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                                                                                     87.8%; Score 1268; DB 2; L
100.0%; Pred. No. 1.3e-112;
ive 0; Mismatches 0;
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/note= "N-myristoylation"
125. .131
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|abel= Signal_peptide
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/label= PRO207
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24. .35
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                                                                                                    Best Local Similarity
Matches 249; Conserv
                                                                 Sequence 249 AA;
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TWEAK protein; immunological disorder; immune response; inflammati TWEAK blocking agent; autoimmune disease; organ transplant rejecti Graft-versus-Host disease; GVHD; lymphoid cell malignancy; shock;

14-JAN-2000; 2000WO-US001044.

WO200042073-A1. Homo sapiens

20-JUL-2000.

99US-0116168P.

15-JAN-1999;

(BIOJ ) BIOGEN INC.

Amino acid sequence of a soluble recombinant human TWEAK protein.

(first entry)

20-OCT-2000

AAB07526;

AAB07526 standard; protein; 249 AA.

RESULT 4

241 TYFGLFQVH 249

1

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foetal kidney CDNA clone (see AAA49717). PRO207 shows uence identity to tumour necrosis factor family members, an lymphotoxin-beta (23.4%) and human CD40 ligand (19.8%). 216. A claimed method for inhibiting the growth of a tumour exposing the tumor cell to PRO179, PRO207, PRO328, PRO310, PRO526, PRO356, PRO356, PRO509 or PRO866 (99), their agonists or chimeric polypeptides incorporating tur is especially a cancer selected from breast, ovarian, tal, uterine, prosetate, lung, bladder and central nervous melanoma and leukaemia. Methods for the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ion to inhibit neoplastic cell growth or for treating tumo rises polypeptides PRO179, PRO207, PRO320, PRO811, PRO526, PRO566, PRO362, PRO365, PRO509 or PRO866.
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Pred. No. 1.3e-112;
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                                                                                               /note= "Asn is N-glycosylated"
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                     128. .134 /
/note= "N-myristoylation"
139. .143
"N-myristoylation"
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ti RM, Wood WI;
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100.0%; Pre
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99US-0144758P.
99US-0145698P.
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  note=
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The present sequence represents a TWEAK protein. The specification describes a method for preventing or treating an immune response in an animal. The method compadministering a TWEAK blocking agent. The method may be used for preventing and TWEAK blocking agent. The method may be used for preventing and treating immune disorders associated with inapproprexpression and/or activity of TWEAK. These disorders include autoidiseases, acute and chronic inflammation, organ transplant rejectifactive compact transplant rejectifactive of shock, loss of immune responsiveness (as seen in himmunedeficiency virus (HIV) infections) and failure of the immune
                                                                                                                                                                                                                                                                                                                                                                                                    Preventing and treating immune responses using modulators, especia antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, useful fc treating e.g. inflammation and graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 MAARRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAC
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100.0%; Pred. No. 1.3e-112;
ive 0; Mismatches 0;
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Gaps

VLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL 275 VLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL 240

FQVH 284

VDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD VDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD

FOVH 284

enign tumour; malignant tumour; lymphoid malignancy; uronal disorder; stromal disorder; blastocoelic disorder; disorder; immune disorder; angiogenic disorder; cytostatic; lard; protein; 249 AA (first entry) polypeptide. FOVH 249

2000WO-US003565

99WO-US012252. 99US-0140650P. 99US-0140653P. 99US-0144758P. 99US-0145698P. 99WO-US020111. 99WO-US021090. 99WO-US028313. 99WO-US028301. 99US-0146222P. 99US-0149395P. 99WO-US005028 99US-0123972P. 99US-0133459P. 99WO-US028634. 2000WO-US000219.

Hillan KJ; Stone DM; Gurney AL, Smith V, d A, Godowski PJ, Pitti RM, Roy MA, Goddard A, Pan J, F Wood WI, TECH INC.

567/26.

ucleic acids encoding PRO polypeptides, useful for treating ignant tumors, leukemias and lymphoid malignancies, angiogenic and immunologic disorders.

nvention relates to the isolation of novel human PRO and the polynuclectide sequences encoding them. The PRO agonists, antagonists or anti-PRO antibodies are useful for on or malignant tunnours (e.g. renal, kidney, bladder, leukaemias and lymphoid malignancies, other disorders such glial, astrocytal, hypothalamic, glandular, macrophagal, lastocoelic disorders, inflammatory, immune and angiogenic e polymucleotide sequences are also useful in gene therapy.

U 36 MAARRSQRRRGERGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPA 1 MAARRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPA 96 VAEEDQDPSEINPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPR 61 VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPR 156 GAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVY 216 LLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKA 181 LLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKA .. Length 249; Human; TWEAK; tumour necrosis factor; ligand; cytostatic; Indels 87.8%; Score 1268; DB 5; L 100.0%; Pred. No. 1.3e-112; ive 0; Mismatches 0; ABR42315 standard; protein; 249 AA. immunomodulator; osteopathic. (first entry) 249; Conservative 241 TYFGLFOVH 249 276 TYFGLFQVH 284 Human TWEAK protein. Query Match Best Local Similarity Homo sapiens. 11-AUG-2003 ABR42315; Matches ABR42315 RESULT 음 셤 ò ద à g 8 à

25-JUL-2002; 2002WO-US023782. 27-JUL-2001; 2001US-0307838P. (HUMA-) HUMAN GENOME SCI INC. ÇA; Hilbert DH, Rosen WO2003040307-A2 15-MAY-2003

New heteromultimeric complex having a first polypeptide member of tumor necrosis factor (TNF) ligand family, and a second different of TNF ligand family, useful for treating cancer, osteoporosis or autoimmune disease.

WPI; 2003-430659/40.

N-PSDB; ACC57901.

Disclosure; Page 368-369; 388pp; English.

The present sequence is the protein sequence for human TWEAK prot invention relates to compositions comprising heterotrimeric complication, necrosis factor (TNF) ligand family members, and their use detection, prevention and treatment of disease. In one embodiment heterotrimeric complex comprises full-length or extracellular por TWEAK and full-length or extracellular portions of other TNF ligationly members, preferably VGGI or VGGI-SV. The heterotrimeric coff the invention are useful for treating an autoimmune disease, osteoporosis, and particularly for inhibiting cancer cell prolife increasing B cell proliferation, or inducing apoptosis of T cells

A.

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Length 249; 0; Indels

87.8%;

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*servative* 

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individual having a disorder associated with excessive bone resorp e.g. osteoporosis, Paget's disease or arterial calcification. Trea individual having a disorder associated with insufficient bone res comprises administering an endokine alpha antagonist, which is the antibody that binds specifically to endokine alpha polypeptide. The present sequence represents the amino acid sequence of a tumour ne factor family ligand.
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                                                                                                                                                                                                                                             36 MAARRSQRRRGRRGEPGTALLVPLALGIGIALACIGLILAVVSLGSRASISAQEPAC
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Best Local Similarity 100.0%; Pred. No. 1.3e-112;
Matches 249; Conservative 0; Mismatches 0;
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                                                                                                                                              Sequence 249 AA;
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10-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wiley SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW29745;
                                                                                                                                                                                                                                                                                                                       96
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                                                                                                                                                                                                                                                                                                                                                                                          156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вb
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          88888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha gene useful for preparing a composition for treating a lated with excessive or insufficient bone resorption e.g., Paget's disease or arterial calcification.
                                                                               ö
                                                                                                                                                                                                                                                                                   VDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD 180
                                                                                                                                                                                                                                                                                                                       VLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL 275
                                                                                                                                                                                                                                                                                                                                           DPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 120
                                                                                                                                                                                                                                                     VDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD 215
                                                                                                                                                                                  UDPSELNPQTEESQDDAPFLNRLVRPRRSAPKGRKTRARRALAAHYEVHPRPGQD 155
                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relates to an isolated nucleic acid molecule encoding a is factor family ligand. A composition comprising the oody or its fragment is used for treating an individual in ased level of endoxine alpha activity. The endoxine alpha resent in a heterotrimeric complex is used for treating an
                                                                                                                                              SORREGERGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEEL
                                                                                                             SORRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEEL
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    necrosis factor, TNF ligand, endokine alpha, resorption disorder, osteoporosis, Paget's disease,
                                                                               .
0
                                              Length 249;
                                                                             Indels
                                             Score 1268; DB 6; L
Pred. No. 1.3e-112;
                                                                             0,
                                                       100.0%; Pred. nc. _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nd family member #12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nardelli
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first entry)

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FOVH 249 FQVH 284

fication.

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TNF; endothelium proliferative agent; TREPA; wound healing; cance:
tissue grafting; vascularisation; apoptosis; autoimmune; birth co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The TNF-related endothelium proliferative agent (TREPA), or its activators or agonists, are used to treat a deficit of TREPA, e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting nucleic acid encoding TREPA - useful for diagnosis treatment of autoimmune disease, tumours and inflammation.
TNF related endothelium proliferative agent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Page 123-4; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00798692.
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Rosen CA,

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healing or tissue grafting, by promoting vascularisation, a apoptosis for treating cancer and eliminating autoreactive a adjunct to cancer chemotherapy or antiviral treatment s can also be used to target cytotoxic agents or for action of the corresponding receptor, the nucleic acid for used to transform tumour cells to render them more TREPA and to screen for TREPA mimics. Ribozymes, antisense iss or peptides, are used to treat TREPA-associated. tumours and metastases (by inhibiting vascularisation), or a wide range of autoimmune conditions, conditions or a wide range of autoimmune conditions or an istimulation of epithelial cells (e.g. ormal stimulation (inhibiting ovulation and placental other anglogenic conditions (e.g. ulcers)
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GVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD 180
                                                                                                                                                                                                                                                                                                                                                                                               GVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL 275
                                                                                                                                                                                              DQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 155
                                                                                                                                                                                                                                               DODPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRALAAHYEVHPRPGQD 120
                                                                                                                                                                                                                                                                                                GVDGTVSGWEBARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD 215
                                                                                                                                             9
                                                                                                 95
                                                                                                                                        RSOKRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEEL
                                                                                                 RSORRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEEL
                                                   Gaps
                                                ó
Length 249;
                                                Indels
                                                      ;
0
87.6%; Score 1265; DB 2;
99.6%; Pred. No. 2.5e-112;
iive 1; Mismatches 0;
                                                      onservative
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# LFQVH 284

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LÈCVH 249

dard; protein; 249 AA.

TNF related endothelium proliferative agent)

TREPA; : necrosis factor, TNF; angiogenesis, wound healing, indothelium proliferative agent; tumour; metastasis;

/label= Extracellular domain Location/Qualifiers

98US-00105343

97US-00798692 98US-00021706

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The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molec designated as TREPA (TNF related endothelium proliferative agent) Soluble biologically active TREPA are used to treat TREPA-associa diseases, tumours or metastases. TREPA is used for inducing angio in human for promoting wound healing and for vascularising grafte for successful grafting and to promote tissue grafts. The present acid sequence is clone ID #690050 human TREPA
                                                                  Inducing angiogenesis in mammal at desired sites for promoting wo healing, by administering soluble fragment of extracellular domaitumor necrosis factor related endothelium proliferative agent pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 MAARRSQRRRGERGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEP?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAARRSQKRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRALAAHYEVHP
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99.6%; Pred. No. 2.5e-112;
iive 1; Mismatches 0;
                                                                                                                                                 Claim 1; Col 75-76; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                2001-280760/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                WPI; 2001-280760/
N-PSDB; AAD04350.
                                                                                                                                                                                                                                                                                                                                                                         Sequence 249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 248;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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## RESULT 10

ADC97712 standard; protein; 249 AA. ADC97712

## ADC97712;

15-JAN-2004 (first entry)

Murine FL-TWEAK.

skeletal muscle disease; adipose tissue disease;
gastrointestinal tract disease; pancreatic disease;
reproductive organ disease; neural disease; cartilage disease;
bone disease; connective tissue disease; cellular death; hepatot:
dermatological; gastrointestinal; osteopathic. Murine, FL-TWEAK, TNF relatedness and weak ability to induce cel. TNF, Tumour Necrosis Factor, TWEAK, fibrosis, cardiac disease, liver disease, lung disease, kidney disease, skin disease, 

WO2003086311-A2.

23-OCT-2003.

09-APR-2003; 2003WO-US011350.

fusion protein.

Homo sapiens.

002US-0371611P

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155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVLALRCLEBFSATAASSPGPQLRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFL 240
                                                                                                                                                                                                                                                                                        ARK-related condition, e.g. liver, gastrointestinal, kidney, i.c. cartilage or neural tissue condition in a subject .nistering to the subject a TWEAK agonist or antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equence is murine transmembrane FL-TWEAK (TNF relatedness ity to induce cell death, where TNF is Tumour Necrosis (is a member of the TNF family. TWEAK agonists or e useful for treating a TWEAK-related condition, e.g. liac disease; liver disease; lung disease; kidney disease; skeletal muscle disease; adipose tissue disease; all tract disease; adipose tissue disease; all disease; cartilage disease; bone disease; cartilage disease; bone disease; cartilage disease; bone disease; cartilage disease; bone disease; cartilage disease; bone disease; cartilage disease; bone disease; cartilage disease; bone disease; cartilage disease; bone disease; cartilage disease; bone disease; cartilage disease; bone disease; cartilage disease; bone disease; cartilage disease; bone disease; cartilage disease; bone disease; cartilage disease; cartilage disease; cartilage disease; bone disease; cartilage disease; cartilage disease; bone disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage disease; cartilage d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         llular domain; tumour necrosis factor; TNF; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSORRRGRRGEPGTALLAPLVLSLGLALACLGLLLVVVSLGSWATLSAQEPSQEEL
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      Hahm K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO 1; 120pp; English.
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      Zheng T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
ubowski A,
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                                                                                                                         56/78.
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The sequence represents a a fusion protein encoded by the express vector pDC409-LZ-TWEAK. The fusion protein comprises a growth hor leader, a leucine zipper multimerisation domain, and the extracel domain of human TWEAK. The fusion protein was used in the isolatic human TWEAK receptor (TWEAKR)-expressing clones from a COS cell human TWEAK receptor (TWEAKR)-expressing clones from a COS cell human TWEAK receptor (TWEAKR)-expressing clones from a COS cell human fusion family and induces angiogenesis: TWEAKR may therefore be us creen for and develop TWEAKR agonists and antagonists for the most close of angiogenesis, to be used in the treatment and diagnosis of hum classe: The disorders mediated by angiogenesis include coular dicharacterised by ocular neovascularisation such as diabetic retin neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retroental fibroplasia, rubeosis, uveitis, macular degeneration corneal graft neovascularisation, and inflammatory diseases such arthritis, rheumatism and psoriasis. Other treatable diseases inc malignant and metastatic conditions such as sarcomas and carcinom benight tumours and preneoplastic conditions, myocardial angiogene hemophilic joints, scleroderma, vascular adhesions, atherosclero plaque neovascularisation, telangiectasia, wound granulation, corestered and ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating anglogenesis in a mammal for treating diseases mediate anglogenesis, e.g. solid tumors and vascular deficiencies of card peripheral tissue, by administering antagonist or agonist of TWEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 SLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 SLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 ARRAIAAHYEVHPRPGODGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 ARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 LYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 LYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.8%; Score 1066; DB 4; Length 273; 100.0%; Pred. No. 3e-93; ive 0, Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLRIRTLPWAHLKAAPFLTYFGLFQVH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLRIRTLPWAHLKAAPFLTYFGLFQVH 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 41; 46pp; English
                                                                                                                                                                                                                                     20-DEC-1999; 99US-0172878P.
10-MAY-2000; 2000US-0203347P.
                                                                                                                                                                                         19-DEC-2000; 2000WO-US034755.
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                                                                                                                                                                                                                                                                                                 (IMMV) IMMUNEX CORP.
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N-PSDB; AAS03964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 273 AA;
                                                                                                      WO200145730-A2
                                                                                                                                                   28-JUN-2001
                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                              Wiley SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258
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RESULT 12

dard; protein; 208 AA.

(first entry)

rotein.

is factor receptor; signal transducer molecule, TNF, APO4; abnormality; gestational abnormalitity; prostate cancer; PO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease; omain; immunogen; antibody preparation; breast carcinoma;

98WO-US018393.

97US-00924634.

WASHINGTON.

191/17.

mosis Factor family receptor polypeptides and ligands - agnosis and treatment of prostate cancer and developmental abnormalities.

y 13A; 156pp; English.

on describes isolated Tumor Necrosis Factor (TNF) family peptides: APO4, APO6, APO8 and APO9 or their active of isolated TNF related ligands I and 3 (TNRL1 and TNRL3) or fragments. APO4 is useful for diagnosing prostate cancer by levels of APO4 in an individual. Prostate cancer can also be polypeptides are also useful for identifying selective by the calls useful in diagnosis/treatment of disease by binding of a polypeptides are also useful for identifying selective the call surface. The binding is preferably performed in alypeptides/active fragment which is extracellular, or the call surface. The binding and observing the changer in APO4 disease are also identified using APO4 polypeptides/active fragment useful in diagnosis or disease are also identified using APO4 polypeptides/active 1 APO4 signal transducer molecules that specifically interact lasmic domain of APO4 and detecting a change in level of APO4 e method is performed in vivo or in vitro. APO polypeptides ul as immunogens for preparing antibodies, APO4 is also iagnosis/treatment of developmental or gestational nduced apoptosis

Tumour necrosis factor related ligand - useful for, e.g. treatin auto-immune disease and immune responses to tissue grafts.

WPI; 1998-145619/13. N-PSDB; AAV18599.

ö 120 RAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLY 196 GSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKT 136 9 0; Gaps Score 1062; DB 2; Length 208; Pred. No. 4.9e-93; 0; Mismatches 1; Indels C 73.5%; Conservative larity

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TRELL; tumour necrosis factor related ligand; tnf; treatment; car autoimmune disease; immune system; stimulation; suppression;
YLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLA
         121 YLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEBFSATAASSLGPQLRLCQVSGLLA
                                                                                                                                   Mus musculus tumour necrosis factor related ligand (TRELL).

    .21
    /note= "hydrophobic, transmembrane domain"

                                 284
                                               181 SSLRIKTLPWAHLKAAPFLTYFGLFQVH 208
                                 SSLRIRTLPWAHLKAAPFLTYFGLFQVH
                                                                                                                                                                                                                                                                                                                        (UYGE-) UNIV GENEVA FACULTY MEDICINE.
                                                                                                                                                                                                     Location/Qualifiers
                                                                                       AAW47524 standard; protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                         Chicheportiche Y, Browning JL;
                                                                                                                                                                                                                                                                                 96US-0023541P.
96US-0028515P.
97US-0040820P.
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                                                                                                                       21-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                 BIOJ > BIOGEN INC.
                                                                                                                                                                       graft rejection.
                                                                                                                                                                                                                                                                    07-AUG-1997;
                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                   07-AUG-1996;
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18-MAR-1997;
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                                                                                                        AAW47524;
                                  257
   197
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The sequence is that of mouse tunnour necrosis factor related lig (TRELL). TRELL or active fragments can be included with a carrie pharmaceutical compositions to treat cancer, autoimmune diseases immune responses to tissue grafts, or to stimulate or suppress to immune responses to tissue grafts, or to stimulate or suppress to system. It is useful to screen for TRELL receptors, by labelling detectable label and screening compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for then be administered, optionally with interferon- gamma, to induce death or treat, suppress or alter immune responses (especially intument adenocarcinoma cells) involving a signal pathway between Tries receptor. It's coding sequence can be used in gene therapy for related disorders in mammals (especially humans), e.g. tunnours, autoimmune and inflammatory diseases or inherited genetic disord introcells, and expressing, therapeutically effective of a vector, e.g. a virus comprising a gene encoding TRELL. It is natural/synthetic DNAs for TRELL-encoding sequences and for anticipal variations. Claim 12; Page 48-50; 69pp; English.

Sequence 225 AA;

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įz,

0 240 ALACIGILLAVVSLGSRASISAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL 120 PRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEBARINSSSPLR 180 PRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLR 121 61 GEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGP ALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFL Gaps . Length 225; QVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 284 OVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFOVH 225 Indels 16; Score 1020; DB 2; Pred. No. 5.7e-89; 9; Mismatches 70.6%; 88.8%; nservative

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lard; protein; 225 AA.

(first entry)

quence of a soluble recombinant murine TWEAK protein.

; immunological disorder; immune response; inflammation; g agent; autoimmune disease; organ transplant rejection; Host disease; GVHD; lymphoid cell malignancy; shock; tumour.

2000WO-US001044.

99US-0116168P

036/41

. treating immune responses using modulators, especially TWEAK, TWEAK receptors and TWEAK ligands, useful for inflammation and graft versus host disease. ਰ ਘੁ

ig 1; 45pp; English.

equence represents a TWEAK protein. The specification ethod for preventing or treating an immunological disorder ting an immune response in an animal. The method comprises a TWEAK blocking agent. The method may be used for distrain immune disorders associated with inappropriate d/or activity of TWEAK. These disorders include autoimmune the and chronic inflammation, organ transplant rejection, Host disease (GVHD), lymphoid cell malignancies, septic and stock, loss of immune responsiveness (as seen in human incy virus (HIV) infections) and failure of the immune umour growth

70.6%; Score 1020; DB 3; Length 225;

Ö 61 LGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDP. 2 ISIGIALACIGLILIVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDV 62 EQLVRPRESAPKGEKARPREALAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSS 121 NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSS YNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAAS ; QLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 284 88.8%; Pred. No. 5.7e-89; ive 9; Mismatches 16; Matches 199; Conservative Best Local Similarity 181 241 à 셤 ò 임 à

RESULT 15 AAW9359

AAW93591 standard; protein; 211 AA.

AAW93591;

18-JUN-1999 (first entry)

Mouse TNRL3 protein.

Tumour necrosis factor receptor; signal transducer molecule; TNF; developmental abnormality; gestational abnormality; prostate ca APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; cytoplasmic domain; immunogen; antibody preparation; breast carci apoptosis; mouse

Mus sp.

WO9911791-A2.

11-MAR-1999

98WO-US018393. 04-SEP-1998; 

97US-00924634. 05-SEP-1997;

(UNIW ) UNIV WASHINGTON.

Chaudhary PM;

WPI; 1999-205191/17. N-PSDB; AAX23425 New Tumor Necrosis Factor family receptor polypeptides and ligand useful for diagnosis and treatment of prostate cancer and develog or gestational abnormalities.

Claim 40; Fig 13B; 156pp; English.

This invention describes isolated Tumor Necrosis Factor (TNF) fan receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and The their active fragments. APO4 is useful for diagnosing prostate of certaining levels of APO4 in an individual. Prostate cancer can created using APO4 aclective binding agents linked to a therapeut moiety. APO4 polypeptides are also useful for identifying selective binding agents, useful in diagnosis/treatment of disease by binding agents to the polypeptide/active fragment which is extracellular, expressed on the cell surface. The binding is preferably performed vivo. APO4 polypeptides/ active fragments are also useful for science for signification of the changes activity. Effective pharmacological agents useful in diagnosis of treatment of disease are also identified using APO4 polypeptides.

APO4 signal transducer molecules that specifically interact asmic domain of APO4 and detecting a change in level of APO4 method is performed in vivo or in vitro. APO polypeptides a simumnosgens for preparing antibodies. APO4 is also agnosis/treatment of developmental or gestational . APO8 was transfected to human breast carcinoma cell line duced apoptosis

0 0; Gaps 67.0%; Score 968; DB 2; Length 211; arity 89.1%; Pred. No. 4.8e-84; Conservative 9; Mismatches 14; Indels /SLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNKLVRPRRSAPKG 133 

ARRAIAAHYEVHPRPGODGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRA 193 

LYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLAL 253

SELRIRIL PWAHLKAAPFLTYFGLFOVH 284

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Description

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        GenCore version 5.1.6 copyright (c) 1993 - 2004 Compugen Ltd.
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GSRASLSGPRQEPRGELVPREDQDPSELNPGTESCOPAPFTRRIARRRSAPKGRKTR
ARRALAHYEVHPREGQDGQAQAGVDGTVSGREEARINSSSPLRYNGLGEFIVTRAGL
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gortiche, Y.; Bourdon, P.R.; Xu, H.; Hsu, Y.M.; Scott, H.; h, C.; Garcia, I. and Browning, J.L.
a new secreted ligand in the tumor necrosis factor family eakly induces apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ted (14-OCT-1997) Cell Biology, Biogen, 12 Cambridge Center,
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18. .767
/hote="ligand in the TNF family; secreted protein; start
codon not verified experimentally"
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a,P., Hession,C., Tizard,R. and Browning,J.
Submission
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/db_xref="taxon:9606"
/chromosome="17"
/map="17p13"
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Location/Qualifiers
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智術質目<sup>3</sup>

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1. F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., (Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Saton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., S., Hanney, Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lewis, L., Liao, D., Mark, M., Robbié, E., Sanchez, C., Ledi, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., T., Vangts, A., Vandlen, R., Watchanbe, C., Wieand, D., Woods, K., J., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., J.A., Wood, W.I. and Godowski, P. Yansura, D. Stocken Discovery Initiative (SPDI), a Large-Scale to Identify Novel Human.
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1 DNA Way, South San Francisco, CA 94080, USA
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GSRASLSAQEPAQEEVVAEEDOPPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTR
ARAZIAAHYEVHPROGAQAGVOGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGL
YYLYCQVHFDDGKAYYLKLDLLVDGYLALRCLEEFSATAASSLGPQLRLCQVSGLLAL
RPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH"
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                                                                              04-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                               ification of a ligand for the death-domain-containing receptor
                                                                                                                                                                                                                                                                                                                             ers, S.A., Sheridan, J.P., Pitti, R.M., Brush, J., Goddard, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="binds to the death-domain-containing receptor
                                                                                                                                                                                                                                                  yota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
lia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Way,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGGAGGACCCGTCGGAACTGAATCCCCAGACAGAAGAAAGCCAGGATCCT
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ers, S.A., Sheridan, J.P., Pitti, R.M., Brush, J., Goddard, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncology, Genentech, 1 DNA
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0
                                                                           372 1368 bp mRNA linear PRI sapiens Apo3/DR3 ligand (APO3L) mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9; Length 1368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Apo3/DR3 ligand"
/protein_id="AAC39724.1"
/db_xref="GI:3108231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
mol type="mRNA"
/db_xref="taxon:9606"
/chromosome="17"
/map="17pl3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (25-MAR-1998) Molecular (Francisco, CA 94080, USA Location/Qualifiers
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355
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58..807
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1 (bases 1 to 1236)
Wiley,S.R.
Member of the TNF family useful for treatment and diagnosi
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ta; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
a, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Length 1421;
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rai,b.J., Marefers,S.A. and Pitti,R.
igand polypeptide
UP 2001522584-A 1 20-NOV-2001;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
                                                                                                                                                                     1421 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     )-OCT-1998 JP 2000516042
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	RESULT 8   BD057124   1236 bp DNA	623  PEATURES  Tocation/Qualifiers.  788  Source  11236  /organism="Homo sapiens" /mol_type="genomic DNA"  848  Query Match  69.8%; Score 958; DB 6; Length 1236;  Best Local Similarity 99.6%; Pred, No. 0;	908  Matches 1208; Conservative ( 803  QY 129 GCGGAGGGGGCCCGGGGGG 968  Db 24 GCGGAGGGGCCCGGGGGG 863  QY 189 GGGCTGGCGGGCTGCCTGCC 863  Db 84 GGGCTGGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTG
e: US 6207642-A 1 27-WAR-2001; Location/Qualifiers 11236 / organism="unknown" / mol_type="unassigned DNA"  69.8%; Score 958; DB 6; Length 1236; arity 99.6%; Pred. No. 0; Conservative 0; Mismatches 5; Indels 0; Gaps SAGGGGCGCGGGGAGCCGGCCTGCTGCTCGCTCGCTGGCTTGTCTCGCTTGGCCTTGTTTTGGCGAGCCTTGTTTTGGCGAGCCTGTTTTTGGCGAGCCTGGTGCTTGTTTTTGGCGAGCCTGGTGCTTGTTTTTGGCGAGCCTGGTGTTTTTTTT	SGAACTIGAATCCCCAGACAGAAGAAAAGCCAGGATCCTGCGGCCTTTCCTGAACCGACT SGAACTGAATCCCCAGACAGAAAAGCCAGGATCCTGCGCGCTTTCCTGAACCGACT CGGCCTCGCAGAAGAAGAAGCCAGGATCCTGCGCCTTTCCTGAACCGACT CGGCCTCGCAAGAGAAGAAGCCAGAAAACCTGCGCTTTCCTGAACCGACT CGGCCTCGAAGAGACACCTAAAGGCCGGAAAACACGGCTGTCGCTCGAAGAGCCAGACTCGCCTCGAAGAGCCAGAACACGGCTCGAAGAGCCAGAACACGGCTCGAAGAGCCAGAACACGGCTCGAAGAGCCAGAACACGGAACACGGAACACGGAACACGAAGACCAGAACACGAACACGAACACGAACACGAACACGAACACGAACACGAACACGAACACGAACACGAACACGAACACGAACACGAACACGAACACACGAACACACACACACACACACACACACACACACACACACACA	SCETTGCCAGAGAATTCTCAGCCACTGCGGCGAGTTCCCTCGGGGCCCAGCTCCGCGCCCAGCTCCGCGCCCAGCTCCGCGCCCAGCTCCGCGCCCAGCTCCGCGCCCAGGTTCCCCTGCGGGCTCCGCCACCTCCCCCGCGGCTCCTGCGGCTCCTCCCTGCGGGCTCCTC	CTGAGGGCCTGGTCTCCCCACAGTCGTCCCAGGCTGCCGGCTCCCTCGACAGCT

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	MACTGAATCCCCAGACAGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACT 368	SGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGAGCGATCGC 428	CATTATGAAGTTCATCACGACCTGGACGGAGGCCCAGGTGTGTGT	909	CATGAGGGGAAGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGTGTGTG	CGCTGCCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGGGCCCCAGCTCCG 728	TGCCAGGTGTCTGGGCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGGATCCGCAC 788	CCTGGGCCCATCTCAAGGCTGCCCCTTCCTCACCTACTTCGGACTCTTCCAGGT 848	TGAGGGCCCTGGTCTCCCCACAGTCCTCCCAGGCTGCCGCTCCCCTCGACAGCT 908	GGGCACCCGGTCCCTCTGCCCCACCTCAGCCGCTTTTGCTCCAGACCTGCCCC 968	TCTAGAGGCTGCCTGGGCCTGTTCACGTGTTTTCCATCCCACATAAATACAGTATT 1028	CTCTTATCTTACAACTCCCCCACCGCCCACTCTCCACCTCACTAGCTCCCCAATCC 1088	CCCTTTGAGGCCCCCAGTGATCTCGACTCCCCCTGGCCACAGACCCCCAGGGCAT 1148	TTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAG 1208	GCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAA 1268	GOGGCGAGAAAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAA 1328	VTATTATTT 1341           VTATTATTT 1236

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QDPAPFLINRLVRPRRSAPKGRKTRARRAJAAHYEVHPRPGQDGAQAGVI
RINSSSPLRYNRQJGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDK
FSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYI
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                                                                                                                                                      TTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTA
                                                                                                                                                                                                         TTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGAGACTGGGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1316 TGGATTTTTAAAACAGATATTATTTTTATTATTATTGTGACAAAATGTTGATAAAT
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/db_xref="G1:15132571"
/db_xref="REMTREMBL:CAC50004"
/translation="WATGSRTSLLLAPGLLCIPWLQEGSATSSDRMKQ:
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                                                                                                                                                                                                                                                                                                                                                                    1486 AGGAGTTCCCAAATGTGAGGGCGAGAAACAAGACAAGCTCCTCCTTGAGAATTT
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100.0%; Pred. No. 0;
tive 0; Mismatches 0; Indels
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IMMUNEX CORPORATION (US)
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/db_xref="LocusID:8742"
/db_xref="MIM:602695"
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/tissue type="Primary B-Cells from Tonsils"
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/db_xref="GI:17512139"
/db_xref="LocusID:8742"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Birren, B. Musbaum, C. Lander, E., Ali, A., Allen, N., Andersc Barna, N., Bastien, T., Boguslavkiy, L., Boukhgalter Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A. Cooke, P., DeArellano, K., Dewar K., Diaz, J.S., Dodg Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafaz, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J. Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihoya, T., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihoya, T., Merga, V., Murphy, T., Naylor, J., Ngyen, C., Nicol, R., Norbu Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J. Peterson, K., Phunkhang, P., Pierre, N., Schauer, S., Schupback, Stojanovic, K., Phunkhang, P., Pierre, N., Schauer, S., Schupback, Stojanovic, N., Tallamas, J., Tesfaye, S., Theodore, J., Topham, Traverre, M., Vasch, M., Vaiel, R., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zchiller, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale, M., Vale,
                   Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rog
Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Seve
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Tal
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainc
Direct Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Only the first 60.3 kilobases of this clone are being submithe remainder overlaps accession number AC113189 [WICGR pro L23113].
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (31-007-2002) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Oct 31, 2002 this sequence version replaced gi:23592141. All repeats were identified sing RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Rese
                                                                                                                                                                                                                                                                                                                                                Submitted (08-OCT-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 60268)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-11 Human Male BAC"
complement(7920. .8209)
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Web site: http://www-seq.wi.mit.edu
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/rpt_family="MIR"
complement (18188. .18483)
/rpt_family="AluSq"
22454. .22535
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/rpt_family="AluSx"
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complement (9356. .9663)
/rpt family="Alusq"
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/db_xref="taxon:9606"
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Center clone name: 186_B_7
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                                                                                                                                                                                  601 CAGGIGCACTITGAIGAGGGGAAAGGCIGICTACCIGAAGCIGGACTIGCIGGAA
                                                                                                                                                                                                     37278 CAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGAACTTGCTGGTGGA
                                                                                                                                                                                                                                         721 CAGCTCCGCCTCTGCCAGGTGTCTGGGCTGTTGGCCCTGCGGGCCAGGGTCCTCCC
                                                                                                                                                                                                                                                                                        781 ATCCCCACCCTCCCCTGGGCCCCATCTCAAGGCTGCCCCCTTCCTCACCTACTTCGC
                                                                                                                                                                                                                                                                                                                                       37098 ATCCGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCCTTCCTCACCTACTTCGC
                                                                                                                                                                                                                                                                                                                                                                      841 TICCAGGIICACTGAGGGGCCCTGGTCTCCCCACAGTCGTCCAGGCTGCGGGCT
                                                                                                                                                                                                                                                                                                                                                                                   901 CGACAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCCACCCTCAGCGGCTCTTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                1141 CAGGGCATTGTGTTCACTGTACTCTGTGGCAAGGATGGGTCCAGAAGACCCCAC
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0
                                                                                                                                     Length 60268;
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                                                                                                                                    Query Match
45.2%; Score 620; DB 9; Length 60
Best Local Similarity 99.6%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 3; Indels
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AY081051
LOCUS
DEFINITION Homo sapiens TWE-PRIL mRNA, complete cds.
41746. .42046

/rpt family="AluSx"

42047. family="L2"

42287. .42581

/rpt family="L2"

42582. .42730

/rpt family="L2"

42730. /rpt family="L2"

43730. .43859

/rpt family="MER94"

44018. .44132
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The sequence data in this record represents an 'enhanced' version of a phase 2 submission. Specifically, the indicat order and orientation of each sequence contigh has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associative, a phrap-derived quality score.
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AC127470.4 GI:31415893
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                                                                                                                                                                                                                                                                                                                                                                                                                               591 CCTGTACTGTCAG 603
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ARRA1AAHYEVHPREGDGAQAGVDGTVSGMEEARINSSSPLRYNROLIGEFIVTRAĞL
YYLYOGSSADALEAMENGERSKRRRALUŢĢKQKKQHSVLHLVPINATSKDDSDVTEVNM
QPALREGRGLQAQCYGRIQDAGVYLLYSQVLFQDDVTFTMGQVVSREQGGRQETLFRC
IRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARAKLNLSPHGTFLGFVKL"
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                                                                                                                                                                                  ta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
a, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Balade,B., Medema,J.P., Lopez-Fraga,M., Lozano,J.C.,
oten,G.M., Picard,A., Martinez-A,C., Garcia-Sanz,J.A. and
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Balade, B., Garcia-Sanz, J.A. and Hahne, M. Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="17"
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/protein_id="AAL90443.1"
/db_xref="G1:24934974"
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Location/Qualifiers
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GI:24934973
                                                                                                      piens (human)
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Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Pan.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 218485)
8 Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjami
Blakesley, K.W., Bouffard, G.G., Brinkley, C., Brooks, S., Car
Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan
Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P.,
Hurle, B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-L
Legaspi, R., Maduro, D.L., Maduro, V.B., Margulies, E.H., Masi
Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portno
Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., S
Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.-J., Tsipour
Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.
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Submitted (05-JUN-2003) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
On Jun 5, 2003 this sequence version replaced gi:26449071.
361 GGCTCGAAGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGACGG
                                                                                                                481 CCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTA
                                                                                                                                                                                                                 CCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCT
                                                                       GCAGGCAGGTGTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCT(
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Pan troglodytes clone RP43-145D13, WORKING DRAFT SEQUENCE,
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Contact: nisc_zco@nhgri.nih.gov
Contact: project Information
Center project name: cms
Center clone name: 145D13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS PHASE2; HTGS DRAFT.
Pan troglodytes (chimpanzee)
Pan troglodytes
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iste of 17 contigs. Gaps between the contigs represented as runs of N. The order of the pieces helieved to be correct as given, however the sizes hely gaps between them are based on estimates that have ided by the submittor; as soon as it is available and accession number will be replaced.

1 Sequence will be replaced
accession number will be preserved.
1 748: contig of 7448 bp in length
1 7549 1317: contig of 7448 bp in length
1 7649 31917: contig of 7448 bp in length
1 7649 31917: contig of 14474 bp in length
1 8043: contig of 14474 bp in length
1 8043: contig of 4674 bp in length
1 8043: contig of 4674 bp in length
1 8043: contig of 4674 bp in length
1 8043: contig of 7848 bp in length
1 8043: contig of 7848 bp in length
1 8043: contig of 1845 bp in length
1 8044: 109973: gap of unknown length
1 8044: 109973: gap of unknown length
1 8044: 109973: gap of unknown length
1 8044: 109973: gap of unknown length
1 8044: 109973: gap of unknown length
1 8045: 128625: contig of 18496 bp in length
1 8046: 128625: contig of 18496 bp in length
1 8046: 128625: contig of 18496 bp in length
1 8046: 128625: contig of 18496 bp in length
1 80476: 18673: contig of 18496 bp in length
1 80476: gap of unknown length
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equencing vector: plasmid; n/a; 100% of reads hemistry: Dye-terminator Big Dye; 100% of reads ssembly program: Phrap; version 0.990319 onsensus quality: 214085 bases at least Q40 onsensus quality: 216265 bases at least Q20 onsensus quality: 216264 bases at least Q20 nest size: 190000; agarose-fp nest size: 216885; sum-of-contigs hality coverage: 12.65x in Q20 bases; sum-of-contigs hality coverage: 11.08x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52645 Grecresceriscereceredadaarrereageeacregegegagreeres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781 ATCCGCACCCTCCCCTGGCCCCATCTCAAGGCTGCCCCCTTCCTCACCTACTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 961 CCTGCCCCCCCTCTAGAGGCTGCCTGGGCCTGTTCACGTGTTTTCCATCCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1021 ACAGIATICCCACTCTIATCTTACAACT-CCCCCACCGCCCACTCTCCACCTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1200 GGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAAGAGACTGGGCCTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICCAGGITCACTGAGGGCCCTGGTCTCCCCACAGGTCGTCCCAGGCTGCCGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           721 CAGCICCGCCICIGCCAGGIGICIGGGCIGITGGCCCTGCGGCCAGGGICCICCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 CGACAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCACCCTCAGCCGCTCTTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 218485;
                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     31.7%; Score 435; DB 2; I 99.3%; Pred. No. 1.1e-230; tive 0; Mismatches 4;
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Matches 755; Conservative
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicat order and orientation of each sequence contigh has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associate with a Phrap-derived quality score. Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Assembly program: Phrzap; version 0.990319
Consensus quality: 178450 bases at least Q40
Consensus quality: 179436 bases at least Q30
Consensus quality: 179435 bases at least Q20
Insert size: 169000; agarose-fp
Insert size: 179622; sum-of-contigs
Quality coverage: 12.21x in Q20 bases; sum-of-contigs \* by the finished sequence as soon as it is available and
the accession number will be preserved.

1 27615: contig of 27615 bp in length
27716 63581: contig of 3886 bp in length
63582 63681: gap of unknown length
63582 79016: contig of 13886 bp in length
79017 79116: gap of unknown length
79017 91018: contig of 1392 bp in length
91019 94188: gap of unknown length
91019 94188: gap of unknown length
91019 94389: contig of 1302 bp in length
91019 94389: gap of unknown length Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipour Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E NISC Comparative Sequencing Initiative consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced Direct Submission Submitted (05-JUN-2003) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA On Jun 5, 2003 this sequence version replaced gi:25447561. Direct Submission Submitted (08-AVG-2002) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 180222) NOTE: This is a 'working draft' sequence. It currently 167164: contig of 72775 bp in length 167264: gap of unknown length 180222: contig of 12958 bp in length. Web site: http://www.nisc.nih.gov Contact: nisc zoo@nbgri.nih.gov 1. .tavzzz /organism="Sus scrofa" Center clone name: 436K21 Location/Qualifiers Center code: NISC (bases 1 to 180222) Unpublished 27616 27716 63582 63682 79017 79117 91119 94290 94390 167165 Green, E.D. Green, E.D. source TITLE JOURNAL TITLE JOURNAL AUTHORS AUTHORS JOURNAL REFERENCE REFERENCE FEATURES COMMENT TITLE Jilis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., iley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., G., Hadnighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q., J., R., Maduro, Q.L., Maduro, V.B., Marquiles, B.H., Massiello, C., Ti, B., McDowell, J., Paquirigan, C., Pearson, R., Portnoy, M.E., I, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., TAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGGCCAGGA 53244 caaargreagegegegagaaacaagacaagcrecerecerreagaarrecererega 53304 92 180222 bp DNA linear HTG 05-JUN-2003 rofa clone RP44-436K21, WORKING DRAFT SEQUENCE, 7 ordered ö GTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCACTTCAGGCACT 1205 GGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCC 1265 CCAAATGTGAGGGGGGAGAAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGA 1319 PAT 18-MAR-2002 gesecresacereseadesaasecaaasaasaasaasaasaasaasecaasaasaasaasaases GTGAGGGGGGGAAAACAAGACAAGCTCCTCCCTTGAGAATTCCCTGTGGATTTTT 1324 96 GTGAGGGGCGAGAAACAAGACTCCTCCTTGAGAATTCCCTGGGATTTTT 195 ota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; ia; Butheria; Cetartiodactyla; Suina; Suidae; Sus. ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; ia; Eutheria; Primates; Catarrhini; Hominidae; Homo. r,M.J., King,G.E., Xu,J. and Secrist,H. itions and methods for the therapy and diagnosis of colon GTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGACCCCCACTTCAGGCACT ô 13.0%; Score 179; DB 6; Length 195; 100.0%; Pred. No. 6.6e-88; 0; Indels linear raaaacagararrarrrarrarrarrargacaaa 53344 PARANCAGATATTATTTTTATTGTGACAAA 1359 DNA 100.0%; Prec. ... WO 0196389-A 66 20-DEC-2001; 195
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92.4 TGS

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ö 0; Gaps Length 180222; 0; Indels 10.6%; Score 145; DB 2; I 100.0%; Pred. No. 1.2e-68; ive 0; Mismatches 0; arity 100.

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secedededrececerecedareceredareces SCACAGCCCCCCGCCCCCATGGCCGCCCGTCGGAGCCCAGAGGCGGAGGGGCGCCGG 144

AGCCGGGCACCGCCTGCTGG 96025 SAGCCGGGCACCGCCCTGCTGG 169

ells, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., sley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., J. Haddighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., E., B., Madluc, C., Madro, P., Laric, P., Laric, P., E., Mallor, C., Maduro, V.B., Margulies, E.H., Masiello, C., ri, B., McDowell, J., Pagnirigan, C., Pearson, R., Portnoy, M.E., d.A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D., Comparative Sequencing Initiative 130254 bp DNA linear HTG 06-JUN-2003 norvegicus clone RP31-258K6 strain Brown Norway, WORKING yota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, lia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, SEQUENCE, 12 ordered pieces. norvegicus (Norway rat) HTGS PHASE2; HTGS DRAFT GI:31442440 ases 1 to 130254) ases 1 to 130254) norvegicus lished

Submitted (06-JUN-2003) NIH Intramural Sequencing Center, Submitted (06-JUN-2003) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA On Jun 6, 2003 this sequence version replaced gi:27753660. Submitted (30-OCT-2002) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 130254) Center: NIH Intramural Sequencing Center Web site: http://www.nisc.nih.gov Center code: NISC Green, E.D. TITLE JOURNAL REFERENCE AUTHORS JOURNAL COMMENT

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicat order and orientation of each sequence contigh has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least BX average in confirmation by PCR testing. In addition, the sequence assemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associate with a Phrap-derived quality score.

Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990119
Consensus quality: 128674 bases at least Q20
Consensus quality: 128674 bases at least Q20
Insert size: 150000; agarose-fp
Quality coverage: 10.78x in Q20 bases; sum-of-contiguation.

NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces

\* is believed to be correct as given, however the sizes of the gaps between them are based on estimates that has provided by the submittor.

\* This sequence will be replaced.

\* This sequence will be preserved.

\* the accession number will be preserved.

\* 10522 10621: contig of 10621 bp in length

\* 10622 13327: contig of 10621 bp in length

\* 1328 13427: gap of unknown length

\* 13428 28924: contig of 15497 bp in length

\* 29025 39201: contig of 15497 bp in length

\* 39102 41906: contig of 2006 bp in length

\* 41007 70095: contig of 2005 bp in length

\* 42007 70095: contig of 2005 bp in length

\* 42007 70095: contig of 2005 bp in length

\* 42007 70095: contig of 2005 bp in length

\* 7762: contig of 2005 bp in length

\* 70096 70195: app of unknown length gap of unknown length contig of 7366 bp in length gap of unknown length contig of 16500 bp in length gap of unknown length contig of 7318 bp in length gap of unknown length contig of 3721 bp in length gap of unknown length 94261: 77561: 77661: 94161: 98082: 70196 94262 97983 77662

of 22355 bp in length

unknown length of 2299 bp in length.

contig gap of

105401 105501 127856 127956

105400: 105500: 127855: 127955:

98083

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Submission

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8.7%: Score 119; DB 2; Length 130254;
100.0%; Pred. No. 3.9e-54;
ive 0; Mismatches 0; Indels 0;
                                    nservative
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                                                                                                                                                                                                                                                                                                                                                  ta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
                                                                                                                                                                                                                                                                                                                                                                                          a; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                     GS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                                                                                                                                                                                                  norvegicus
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COMMENT

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, V., Chavez, D., Chen, C., Chople, M., Cree, A., D'Sou Clacko, J., Chavez, D., Chen, C., Coople, M., Cree, A., D'Sou Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederic Delgade, O., Denson, S., Deramo, C., Ding, Y., Dinh, M., Divya, K. Drapar, H. Bescotto, M., Eugene, C., Evane, C. A., Falls, T., Fan, G. Franer, H. Dugan, Rocha, S., Dunn, A., Durbin, K., Duval, B., Ea Bran, A., Eascotto, M., Eugene, C., Evane, C. A., Falls, T., Fan, G. Franer, C. M., Cablsi, A., Canta, R., Garcia, A., Garner, T., Gar Gebregoorgis, B., Geer, K., Gill, R., Gracia, A., Garner, T., Gar Gunaratne, P., Havlak, P., Hamil, C., Hamilton, C., Hamilton, K., Hennandez, R., Hines, S., Hilly, M., Hamil, C., Hamilton, C., Hamilton, K., Hennandez, R., Hines, S., Hilly, S., Khan, Z., King, L., Kovar, C. Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Ichain, J., Li, Z., Liu, W., Lilu, W., Lilu, Y., Londsock, H., Donason, M., Martin, E., Martin, R., Marti Direct Submitted (19-NOV-2002) Human Genome Sequencing Center, Der Submitted (19-NOV-2002) Human Genome Sequencing Center, Der of Molecular and Human Genetics, Baylor College of Medicine Baylor Plaza, Houston, TX 77030, USA on Nov 19, 2002 this sequence version replaced gi:23616728. The sequence in this assembly is a combination of BAC basec and whole genome shotgun sequencing reads assembled using and whole genome shotgun sequencing reads assembled using and therp://www.hgsc.bom.tmc.edu/projects/rat/). Each contig assembly (a 'contig-scaffold'). Within each contig di individual sequence contigs are ordered and oriented, and individual sequence contigs are ordered and oriented, and systed gaps filled with Ns to the estimated size. The sec may extend beyond the ends of the clone and there may be se Submitted (25-APR-2002) Human Genome Sequencing Center, Der of Molecular and Human Genetics, Baylor College of Medicine Baylor Plaza, Houston, TX 77030, USA (bases 1 to 16516) (Bat Genome Sequencing Consortium. contigs within a contig-scaffold that consist entirely of v genome shotgun sequence reads. Both end sequences and whole shotgun sequence only contigs will be indicated in the feat table. (bases 1 to 165316) Direct Submission Unpublished Worley, K.C. Direct Submission AUTHORS TITLE JOURNAL TITLE JOURNAL REFERENCE AUTHORS REFERENCE

Center: Baylor College of Medicine Center code: BCM

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Manmalls; burderls; Rocentis; Sciulogiachii; Mulicae; Mainis, C., Marris, C., Marris, C., Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwunnu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Br. Buhay, C., Burac, C., Burkett, C., Chacko, J., Chen, G., Cox, C., Davis, C., Delagado, O., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R., Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogue Hosak, H., Hou, X., Huber, J., Jackson, J., Jia, W., Kolly, J., Kovar, C., Liu, J., Lulu, W., Loulseeged, H., Lozado, R.J., Marti Massey, E., McLeod, M.P., Mei, G., Mover, S., Morgan, M., Morri Neal, D., Nelson, A., Myuyen, R., Nguyen, N., Oguh, M., Parish, Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Wallingt Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A., Wolley, K. and Gibbs, R.
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(C) (bases 1 to 203083)

Worley, K.C.

Direct Submission

Submitted (31-MAY-2000) Human Genome Sequencing Center, De

(Molecular and Human Genetics, Baylor College of Medicin

Baylor Plaza, Houston, TX 77030, USA

On Jun 25, 2001 this sequence version replaced gi:12621364
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                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murin
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g of 22576 bp in length
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Contact: hgsc.help@bcm.tmc.edu
Contact: hgsc.help@bcm.tmc.edu
Center project Information
Center project name: MAFO
HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP
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Center code: BCM
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This is a "working draft' sequence It currently ists of 5 contigs. The true order of the pieces of known and their order in this sequence record is trary. Gaps between the contigs are represented as of N, but the exact sizes of the gaps are unknown. record will be updated with the finished sequence oon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                              timated insert size: 159662; sum-of-contigs estimation ality coverage: 7x in Q20 bases; sum-of-contigs estimation
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100.0%; Pred. No. 3.9e-54;
iive 0; Mismatches 0; Indels
                                                                                                                                                                nter clone name: CH230-320N23
------ Summary Statistics
sembly program: Phrap; version 0.990329
nsensus quality: 155971 bases at least Q40
nsensus quality: 157321 bases at least Q30
nsensus quality: 158253 bases at least Q20
    b site: http://www.hgsc.bcm.tmc.edu/
ntact: hgsc-help@bcm.tmc.edu
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/mol_type="genomic DNA"
/db xref="taxon:10116"
                                                                                           ----- Project Information
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clone_end:T7"
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/note="clone_boundary
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                                                                                                                                                                                                     GTCGGAGCCAGAGGCGGAGGGGGCGCCGGGGGGAGCCGGGCACCGCCCTGCTGG 169
                                                                                                                                                                         Gaps
                                                                                                                                                                        ٥;
                                                                                                                                     Score 119; DB 2; Length 203083;
Pred. No. 4e-54;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRAFT; HTGS FULLTOP.
                                                                                                                               8.7%; Scor.
100.0%; Pred. No. ac.
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Location/Qualifiers
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                 .203083
                                                                                                                                                                         nservative
                                                                                                                                                                                                                                                                                                                                                                                                            ed pieces.
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norvegicus clone CH230-154B15, WORKING DRAFT SEQUENCE, 3
norvegicus clone CH230-154B15, WORKING DRAFT SEQUENCE, 3
sed pieces.

Sa G1:30521223
SPHSEL; HTGS_DRAFT; HTGS_FULITOP.

Norvegicus (Norway rat)
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static 223877)
Naric Metazos, Chanch, Maric Manna, Arguiano, D.
Naric Metazos, Charler, M. Barnstead, M. Benhmed, F.,
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/organism="Rattus norvegicus"

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Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D. Sneetly, A., Sodergren, E., Song, X.-Z., Sozelle, K., Sosa, J., Steimle, M., Strong, R., Sutton, A., Tabor, P., Tabor, P., Tay, Taylor, T., Thomas, N., Tingey, A., Trejos, Z., Usmi Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wai Wang, G., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Weczyk, R., Wooden, H., Worley, R., Wight, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., You, Y., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H. Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Molecular and Human Genetics, Baylor College of Medicini
Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this ascembly is a combination of BAC bases
The sequence in this ascembly is a combination of BAC bases
and whole genome shotgun sequencing reads assembled using,
(http://www.hgsc.bom.tmc.edu/projects/rat/). Each contig
in the feature table below represents a scaffold in the At
assembly (a 'contig-scaffold') Within each contig-scaffol-
individual sequence contigs are ordered and oriented, and
by sized gaps filled with Ns to the estimated size. The se-
may extend beyond the ends of the clone and there may be s-
contigs within a contig-scaffold that consist entirely of
genome shotgun sequence reads. Both end sequences and whol-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-NOV-2001) Human Genome Sequencing Center, Del of Molecular and Human Genetics, Baylor College of Medicin Baylor Plaza, Houston, TX 77030, USA (DABESE 1 to 223877)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: Estimated insert size may differ from sequence len (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_da * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center clone name: CH230-154815
Center clone name: CH230-154815
Assembly program: Atlas 3.0;
Consensus quality: 214785 bases at least Q40
Consensus quality: 216908 bases at least Q30
Consensus quality: 218593 bases at least Q20
Bstimated insert size: 227169; sum-of-contigs estimati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-MAY-2003) Human Genome Sequencing Center, De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality coverage: 7x in Q20 bases; sum-of-contigs esti
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8 221427: gap of unknown length
8 222652: contig of 1225 bp in length
3 222552: gap of unknown length
3 223877: contig of 1125 bp in length
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------- Project Information
Center project name: GIOK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 223877)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Worley, K.C.
Direct Submission
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222753
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JOURNAL
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C., Aller, H., Alsbrooks, S., Amin, A., Anguiano, D.,

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lia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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3 norvegicus clone CH230-46E21, WORKING DRAFT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 223877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.7%; Score 119; DB 2; Length 223
100.0%; Pred. No. 4e-54;
ive 0; Mismatches 0; Indels
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IGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
norvegicus (Norway rat)
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(X)

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* NOTE: Estimated insert size may differ from sequence le (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_d * NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that ha provided by the submittor.

* This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.

* Location/Qualifiers
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Rigg Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J. Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, I. Sneety, J., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Tingey, A., Tabor, P., Tay Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usr Valas, R., Veray, V., Villasana, D., Walker, B., Wa Wang, C., Walker, B., Wa Wang, C., Wang, S., Warren, R., Woden, H., Worley, K., Wijht, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Ye, R., Zhang, J., Zhou, X., Zhou, S., Yan, C., Yoon, L., Ye, R., Smith, E., Wainser, C., Mang, S., Raits, R., Smith, E., Naist, C., Whiles, R., Smith, E., Wainser, C., Shin, Santh, E., Santh, E., Smith, E., Stand, S., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E., Santh, E
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On May 10, 2003 this sequence version replaced gi:25188701 The sequence in this assembly is a combination of BAC base and whole genome shorgun sequencing reads assembled using (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig (in the feature table below represents a scaffold in the Aliassembly (a 'contigs ecaffold'). Within each contig contig are ordered and coriented, and by sized gaps filled with Ns to the setimated size. The Sympy extend beyond the ends of the clone and there may be contigs within a contig-scaffold that consist entirely of genome shotgun sequence reads. Both end sequences and who shotgun sequence eadds. Both end sequences and who shotgun sequence cadds. Both end sequences and who shotgun sequence eadds. Both end sequences and who shotgun sequence cadds.
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Direct Submission
Submitted (06-NOV-2002) Human Genome Sequencing Center, De of Molecular and Human Genetics, Baylor College of Medicir Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 225077)
Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 8x in Q20 bases; sum-of-contigs est
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Center code: BCM
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/note="Sequence from uni-directional primer reads and dGTP
big dye terminator reads only."
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a; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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ne RPCI-23 Mouse PAC Library
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                                                                                                                                                                                             8.7%; Score 119; DB 2; Length 225077;
100.0%; Pred. No. 4e-54;
iive 0; Mismatches 0; Indels 0;
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db xref="taxon:10116"
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/clone_lib="RPCI-23"
                                /clone="CH230-46E21"
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

I (bases 1 to 212093)
S. Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjami.
Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Car Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan Gupta, J., Han, D., Han, D., Han, D., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Liegaspi, R., Maduro, L.B., Maduro, L.B., Margulies, B.H., Masi Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portno Praead, A., Reddix-Duger, N., Schandler, K., Schweler, M.G., Sison, C., Stantripoy, S., Thomas, J.W., Thomas, P.J., Taipour Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E., Tann, J., A., Missins, L., Young, A. and Green, E., Mark, J., A., Missins, L., Young, A. and Green, E., Mark, J., A., Missins, L., Young, A. and Green, E., Mark, J., A., A., Missins, L., Young, A. and Green, E., Mark, J., A., Missins, L., Young, A. and Green, E., Mark, J., A., Missins, L., Young, A., and Green, E., Mark, J., A., Missins, L., Young, A., and Green, E., Missins, L., A., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Young, A., and Green, E., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Young, A., and Green, E., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Young, A., and Green, E., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Young, A., and Green, E., Missins, L., Missins, L., Young, A., and Green, E., Missins, L., Missins, L., Missins, L., Young, A., and Green, E., Missins, L., Missins, L., Missins, L., Missins, L., Young, A., and Green, E., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, L., Missins, Missins, L., Missins, L., Missins, Missins, L., Missins, Missins, Mis
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Submitted (06-JUN-2003) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
On Jun 6, 2003 this sequence version replaced gi:27476131.
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                                                                                                                                                                                                                                  111 CGCCCGTCGGAGCCAGAGGCGGAGGGGCCCCGGGGGGGAGCCGGGCACCGCCCTGC
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Canis familiaris clone RP81-414022, WORKING DRAFT SEQUENCE
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                Length 234182;
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                                                                                                                                  0; Indels
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                                                                                    4.le-54;
                                 DB 10;
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B.7%; Scor.
100.0%; Pred. No. *...
... 0; Mismatches
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------ Project Information
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HTG; HTGS PHASE2; HTGS_DRAFT.
Canis familiaris (dog)
Canis familiaris
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/note="assembly\_fragment"

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VERSION
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AF030100
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126505. 212093
/note="Clone overlaps with GenBank Accession Number
AC126925 clone RP81-332E11 (center project name cwp)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jeeguance will be resplaced
accession number will be preserved.

1485
1584: contig of 1484 bp in length
3485
1584: gap of unknown length
18900: contig of 24725 bp in length
18910: gap of unknown length
18901: gap of unknown length
18901: gap of unknown length
18901: gap of unknown length
18901: gap of unknown length
18901: gap of unknown length
18902: contig of 64694 bp in length
18055: gap of unknown length
18056: s7955: contig of 61461 bp in length
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                                                                                                                                                                                                                                                                                                                          sists of 15 contigs. Gaps between the contigs represented as runs of N. The order of the pieces believed to be correct as given, however the sizes the gaps between them are based on estimates that have sided by the submittor.
Chemistry: Dye-terminator Big Dye; 100% of reads ussembly program: Phrap; version 0.990319
Consensus quality: 209634 bases at least Q40
Consensus quality: 209673 bases at least Q30
Consensus quality: 210263 bases at least Q20
Consensus quality: 210263 bases at least Q20
Consert size: 196000; agarose-fp
Consert size: 210693; sum-of-contigs
Conlity coverage: 16.73x in Q20 bases; sum-of-contigs
Consensus Consensus Contigs
                                                                                                                                                                                                                                                                                                    3: This is a 'working draft' sequence. It currently
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/organism="Canis familiaris"
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/db_xref="taxon:9615"
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/clone_lib="RP81"
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vector_side:left"
3585, .28309
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Eutel Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Muri I bases I to 1239 I to 1239 I to 1239 I to 1239 I to 1240 I the session, C., Garcia, I. and Browning, J.L. TWEAK, a new secreted ligand in the tumor necrosis factor That weally induces apoptosis J. Biol. Chem. 272 (51), 32401-32410 (1997)
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Submitted Submitsbard.
Submitted Submitsbard.
Submitted, MA 02142, USA
3 (bases 1 to 1239)
Chicheportiche, Y., Bixler, S., Tizard, R. and Browning, J. Direct Submitsbard.
Submitted (30-JUL-2003) Cell Biology, Biogen, 12 Cambridg Sequence update by submitter by submitter by submitter by submitter by submitter by submitter by submitter by submitter by submitter.
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Chicheportiche, Y., Bixler, S., Tizard, R. and Browning, J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 212093;
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1 Similarity 100.0%; Pred. No. 6e-24;
65; Conservative 0; Mismatches 0; Indels
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/mol_type="mRNa"
/db_xref="taxon:10090"
/cell_type="peritoneal macrophages"
1.750
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146963. .152584-
/note="assembly fragment"
|152685. .15568
/note="assembly fragment"
|155769. .176557
/note="assembly_fragment"
                                                                                                                                                                                                           /note="assembly_fragment"
195138 .200818
/note="assembly_fragment"
200919 .204476
/note="assembly_fragment"
204577 .212093
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/note="assembly_fragment"
184192. .195037
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AF030100,2 GI:33348855
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Best Local Similarity
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lis, A., Ayele, K., Beckstrom-Sternberg, S. M., Benjamin, B., ley, R. W., Bouffard, G. G., Brinkley, C., Brooks, S., Gariaga, K., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., B., Idol, J. R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q., R., Maduro, Q. L., Maduro, V. B., Margulies, E. H., Masiello, C., M., McCowell, J., Paguirigan, C., Pearson, R., Portnoy, M. E., A., Reddix-Dugue, N., Schandler, K., Schueler, M. G., Shah, K., C., Stantripop, S., Thomas, J. W., Thomas, P. J., Tsipouri, V., L., Wetherby, K. D., Wiggins, L., Young, A. and Green, E. D. omparative Sequencing Initiative
                                                                                              /trānslation="MAARRSQRRRGRRBGFPGTALLAPIVLSLGLALACIGLLLVVVSL
GSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRSAPKGRKAR
PRRALAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 148555 bp DNA linear HTG 06-JUN-2003 urus clone RP42-45D24, WORKING DRAFT SEQUENCE, 11 ordered
                                                                                                                                                                                                YYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSGLLPL
RPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH"
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Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ted (10-JUL-2002) NIH Intramural Sequencing Center, 8717 ont Circle, Gaithersburg, MD 20877, USA ses 1 to 148555)
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6, 2003 this sequence version replaced gi:24137427
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                                                                                                                                                                                                                                                                                                                                  4.7%; Score 64; DB 10; Length 1239;
100.0%; Pred. No. 1.4e-23;
ive 0; Mismatches 0; Indels (
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/product="TWEAK"
/protein_id="AAC53517.2"
/db_xref="GI:33348856"
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11.13 to 40 E1.13

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data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associate with a Phrap derived quality score.

Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319

Consensus quality: 144765 bases at least Q30

Consensus quality: 146165 bases at least Q20

Insert size: 147555; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence will be replaced

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 41912 42011: contig of 41911 bp in length

* 42012 58978: contig of 16867 bp in length

* 58979 59078: contig of 16867 bp in length

* 58979 59078: contig of 6747 bp in length

* 5926 65925: gap of unknown length

* 5526 73946: contig of 8021 bp in length

* 74047 89416: contig of 18370 bp in length

* 74047 89416: contig of 18370 bp in length

* 89417 89516: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     consists of 11 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that hav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 8.83x in Q20 bases; agarose-fp Quality coverage: 9.03x in Q20 bases; sum-of-contigs
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109990. .126878
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/note="assembly_fragment
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/db_xref="taxon:9913"
/clone="RP42-45D24"
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ages 1 to 17628)
alis, A. Ayele, K. Beckstrom-Sternberg, S.M., Benjamin, B.,
sley, R.W., Bonffard, G.G., Brinkley, C., Brooks, S., Cariaga, K.,
Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X.,
J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P.,
B., Idol, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q.,
P.R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C.,
ri, B., McDowell, J., Paquirigan, C., Pearson, R., Portnoy, M.E.,
d.A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K.,
J.L., Wetherby, S., Thomas, J.W., Thomas, P.J., Tsipouri, V.,
J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
Comparative Sequencing Initiative
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familiaris clone RP81-332E11, WORKING DRAFT SEQUENCE, 12
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lia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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tted (10-UJU-2002) NIH Intramural Sequencing Center, 8717
mont Circle, Gaithersburg, MD 20877, USA
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     indicated
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Center code: NISC
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HTGS PHASE2; HTGS DRAFT.
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familiaris
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파무크표 KR4,110

显真显微

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**NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that has provided by the submittor.

**Provided by the submittor.**

**Provided by the submittor.**

**Intage sequence as soon as it is available and the accession number will be preserved.

**Intage contig of 11425 bp in length 11526 27554; contig of 1425 bp in length 27555 29975 contig of 16029 bp in length 27655 29975 contig of 2320 bp in length 27655 29975 contig of 6167 bp in length 36241; contig of 6167 bp in length 36241; contig of 6167 bp in length 36242 77002; contig of 40661 bp in length 36242 77002; contig of 40661 bp in length 36242 77002; contig of 40661 bp in length 36242 77002; contig of 40661 bp in length 36242 77002; contig of 40661 bp in length 36242 77003; contig of 40661 bp in length 36242 77003; contig of 40661 bp in length 36242 77003; contig of 40661 bp in length 36242 77003; contig of 40661 bp in length 36242 77003; contig of 40661 bp in length 47002; contig of 40661 bp in length 47002; contig of 40661 bp in length 47002; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 47003; contig of 40661 bp in length 470
              1. 88033
/note="clone overlaps with GenBank Accession Num
AC126237 clone RP81-414022 (center project name
established using one or more of the following: read-pair
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of 39916 bp in length
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of 39247 bp in length
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contig of 9545 bp in length
gap of unknown length
contig of 2583 bp in length
gap of unknown length
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of 1923 bp in length
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contig of 1729 bp in l
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30075. .36241
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clone_end:SP6
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/db_xref="taxon:9615"
/clone="RP81-332E11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 149736 bp DNA linear HTG 06-JUN-2003 catus clone RPB6-474H17, WORKING DRAFT SEQUENCE, 12 ordered
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ia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rgcactttgatgagggaaggctgtctacctgaagctggacttgctggatg 658
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ontact: nisc_zoo@nhgri.nih.gov
                                                                                                                                           /note="assembly fragment"
119142. .158388 / note="assembly fragment"
158489. .168033 / note="assembly fragment"
168134. .170716
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enter project name: daa
enter clone name: 474H17
                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
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                                                                                       /note="assembly_fragment"
117119. .119041
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IGS_PHASE2; HTGS_DRAFT.
catus (cat)
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicat order and orientation of each sequence contigh has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associate with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator: Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 1480%1 bases at least Q40
Consensus quality: 1485%8 bases at least Q30
Consensus quality: 1485%8 bases at least Q20
Insert size: 126000; agarose-fp
Insert size: 14863%; sum-of-contigs
Quality coverage: 15.56x in Q20 bases; sum-of-contigs
Quality coverage: 13.19x in Q20 bases; sum-of-contigs
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1 484 583: gap of unknown length 584 19266: contig of 18683 bp in length 19267 21971: contig of 2605 bp in length 21972 22071: gap of unknown length 22072 22071: gap of unknown length 2417 24416: gap of unknown length 2417 36979: contig of 2265 bp in length 2417 36979: contig of 12563 bp in length 36980 37079: gap of unknown length 42620 42719: gap of unknown length 42620 42719: gap of unknown length 4665 61551: contig of 3745 bp in length 4665 61551: contig of 3745 bp in length 4665 61551: contig of 14987 bp in length 4665 61551: contig of 14987 bp in length 4665 61551: contig of 11134 bp in length 110460 110559: gap of unknown length 110460 110559: gap of unknown length 110460 110559: gap of unknown length 110460 147587: contig of 37028 bp in length 110468 147587: contig of 37028 bp in length 147588 147687: gap of unknown length 147687: gap of unknown length 147689 147587: contig of 2049 bp in length 147689 147587: contig of 2049 bp in length 147689 147587: contig of 2049 bp in length 147689 147587: contig of 2049 bp in length 147689 147587: contig of 2049 bp in length 147689 147687: gap of unknown length 147689 147587: contig of 2049 bp in length 147689 147587: contig of 2049 bp in length 147689 147587. contig of 2049 bp in length 147689 147587. contig of 2049 bp in length 147689 147587. contig of 2049 bp in length 147689 147687.
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22072. .24316
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/db_xref="taxon:9685"
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1. .483
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584. .19266
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/organism="Felis catus"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. I (Dases 1 to 163542)

R thoses 1 to 163542)

R Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gu Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karl Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Velterby, K.D., Wiggins, L., Young, A. and Green, E.D.
                                                                                                                                                                           Unknown
JP 2001522584-A/3
20-NOV-2001
20-NOV-2001
09-OCT-1997 US 60/062037,17-DEC-1997 US 60/0698
10-OCT-1997 US 60/062037,17-DEC-1997 US 60/0698
COTSTAIS,09,A61K3B/00,C07K14/705,C07K16/24,C12N15/00,A8
Description of Unknown Organism:Unknown
Location/Qualifiers
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Submitted (11-DEC-2002) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
On Dec 11, 2002 this sequence version replaced gi:2195501
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Pan troglodytes clone RP43-149M23, WORKING DRAFT SEQUENCE
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Center: Ods: NISC
Web site: http://www.nisc.nih.gov
unclassified.

1 (bases 1 to 50)
Ashenazi,A.J., Marsters,S.A. and Pitti,R.
Apo-3 ligand PolyPeptide
Patent: JP 200152584-A 3 20-NOV-2001;
GENENTECH INC
OS UDKNOWN
PN JP 2001522584-A/3
PD 2001522584-A/3
PD 2001522584-A/3
PD 2001522584-A/3
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PD 2001522584-A/3
PD 2001522584-A/3
PD 2001522584-B/3
PD 2001522584-B/3
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PD 2001528
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HTG; HTGS PHASE2; HTGS_DRAFT.
Pan troglodytes (chimpanzee)
Pan troglodytes
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Best Local Similarity
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1,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
P.M., Watanabe,C.K. and Wood,W.I.
sitions and methods for the treatment of tumour
NO 0153486-A 74 26-JUL-2001;
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larity 100.0%; Pred. No. 3e-17;
Conservative 0; Mismatches 0; Indels 0;
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//mol type="unassigned DNA"
/db_xref="rexon:32630"
/noTe="Synthetic Oligonucleotide Probe."
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tive 0; Mismatches
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/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                            'note="assembly_fragment"
110560. .147587
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
147688. .149736
                                           24417. 36979
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                                                                                                                                                                                                                                                                                                              note="assembly_fragment"
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                     'note="assembly_fragment"
                                                                                                                                        note="assembly_fragment"
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30e 74 from Patent W00153486.
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                                                                                                                                                                                                                                                                                                                                                      9326. .110459
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                                                                                                         .42619
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misc_feature
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                                                                                                                                                                                                                       puence data in this record represents an 'enhanced' nof a Phase 2 submission. Specifically, the indicated and orientation of each sequence contigh has been ished using one or more of the following: read-pair com individual subclones, overlaps with neighboring alignment with available reference sequence (e.g., and/or confirmation by PCR testing. In addition, quence assembly is based on at least 8X average je in Q20 bases and has been reviewed to rule out misassemblies, the low-quality ends of sequence have been trimmed away, and each base is associated Phrap-derived quality score.

------ Summary Statistics aguainty by 100% of reads aguacing vector: plasmid; n/a; 100% of reads agencing vector: plasmid; n/a; 100% of reads agencing quality: 159675 bases at least Q40 nnsensus quality: 159675 bases at least Q20 nnsensus quality: 161608 bases at least Q20 nnsensus quality: 161608 bases at least Q20 nnsensus quality: 16108 bases at least Q20 nnsensus quality: 16108 bases at least Q20 nnsensus quality: 16108 bases at least Q20 nnsensus quality: 16108 bases at least Q20 nnsensus quality: 16108 bases at least Q20 nnsensus quality: 16108 bases at least Q20 nnsensus quality: 16108 bases at least Q20 nnsensus quality: in Q20 bases; sum-of-contigs wality coverage: 8.47x in Q20 bases; sum-of-contigs
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Sequence will be replaced a cession number will be preserved.

1 10517; contig of 10517 bp in length of 10617 gap of unknown length of 10617; gap of unknown length of 10617; gap of unknown length of 10617; gap of unknown length of 10617; gap of unknown length of 10617; gap of unknown length of 10617; gap of unknown length of 2529; contig of 2467 bp in length of 2792; contig of 28005 bp in length of 2796; gap of unknown length of 2796; gap of unknown length of 2796; gap of unknown length of 1287; contig of 22622 bp in length of 1287; contig of 22622 bp in length of 1287; contig of 22622 bp in length of 114016; contig of 2383 bp in length of 114016; contig of 2383 bp in length of 114016; contig of 2383 bp in length of 114016; contig of 2383 bp in length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unknown length of 114016; gap of unkn
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1. .10517

/note="assembly_fragment

missing T7 clone end on 5' end of insert"

nosing T7 clone end on 5' end of insert"

nosing 25192
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     ntact: nisc zoo@nhgri.nih.gov
                                                        Project Information
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'db_xref="taxon:9598"
'clone="RP43-149M23"
                                                                                                 inter project name: cmt
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OS TNF family related protein
PN JP 2001505407-A/1
PD 24-APR-2001
PP 07-APG-1997 JP 1998508239
PR 07-APG-1996 US 60/023541,18-OCT-1996 US 60/028E
PR 07-APG-1996 US 60/040820
PR WAR-1997 US 60/040820
PP C12NJ5/28, CO7K14/525, GO1N33/68, CO7K16/24, C12N15/11, A6
PC C12NJ5/19, A61K39/395, A61K38/19, CO7K14/705, C12N15/12
CC Strandedness: Double;
CC Strandedness: Double;
CC TOPOLOGY: Linear;
FH Key
CT CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 1168)
Chicheportiche, Y. and Browning, J.L.
A tumor necrosis factor related ligand
Patent: JP 2001505407-A 1 24-APR-2001;
BIOGEN INC, THE FACULTY OF MEDICINE OF THE UNIVERSITY OF GE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.4%; Score 46; DB 6; Length 1168; 100.0%; Pred. No. 1.6e-13; Live 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A tumor necrosis factor related ligand.
                                                                                                                                                                                      /note="assembly_fragment"
114117. .116474
/note="assembly_fragment"
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61388. .84039
                                                                                                                                                   /note="assembly_fragment"
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154300, 163542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
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Location/Qualifiers
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JP 2001505407-A/1.
unidentified
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Best Local Similarity
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BD062757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
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Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:23267374
The sequence in this assembly is a combination of BAC base and whole genome shotgun sequencing reads assembled using (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig (assembly (a contig-scaffold in the At assembly (a contig-scaffold). Within each contig-scaffol individual sequence contigs are ordered and oriented, and by sized gaps filled with Ns to the estimated size. The stands watchard beyond the ends of the clone and there may be contigs within a contig-scaffold that consist entirely of genome shotgun sequence reads. Both end sequences and who.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence legent by the sequence legent this is a "working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Submitted (15-APR-2002) Human Genome Sequencing Center, De of Molecular and Human Genetics, Baylor College of Medicir Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: phrap; version 0.990329
Consensus quality: 227577 bases at least Q40
Consensus quality: 220382 bases at least Q30
Consensus quality: 213817 bases at least Q20
Estimated insert size: 239036; sum-of-contigs estimat
Quality coverage: 5x in Q20 bases; sum-of-contigs est
                                                                                                                          Rat Genome Sequencing Consortium.

Direct Submission
Submitted (13-NOV-2002) Human Genome Sequencing Center, Df
Molecular and Human Genetics, Baylor College of Medicir
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162694: contig of 162694 bp in length 162794: gap of unknown length 225525: contig of 62831 bp in length 225725: gap of unknown length 231241: contig of 5516 bp in length 231341: gap of unknown length 232740: gap of unknown length 232740: gap of unknown length 232740: contig of 2061 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor College of Medicine
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Center clone name: CH230-212018
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/note="wgs_end_extension
clone_end:T7"
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/db_xref="taxon:10116"
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Molecular Engines Laboratories (FR)
Location/Qualifiers
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Sequence 135 from Patent WO02064731.
AX522465
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                                                                                                                 AX522345 145 bp I Sequence 15 from Patent WO02064731.
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/organism="Homo sapiens"
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 2.3%; Score 31; DB 2; Length 234801; 00.0%; Pred. No. 6e-05; ve 0; Mismatches 0; Indels 0
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.ive 0; Mismatches 0; Indels
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/organism="synthetic construct"
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lar Engines Laboratories (FR)
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ce 138 from Patent W00153486.
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Lobases 1.C. 353/
Strausberg, R.L., Feringold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schn
Altschul, S.F., Zeebergy, B., Butcow, K.H., Schaefer, C.F., Bhi
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hang,
Stapleton, M., Marusina, K., Farmer, A.A., Rubin, G.M., Hong,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peter:
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gay, L.J., Hulyk, S.W.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villano, D.K., Maran, D.M., Sodergren, E.J., Lu, X., Gibbs, R.
Fahey, J., Helton, E., Ketteman, M., Young, A.C., Shevchenko,
Boutfard, G.G., Blakeeley, R.W., Touchman, J.W., Green, B.D.,
Butterfield, Y.S., Rozywinski, M.I., Skalska, U., Smailus, D.)
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-
human and mouse cDNA sequences
I proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfie Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfie Susamna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ra Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver L Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Sacedi, J Schein, Duane Smailus, Michael Smith, Lorraine Spence, Je Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jil George Yang, Scott Zuyderduyn, Marco Marra.
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through the I.M.A.G.E. Consortium/LIML at: http://lmage.l
Series: IRAL Plate: 51 Row: Column: 23
This clone was selected for full length sequencing becaus
passed the following selection criteria: Hexamer frequenc
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/clone="IMAGE:333215"
/tisus type="Skin, melanotic melanoma, high MDR
/clone_lib="NIH_MGC_62"
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Submitted (17-NOV-2003) National Institutes of Health, Mar
Gene Collection (MGC), Cancer Genomics Office, National C
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 2089
               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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1.9%; Score 26; DB 9; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 26; Conservative 0; Mismatches 0; Indels
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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JOURNAL
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COMMENT
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                               PAT 07-JAN-2002
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lia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                        ota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
.ia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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solecules to be used as indicators of the functional and
itional state of t-lymphocytes
:: EF 1162276-A 168 12-DEC-2001;
[Terapeutics 6mbH (DE)
Location/Qualifiers
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100.0%; Pred. No. 0.021;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.02;
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/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                     153 bp I
168 from Patent EP1162276.
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sapiens (human)

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sapiens

Conservative

CORPORATION

Conservative

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sapiens (human)

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 0.022;
ive 0; Mismatches 0; Indels
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1.9%; Score 26; DB 6; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels
1.9%; Score 26; DB 6; Length 387;
100.0%; Pred. No. 0.022;
tive 0; Mismatches 0; Indels
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1 (bases 1 to 416)

Edwards, J. B. D. M., Jobert, S. and Giordano, J.-Y.

EST's and encoded human proteins

Patent: US 6639063-A 18519 28-OCT-2003;

Location/Qualifiers
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                                                                                                                                                                                                 DNA
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Patent: WO 0151513-A 961 19-JUL-2001;
CORIXA CORPORATION (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                               391 bp | Sequence 961 from Patent W00151513.

    .391
    /organism="Homo sapiens"

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/mol_type="genomic DNA"
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AX198506.1 GI:15388827
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Homo sapiens
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Best Local Similarity 100.0%
                                   26; Conservative
                  Best Local Similarity
Matches 26; Conserv
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   Query Match
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KEYWORDS
SOURCE
ORGANISM
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BD122575
LOCUS
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2N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC
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a, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Pred. No. 0.022;
ive 0; Mismatches 0; Indels
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i.d.-B.D.M., Jobert,S. and Giordano,J.-Y.
und encoded human proteins
US 663963-A 18517 28-OCT-2003;
Location/Qualifiers
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3,0.8.D.M., Jobert,S. and Giordano,J.E.
6 mecoded human protein
JP 2002010789-A 14650 15-JAN-2002;
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3Y Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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7-AUG-2000 JP 2000280989
5-AUG-1999 US 60/147499
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                                        387 bp
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9 2002010789-A/14650
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2010789-A/14650.
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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B. Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brochetrich, N. L., Granite, S., Guan, X., Gught, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legas Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McClos Mrobwell, J., Pearson, R., Stantripo, S., Thomas P.J., Touck Tsurgeon, C., Yogf, J.L., Walker, M.A., Wetherby, K.D., Wiggir Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information car through the I.M.A.G.B. Consortium/LLNL at: http://image.ll series: TRAK Plate: 64 Row. 1 Collumn: 24 Parties clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Unknown (protein for IMAGE:5214272)"
/protein_id="AAH32480:1"
/db_xref="G1:21619103"
/tbaslation="RSVVILLVAVRLHTLLSCPLEQPAGTEWILEEGV
DIYNLRSpDENWRWNWRGALWKEKDRPCAFMKVKIWLNQFHKVTVYIA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
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1.9%; Score 26; DB 9; Length 418;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:5114272"
/tissue type="Blood, adult leukocytes"
/clone_lib="NIH_MGC_118"
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100.0%; Pred. No. 0.022;
tive 0; Mismatches 0
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Location/Qualifiers
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Seguence 1027 from Patent WO0194629.
AX330518
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/db_xref="taxon:9606"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                   ora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
.ia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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35-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
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ive 0; Mismatches 0; Indels
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is,J.B.D.M., Jobert,S. and Giordano,J.E.
is,J.B.D.M., Jobert, John Giordano,J.E.
is J.C. 15-JAN-2002;
i. JP 2002010789-A 14652 15-JAN-2002;
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1: cgapbs-r@mail.nih.gov
le Procurement: Life Technologies, Inc.
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site: http://www.nisc.nih.gov/
act: nisc_mgc@nhgri.nih.gov
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TP 2002010789-A/14652
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 452)
Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 6913 02-OCT-2001;
                                                                                                                                                                                                                               Homo sapiens (human)
JP 2001269182-A/6913
02-CCT-2001
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEA
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1.9%; Score 26; DB 6; Length 483;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.022;
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CORIXA CORPORATION (US)
Location/Qualifiers
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Sequence 558 from Patent W00212280.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
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            BD030667.1 GI:22572409
JP 2001269182-A/6913.
Homo sapiens (human)
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cive 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
/mol_type="taxon:9606"
/noce="EMBL/GenBank Accession No. N98464"
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    ATTGTTAGACTTTGAAATTTC 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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34.1 GI:40050018

onservative

arity

K

.. .439

apiens (human)

apiens

07-NOV-2001 (first entry)

lard; DNA; 153 BP.

(first entry)

ell derived DNA fragment #168.

ell; immunosuppressive; immunostimulant; antiinflammatory; ene therapy; vaccine; allergen; transplant rejection; nost disease; malignant disease; ds.

2000DE-01021834.

2000DE-01021834.

THERAPEUTICS GMBH

Reinartz J; inter H,

ative of T cell activation and functional status, useful and therapy e.g. of autoimmunity or transplant rejection. cative

48; 94pp; German.

the activation and functional status of T calls, that have reduced expression, and are present at higher or lower reduced expression, and are present at higher or lower cauches to any of 334 sequences, reproduced, or their complements or fragments. The products of the invention have sive, immunostimulant, antinflammatory and cytostatic can be used for gene therapy. The polynuclectides of the invention have sive, immunostimulant, antinflammatory and cytostatic can be used for gene therapy. The polynuclectides of the sells, for diagnosis, therapy, modulation or control of the ises of (auto) immunoly (against microorganisms, vaccines or ransplant rejection; immunologically-related inflammation; sion; immuno system; (ii) for identifying agents, ranaceuticals, that bind to (II) or derived polypeptides to prepare kits for measuring gene expression profiles in the, especially T, cells; (iv) to raise antibodies (Ab) nst (III); and (v) to prepare binding molecules (IV)

(III) Ab and (IV) are also useful for detecting and heart, which activated T-cell derived polynucleotide fragments essent the activated T-cell derived polynucleotide fragments represents a novel messenger RNA, (mRNA), (I), for use as the method of the invention

BP; 43 A; 23 C; 28 G; 59 T; 0 U; 0 Other;

Gaps ; 1.9%; Score 26; DB 6; Length 153; .arity 100.0%; Pred. No. 0.11; .onservative 0; Mismatches 0; Indels

CATTGTTAGACTTTGAAATTTC 26 CATTGTTAGACTTTGAAATTTC 55

ndard; cDNA; 281 BP.

Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; gene therapy; cytostatic; T-cell expansion; nucleic acid hybridis Human ovarian PCR-subtracted cDNA library clone #890. 05-FEB-2001; 2001WO-US003733. 04-FEB-2000; 2000US-0180403P. 28-MAR-2000; 2000US-0192745P. Mannion J; (CORI-) CORIXA CORP WPI; 2001-488879/53. WO200157207-A2. primer; probe. Homo sapiens. 09-AUG-2001 Algate PA, 

New polynucleotides encoding ovarian tumor proteins, useful for ovarian cancer, and as probes, primers, and markers of cancer progression.

Example 1; Page 253; 378pp; English.

proteins, their associated polynucleotides, or immunogenic portic proteins, their associated polynucleotides, or immunogenic portic the proteins. The ovarian tumour polynucleotides and polypeptides useful for stimulating and/or expanding T cells specific for a ty protein. They are also useful for inhibiting the development of a patient with an ovarian tumour DNA or protein by incubating is cells allowing them to proliferate, and administering to the patisequenes can be used as markers for cancer, for example, to monjovarian cancer progression. Probes and primers are useful in nucl hypridistation, in detecting the presence of complementary sequence given sample, for preparing mutant species and for preparing othe genetic constructions. Sequences AAS:3320.AAS:25211 and AAS:53328-1 The invention comprises compositions used for the therapy and dis represent human ovarian tumour protein cDNA clones

Sequence 281 BP; 98 A; 49 C; 59 G; 74 T; 0 U; 1 Other;

. 0 1.9%; Score 26; DB 4; Length 281; .00.0%; Pred. No. 0.11; 0; Indels 100.0%; Prec. ... Query Match Best Local Similarity 100. Matches 26; Conservative

Š q

ABQ60530 standard; cDNA; 386 BP. RESULT 40 ABQ60530

ABQ60530; 

ö

02-AUG-2002 (first entry)

Human colon cancer related nucleotide sequence SEQ ID NO:4225.

Human; colon cancer; cancer; tissue profiling; forensic; mapping genetic analysis; diagnostic; antisense therapy; gene; ss.

Homo sapiens.

WO200229086-A2.

001WO-US030732.

000US-0237271P.

CORP.

Catino TJ, Dwivedi P, Molino GA; Carroll E, Lewis ME; tle JH,

15/45.

uncleic acid that is differentially expressed in cancer. for determining the presence of colon cancer in a cell or and in antisense therapy.

.; 796pp; English.

MOE0787 represent isolated nucleic acids (I) differentially cancer tissues. ABB7893 to ABB79004 represent proteins \*\* ABG60787 nucleic acid sequences. (I) can be made therapy. An antibody immunoreactive with a polypeptide is useful for detecting cancer in a patient sample, and the presence or absence of a polymucleotide encoded by a which hybridises to (I) in a cell. A probe/primer derived be used for determining the presence of a nucleic acid which (I), and for determining the phenotype of cells in a sample a patient. (I) is useful for determining the presence of n a cell or tissue type, for determining the presence or type of cancer, in antisense therapy, to generate it a solid surface, to identify a chromosome on which the gene resides, and in tissue profiling, forensics, genetic ming and diagnostic applications. (I) can be used to raise if to screen for peptide analogues and antagonists

P; 128 A; 72 C; 85 G; 99 T; 0 U; 2 Other;

Gaps . 0 Score 26; DB 6; Length 386; 0; Indels Pred. No. 0.11; 

0;

ATTGTTAGACTTTGAAATTTC 343 ATTGTTAGACTTTGAAATTTC 26

lard; cDNA; 391 BP

(first entry)

tumour associated polynucleotide sequence SEQ ID NO:961.

n tumour; ovarian cancer; diagnosis; gene therapy;

2001WO-US001575.

2000US-0176722P.

vaccine; ss.

A CORP.

WPI; 2001-425866/45. Algate PA;

Novel ovarian tumor proteins, and nucleic acids encoding them, use treat and diagnose cancers, particularly ovarian cancer.

Claim 5; Page 239; 338pp; English.

AAH82377 to AAH83878 represent human ovarian tumour-associated polymucleotide sequences which encode ovarian tumour proteins. The ovarian tumour protein and polymucleotide sequences have cytostat activity, and can be used in gene therapy and vaccine production. ovarian tumour proteins and polymucleotides can be used to inhibit development of cancer, particularly ovarian cancer. They can also to diagnose the onset and progression of cancer

Sequence 391 BP; 118 A; 80 C; 88 G; 97 T; 0 U; 8 Other;

Ű 0 1.9%; Score 26; DB 5; Length 391; 100.0%; Pred. No. 0.11; ive 0; Mismatches 0; Indels Local Similarity 100. nes 26; Conservative Query Match Best Loc Matches

8 d

ABX74646/c RESULT 42

ABX74646 standard; cDNA; 425 BP.

ABX74646;

21-MAR-2003 (first entry)

Human cDNA sequence #113 up-regulated in CC-RCC patients.

differential expression profile; aggressive CC-RCC tumour type; non-aggressive CC-RCC tumour type; clear cell renal carcinoma; gene expression profiling; tumour tissue; gene; ss. microarray; solid surface; immobilised probe; CC-RCC;

Homo sapiens.

WO200279411-A2.

10-OCT-2002.

29-MAR-2002; 2002WO-US009576. 

29-MAR-2001; 2001US-0279411P.

(VAND-) VAN ANDEL INST.

Takashi M; Teh BT, Haab B, Rhodes D,

WPI; 2003-040679/03.

New microarray, comprising a matrix of cDNA probe from a set of p immobilized to a solid surface in predetermined order, useful in prognosis of patients with clear cell renal carcinoma.

Claim 35; SEQ ID NO 223; 179pp; English.

The present invention relates to a microarray comprising a matrix least one cDNA probe from a set of probes immobilised to a solid in a predetermined order, where a row of pixels corresponds to re of one distinct probe from the set. The probes are complementary nucleic acid sequences that are expressed differentially in aggree compared to non-aggressive types of clear cell renal carcinoma (campared to probe under high stringency conditions microarray is useful for the prognosis of patients with CC-RCC, w

Halanda kanada kanada kanada kanada kanada kanada kanada kanada kanada kanada kanada kanada kanada kanada kana ×면목본위본욕확권리감외교육본芹首务旅육법방리점등급급급급급급급급급급급급급급

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id non-aggressive CC-RCC tumour types are characterised by expression profiles of genes that hybridise with one or more. Lised on the microarray. The arrays are useful for gene rofiling of tumour and normal tissues. The present sequence human CDNA sequence up-regulated in CC-RCC patients
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BP; 118 A; 91 C; 78 G; 138 T; 0 U; 0 Other;

Gaps ; 0 DB 7; Length 425; 0.11; 0; Indels 100.0%; Pred. w.. 1.9%; Score 26; 100.0%; Pred. No. Conservative

ö

CATTGTTAGACTTTGAAATTTC 26 CATTGTTAGACTTTGAAATTTC 45

dard; DNA; 439 BP

(first entry)

arcinoma related gene sequence SEQ ID NO:1027.

r; colon; breast; ovary; oesophagus; kidney; thyroid; 3; prostate; pancreas; carcinoma; antitumour; cancerous; gene therapy; antineoplastic; Milm's tumour; adenocarcinoma; colon; breast; ovary; oesophagus; kidney; thyroid;

2000US-0235082P. 2000US-0235134P. 2000US-0235280P. 2000US-0235637P. 2000US-0234923P. 2000US-0234924P. 2000US-0235077P. 0000US-0234567P 2000US-0235711P. 2000US-0235720P 2000US-0235840P 2000US-0235863P 2000US-0234034P 2000US-0235638P 2000US-0234509P

2000US-0236028P

02-0CT-2000; 2000US-0237316P. 03-0CT-2000; 2000US-023759BP. 03-0CT-2000; 2000US-0237504P. 03-0CT-2000; 2000US-0237604P. 03-0CT-2000; 2000US-0237606P. 01-0CT-2000; 2000US-023760BP. 01-NOV-2000; 2000US-0244687P. 02-OCT-2000; 

(AVAL-) AVALON PHARM.

Carter KC, Ebner R, Endress G, Horrig Augustus M, Weaver Z; Young PE, H Soppet DR,

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a agent to be tested for anti-neoplastic activity, and determining in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 1027; 44pp; English

The present invention describes a method (M1) for screening for neoplastic agent. The method involves exposing cells to a chemic to be tested for anti-neoplastic activity, determining a change expression of at least one gene (I) of a signature gene set, whe comprises a sequence (S) selected from 8447 sequences (given in . to ABL70110), or is at least 95% identical to (S), where a change expression is indicative of anti-neoplastic activity. (I) has cyactivity and can be used in gene therapy. MI can be used for scranti-neoplastic agent, and can be used for producing a product with data collected with respect to the anti-neoplastic agent as of MI, and the data is sufficient to convey the chemical structup properties of the agent. MI can be used in the treatment of cancerparts. scolon, breast, stomach, lung, thyroid, oesophageal, ovarian, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cancer, infiltrating ductal cancer, infiltrating lobular cancer, cell carcinoma, neuroendocrine carcinoma, papillary carcinoma an

Sequence 439 BP; 118 A; 101 C; 83 G; 137 T; 0 U; 0 Other;

DB 6; Length 439; 0.11; 0; Indels Query Match 1.9%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.1 Matches 26; Conservative 0; Mismatches

ö

g

ABN96246 standard; DNA; 439 BP. RESULT 44 ABN96246/ ID ABN96

ABN96246;

13-AUG-2002 (first entry)

Gene #2744 used to diagnose liver cancer.

Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease disease progression; drug toxicity; drug efficacy; drug metaboli

Homo sapiens.

WO200229103-A2 

11-APR-2002.

02-OCT-2001; 2001WO-US030589.

8888888

2000US-0237173P. 2000US-0237278P. 2000US-0237294P.

2000US-0236034P. 2000US-0236109P.

2000US-0236111P

2000US-0236033P

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:000US-0237054P.
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OGIC INC.

Vockley JG; Peres-Da-Silva S, ares C,

119/45

d detecting the progression of liver cancer, hepatocellular netastatic liver tumor in a patient, involves detecting the assion of two or more genes in a liver tissue sample.

ID NO 2744; 298pp; English

relates to a novel method for diagnosing and detecting the fliver cancer, hepatocellular carcinoma or metastatic liver atlent, and differentiating metastatic liver cancer from reactinoma in a patient, involving detecting the level of two or more genes represented in ABN93503-ABN97455 in a The method of the invention has hepatotropic, and livity. The method is useful for diagnosing and detecting on of liver cancer, hepatocellular carcinoma and metastatic main a patient. The method is useful for identifying of liver serve as useful diagnostic markers as well as can be used to monitor disease states, disease progression, drug efficacy and drug metabolism. Note: The sequence data at diad not form part of the printed specification, but was sub/published\_pct\_sequences

3P; 118 A; 101 C; 83 G; 137 T; 0 U; 0 Other;

Gaps 0 Score 26; DB 6; Length 439; 0; Indels arity 100.0%; Pred. No. 0.11; onservative 0; Mismatches 1.9%;

CATTGITAGACTTTGAAATTTC 47 CATTGTTAGACTTTGAAATTTC 26

'n

lard; cDNA; 452 BP.

(first entry)

1 protein 5' EST, SEQ ID NO: 10997.

expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.

2000EP-00200610.

99US-0122487P.

Giordano J; Duclert A, dwards J,

381/45

end that is a 5' expressed sequence tag (5' EST) for as and genomic DNAs that correspond to 5'ESTs and for

diagnostic, forensic, gene therapy and chromosome mapping procedu Claim 1; SEQ ID NO 10997; 71pp + Sequence Listing; English. The present sequence is one of a large number of 5' ESTS derived mRNAs encoding secreted proteins. No ORF has yet been conclusivel identified within the present sequence. The 5' ESTS were prepared total human RNAs or polyA+ RNAs derived from 30 different tissues sequences usually correspond mainly to the 3' untranslated region of the mRNA because they are often obtained from oligo-dT primed libraries. Such ESTS are not well suited for isolating cDNA sequences have been obtained, the full 5' UTR is rarely incl C BSTs are derived from mRNAs with intext 5' ends and can therefore to obtain full length cDNAs and genomic DNAs. 5' ESTs are also us diagnostic, forensic, gene therapy and chromosome mapping procedu They are used to obtain upstream regulatory sequences and to desi expression and secretion vectors

Sequence 452 BP; 122 A; 95 C; 112 G; 122 T; 0 U; 1 Other;

Q .. 1.9%; Score 26; DB 3; Length 452; 00.0%; Pred. No. 0.11; 0; Indels 100.0%; Pred No. v.-Query Match Best Local Similarity 100.0 Matches 26; Conservative

g

RESULT 46 ABV86720

ABV86720 standard; cDNA; 469 BP.

ABV86720;

o O

(first entry) 13-DEC-2002 Human colon cancer related cDNA SEQ ID NO 31.

Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine;

Homo sapiens.

WO200258534-A2. 

01-AUG-2002.

16-NOV-2001; 2001WO-US043704.

20-NOV-2000; 2000US-0252222P. 06-FEB-2001; 2001US-026701IP. 28-MAR-2001; 2001US-0379670P. 10-JUL-2001; 2001US-0304037P.

CORI-) CORIXA CORP

GE) Secrist H, Stolk JA, Xu J, Chenault RA, Meagher MJ,

WPI; 2002-608400/65.

New isolated tumor colon polynucleotide and polypeptide, useful diagnosis, prevention and/or treatment of cancer, in particular

Claim 1; SEQ ID NO 31; 266pp + Sequence Listing; English.

The invention relates to a human colon tumour expressed polynucle (I) encoding a polypeptide (II, ABP67991-ABP67996) comprising: (1 2600 fully) defined nucleotide sequences (ABV8669-ABV892899); (ii) complements of (i); (ii) asst 20 contiguous residues of (i); sequences that hybridize to (i), under moderately stringent condi

ariants of (i). The compositions and methods of the present e useful for the diagnosis, prevention and/or treatment of icularly colon cancer. (I) can be used in gene therapy and are useful in pharmaceutical compositions such as vaccines. quence data for this patent did not form part of the printed n, but was obtained in electronic format directly from WIPO s having at least 75% or 90% identity to (i); or (vi) int/pub/published\_pct\_sequences

BP; 142 A; 94 C; 111 G; 122 T; 0 U; 0 Other;

Gaps .; 0 Length 469; 0; Indels DB 6; 0.11; 0; Mismatches Score 26; Pred. No. 100.0%; Conservative larity

0

ICATTGTTAGACTTTGAAATTTC 425 TCATTGTTAGACTTTGAAATTTC 26

ndard; cDNA; 483

(first entry)

cancer-associated cDNA, SEQ ID No 558.

88. cancer; immunogenic; vaccine; tumour; gene;

42

2001WO-US023826

2000US-0237406P. 2001US-0277495P. 2000US-0223265P

2001US-0302702P

KA CORP.

J, Secrist H;

7462/30.

leotide encoding colon tumor polypeptides, useful as treating colon cancers.

e 309; 425pp; English

a relates to isolated polynucleotides (I) encoding colon spitdes (II) (I) is useful for stimulating an immune a patient and treating colon cancer in a patient and treating colon cancer in a patient. a patient. (I) and (II) are useful in pharmaceutical e.g. vaccines, and other compositions for the diagnosis and colon cancer. A composition comprising a first component m physiologically acceptable carriers and immunostimulanes, en.presenting cell expressing (II) is useful for inhibiting of cancer in a patient. (I) is useful in the design and of ribozyme molecules for inhibiting expression of tumour and (I). ABK54531-ABK55464 represent human colon cancer cDNA the invention

BP; 155 A; 97 C; 112 G; 119 T; 0 U; 0 Other;

0

0; Indels

DB 3; Length 486;

Score 26;

1.98:

0.11;

100.0%; Preu. ...

Local Similarity 100. tes 26; Conservative

Matches

ð g

Query Match

400 AIGICALIGITAGACITIGAAAITIC 425

1 AIGICATIGITAGACTITGAAATITC 26

DB 6; Length 483; 1.9%; Score 26;

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The present sequence is the human hypoxia response regulating ge tralated CDMA clone 3D. The gene 7744 has similarity to steroid r transcriptional co-activator, SRA function and can serve as a co in some transcriptional complexes. It has vasotropic, cardiant, ophthalmological, cytostatic and cerebroprotective activity. Ant of the encoded protein, functions as a regulator of apoptosis or angiogenesis. The protein encoded by this polynucleotide, the biologically active product from enzymatic activity of the protein inhibitor of the enzymatic activity is useful for regulating hyp and treatment of tumour growth and ischaemia, e.g., retinopathy, myocardial infarction and stroke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiant; apoptosis; vasotropic; cytostatic; ophthalmological; scenebroprotective; antagonist; regulator; inhibitor; treatment; hypoxia associated pathology; HAPP; gene therapy; diagnosis, retisteroid receptor coactivator; SRA; ischaemia; myocardial infarct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypoxia response regulating gene; gene 77H4; human; EST 3D; angi
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                        Pred. No. 0.11;
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100.0%; Pr
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99US-0132684P.
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                                                           26; Conservative
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dard; DNA; 487 BP.

(first entry)

1 to diagnose liver cancer.

ancer; ds; hepatocellular carcinoma; hepatotropic; ex tumour; cytostatic; expression profile; disease stassion; drug toxicity; drug efficacy; drug metabolism.

2001WO-US030589.

2000US-0237054P.

OGIC INC

Vockley JG; Peres-Da-Silva S, tres C,

119/45.

i detecting the progression of liver cancer, hepatocellular metastatic liver tumor in a patient, involves detecting the ission of two or more genes in a liver tissue sample.

NO 729; 298pp; English.

relates to a novel method for diagnosing and detecting the liver cancer, hepatocellular carcinoma or metastatic liver itient, and differentiating metastatic liver cancer from carcinoma in a patient, involving detecting the level of two or more genes represented in ABN93503-ABN97455 in a The method of the invention has hepatocropic, and invity. The method is useful for diagnosing and detecting n of liver cancer, hepatocellular carcinoma and metastatic a in a patient. The method is useful for identifying files which serve as useful diagnostic markers as well as an be used to monitor disease states, disease progression, drug efficacy and drug metabolism. Note: The sequence data it did not form part of the printed specification, but was ectionic format directly from WIPO at ub/published\_pct\_sequences

P; 141 A; 97 C; 118 G; 131 T; 0 U; 0 Other;

.; 0 Score 26; DB 6; Length 487; Pred. No. 0.11; Indels . 0 1.9%; scc. 100.0%; Pred. No. v. 0; Mismatches nservative

Arrgiragacrirgaaarirc 452 ATTGTTAGACTTTGAAATTTC 26

ard; cDNA; 498

ន្លឺដូលស្នកម

first entry)

Human; ss; sequencing by hybridisation; SBH; expressed sequence t genome mapping; biodiversity; genetic disorder. Jones LW; Dickson MC, Stache-Crain B, Human endothelial cell cDNA #4820 30-JUL-2001; 2001US-00918995. 30-JUL-2001; 2001US-00918995. Drmanac RT, Labat I, (LABA/) LABAT I. (STAC/) STACHE-CRAIN ) (DICK/) DICKSON M C. (JONE/) JONES L W. DRMA/) DRMANAC R T. US2003073623-A1 Homo sapiens. 17-APR-2003. 

New polynucleotide sequences obtained from various cDNA libraries as hybridization probes, as oligomers for PCR, for chromosome and mapping, in the recombinant production of protein, or in generatiantsense DNA or RNA.

WPI; 2003-615964/58.

Claim 1; SEQ ID NO 23899; 44pp; English.

The invention relates to an isolated polynuclectide comprising an 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose seque determined by the technique of SBH (sequencing by hybridisation). Included is a purified polypeptide comprising a sequence correspons reading frame of the novel polynuclectide. The nucleic acid sequence tust useful in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human in forensics, in assessing biodiversities, or in identifying muta responsible for genetic disorders and other traits. The nuclectid sequences are also useful as hybridisation probes, as oligomers for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or NNA. The purified poly is useful for generating antibodies specific for it. The present is one of the 38043 isolated cDNA.FST sequences. Note: The sequence for this patent did not form part of the printed specification, by obtained in electronic format directly from USPTO at segdata.uspto.gov/seguence.html?DocID=20030073623

Sequence 498 BP; 152 A; 119 C; 117 G; 107 T; 0 U; 3 Other;

. 0 1.9%; Score 26; DB 8; Length 498; 100.0%; Pred. No. 0.11; tive 0; Mismatches 0; Indels 0; Indels 26; Conservative Query Match Best Local Similarity Matches

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ð d

0;

Gaps

AAC01272 standard; cDNA; 516 BP AAC01272; (first entry) 06-OCT-2000

Human secreted protein 5' EST, SEQ ID NO: 1270.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA isol gene therapy; chromosome mapping; ss. **\$\$\$\$\$\$\$\$\$\$**\$\$\$\$\$

dwards J, 381/45

Secrist H;

Xu J,

Novel polynucleotide encoding colon tumor polypeptides, useful as vaccines for treating colon cancers. Claim 1; Page 403; 425pp; English. 03-JUL-2001; 2001US-0302702P. (CORI-) CORIXA CORP. WPI; 2002-257462/30. Pyle RA, Matches RESULT 53 셤 Š equence is one of a large number of 5' ESTs derived from g secreted proteins. An ORF has been identified within the 5' ESTs were prepared from total human RNAs or polyAt RNAs 3' different tissues. EST sequences usually correspond 3' untranslated region (UTR) of the mRNA because they are d from oligo-dT primed cDNA libraries. Such ESTs are not or isolating cDNA sequences derived from the 5' ends of nin those cases where longer cDNA sequences have been full 5' UTR is rarely included. 5' ESTs are derived from tact 5' ends and can therefore be used to obtain full length . 0 omic DNAS. 5' ESTS are also used in diagnostic, forensic, and chromosome mapping procedures. They are used to obtain latory sequences and to design expression and secretion cid that is a 5' expressed sequence tag (5' EST) for the and genomic DNAs that correspond to 5'ESTs and for orensic, gene therapy and chromosome mapping procedures. Gaps . 0 cancer; immunogenic; vaccine; tumour; gene; ss. ID NO 1270; 71pp + Sequence Listing; English. BP; 134 A; 106 C; 131 G; 145 T; 0 U; 0 Other; Score 26; DB 3; Length 516; Pred. No. 0.11; 0; Indels ancer-associated cDNA, SEQ ID No 877. Duclert A, Giordano J; 1.9%; Scc. 100.0%; Pred. No. c 0; Mismatches CATTGTTAGACTTTGAAATTTC 503 CATTGTTAGACTTTGAAATTTC 26 2000EP-00200610. 99US-0122487P. dard; cDNA; 531

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The invention relates to isolated polynucleotides (I) encoding oc tumour polypeptides (II). (I) is useful for stimulating an immune response in a patient, and treating colon cancer in a patient.

Oligonucleotides derived from (I) are useful for determining the of cancer in a patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines, and other compositions for the diagratement of colon cancer. A composition comprising a first composition cancer in a patient. (I) is useful for inhical and antigen-presenting cell expressing (II) is useful for inhical and the conformation of cancer in a patient. (I) is useful in the design of preparation of ribozyme molecules for inhibiting expression of tupolypeptides and (I). ABK5531-ABK55464 represent human colon cares sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                        ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; 5' EST; expressed sequence tag; secreted protein; cDNA isc gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo diagnostic, forensic, gene therapy and chromosome mapping procedu
                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                      1.9%; Score 26; DB 6; Length 531;
100.0%; Pred. No. 0.11;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                             Sequence 531 BP; 153 A; 105 C; 128 G; 143 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SBQ ID NO 1269; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein 5' EST, SEQ ID NO: 1269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        459 ATGTCATTGTTAGACTTTGAAATTTC 484
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGTCATTGTTAGACTTTGAAATTTC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC01271 standard; cDNA; 540 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2000; 2000EP-00200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0122487P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAG01265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC01271;
                                                                                                                                                                                                                                                                                                                                                        Query Match
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2000US-0223265P. 2000US-0237406P. 2001US-0277495P.

2001WO-US023826.

(first entry)

onservative

arity

equence is one of a large number of 5' ESTS derived from 9 secreted proteins. An ORF has been identified within the 5' ESTS were prepared from total human RNAs or polyA+ RNAS 30 different tissues. EST sequences usually correspond from oligo-dT primed cDNA libraries. Such ESTs are not or isolating cDNA sequences derived from the 5' ends of n in those cases where longer cDNA sequences have been full 5' UTR is rarely included. 5' ESTs are derived from tact 5' ends and can therefore be used to obtain full length omic DNAs. 5' ESTs are also used in diagnostic, forensic, and chromosome mapping procedures. They are used to obtain latory sequences and to design expression and secretion g secreted pr 5' ESTS

3P; 135 A; 110 C; 137 G; 152 T; 0 U; 6 Other;

·, Score 26; DB 3; Length 540; Pred. No. 0.11; 0; Indels 100.0%; Prec. ... onservative

Gaps

PATTGATAGACTTTGAAATTTC 527 56 CATTGTTAGACTTTGAAATTTC

lard; cDNA; 570 BP.

first entry)

ssociated gene sequence SEQ ID NO:292.

associated gene; cancer antigen; detection; cancer; ostatic; proliferative; vulnerary; immunomodulator; antiatehmatic; antirheumatic; antiarthritic; antiviral; ry; antithyroid; antialergic; antibacterial; cardiant; neuroprotective; thrombolytic; coagulant; noctropic; tipporiatic; antiangiogenic; gene therapy; inflammation; r; haematopoietic cell disorder; autoimmune disorder; ion; graft versus host disease; organ rejection; hrombolytic; cardiovascular disorder; infection; isease; drug screening; ss.

000WO-US005882.

99US-0124270P.

GENOME SCI INC.

en SM;

33/55.

nucleic acids comprising sequences encoding peptides ating or diagnosing e.g. cancer.

853; 2352pp; English.

C78448 encode the human cancer associated proteins given in B44239. The proteins can have activities based on the lls the genes are expressed in. Example of activities

antidiabetic; antiathments, variety, tamestry, tamestry, antidiabetic; antiathments; antidiabetic; antiathments; antidiabetic; antiathments; antidiabetic; antiathments; antihytoid; antiallergic; antibacterial; antiversatiological; neuroprotective; cardiant; thrombolytic; coagular nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, trea amedical conditions and diagnosing pathological conditions and diagnosing pathological conditions and present invention may be used to treat immune disorders by actinibiting the proliferation, differentiation or mobilisation immune cells, antibodietic cells, autoimmed isorders, allergic reactions, graft versus host disease and organismation, cancers, candioversor by the present invention and organism disorders, allergic reactions, graft versus host disease and organismation, cancers, cardiovascular disorders, meurological disorders and antagonists may be also be used in drug screens. And ARA4420 represent sequences used in the exemplifica cytostatic; proliferative; vulnerary; immunomodulator; the present invention 8555555555555555555555

Sequence 570 BP; 171 A; 112 C; 139 G; 145 T; 0 U; 3 Other;

1.9%; Score 26; DB 3; Length 570; 0; Indels 100.0%; Pred. No. 0.1 tive 0; Mismatches 26; Conservative Query Match Best Local Similarity Matches

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AAZ51562 RESULT

AAZ51562 standard; cDNA; 580

21-JUN-2000 (first entry)

Hypoxia response regulating gene; gene 77H4; human; EST 18E; card: apoptosis; angiogenesis; vasotropic; cytostatic; ophthalmological cerebroprotective; antagonist; regulator; inhibitor; treatment; ti hypoxia associated pathology; HAP; gene therapy; diagnosis; ischaisteroid receptor coactivator; SRA; retinopathy; myocardial infarci

Homo sapiens.

polyA\_signal

WO200012525-A1.

09-MAR-2000.

Einat P, Skaliter R,

WPI; 2000-256577/22.

Novel polynuclectides capable of regulating angiogenesis or apoptouseful for diagnosis and treatment of hypoxia, ischemia and tumor

Claim 1; Fig 7a; 78pp; English.

Ü

AAZ51562;

Human hypoxia response regulating gene, 77H4 related cDNA clone  $1^{1}$ 

stroke; ss.

Location/Qualifiers 536. .541 /\*tag= a

99WO-US020394. 27-AUG-1999;

98US-0098158P. 99US-0132684P. (QUAR-) QUARK BIOTECH INC. (KOHN/) KOHN K. 27-AUG-1998; 05-MAY-1999;

Feinstein E;

ã

Sequence is the human hypoxia response regulating gene, 77H4, clone 18E. The gene 77H4 has similarity to steroid receptor hal co-activator. SRA function and can serve as a coactivator scriptional complexes. It has vasorropic, cardiant, cloal, cytostatic and cerebroprotective activity. Antagonist of protein, functions as a regulator of apoptosis or The protein encoded by this polynucleotide, the active product from enzymatic activity of the protein or the enzymatic activity is useful for regulating hypoxia athologies (HAP). It is useful for gene therapy, diagnosis of tumour growth and ischaemia, e.g., retinopathy, farction and stroke

BP; 177 A; 111 C; 134 G; 158 T; 0 U; 0 Other;

Gaps ., DB 3; Length 580; 0.11; 0; Indels 100.0%; Pred. ... Score 26; Pred. No. conservative

CATTGITAGACTITGAAATITC 512 CATTGTTAGACTTTGAAATTTC 26

ndard; cDNA; 580 BP

744 gene sequence.

ia-regulated activity, neurotoxic stress; hypoxia; ischaemia; osis; angiogenesis; cerebroprotective; gene therapy; inhibitor of oxidative stress-mediated apoptosis; ingiogenesis; gene 7744; gene; ss.

2001US-00802472

97US-0056453P 98US-00138109, 98US-0098158P, 99US-0132684P 99US-00384096

æ

TEIN E

Feinstein E; iliter R,

ed polypeptides and genes associated with hypoxia-regulated for treating stroke, hypoxia and ischemia. : 61; 72pp; English. nvention relates to a new polypeptide associated with ated activity. The invention is useful in diagnostic assays. Its further useful as a diagnostic tool which can be used to ix presence in a cell. The invention is also useful for sodies that could be used in diagnostic assays for the the protein and for determining if any given cell had been

subjected to neurotoxic stress. The invention can be used to proneural cells from, and ameliorate the effects of, hypoxia and is and thus in the treatment of stroke, hypoxia and ischaemia. The is also useful to prevent apoptosis and promote angiogenesis. The invention can be used in diagnostic assays for cells that have b subjected to hypoxia or ischaemia, and in screening assays to id agents capable of enhancing gene expression. The present nucleic sequence represents the human gene 7744 gene of the invention. N specification states that this sequence encodes the human gene 7 protein (ABG71808) but this does not appear to be the case 8888888888888

Sequence 580 BP; 177 A; 111 C; 134 G; 158 T; 0 U; 0 Other;

. 0 Length 580; 0; Indels DB 7; 0.11; 1.9%; Scc. 100.0%; Pred. No. v.. '~ 0; Mismatches 26; Conservative Query Match Best Local Similarity Matches

ð g

.; 0

ABQ58318/

ABQ58318 standard; cDNA; 400 BP

ABQ58318;

02-AUG-2002 (first entry)

Human colon cancer related nucleotide sequence SEQ ID NO:2013.

Human; colon cancer; cancer; tissue profiling; forensic; mapping genetic analysis; diagnostic; antisense therapy; gene; ss.

Homo sapiens.

WO200229086-A2.

11-APR-2002.

02-OCT-2001; 2001WO-US030732. 02-OCT-2000; 2000US-0237271P

(FARB ) BAYER CORP.

Burgess C, Astle JH, Ca Thiaglingam A, Lewis ME;

Dwivedi P, Molina

Catino TJ,

Carroll E,

WPI; 2002-426115/45. 

New isolated nucleic acid that is differentially expressed in car tissues useful for determining the presence of colon cancer in a tissue type, and in antisense therapy.

Claim 1; Fig 1; 796pp; English

ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differe expressed in cancer tissues. ABB7893 to ABB79004 represent prote expressed in cancer tissues. ABB78993 to ABB79004 represent prote encoded by the ABG60776 to ABG60787 unaleic acid sequences. (I) oused in antisense therapy. An antibody immunoreactive with a polyneled by (I) is useful for detecting cancer in a patient sample for detecting the presence or absence of a polynucleotide encoded mucleic acid which hybridises to (I) in a cell. A probe/primer defrom (I) can be used for determining the presence of a nucleic acid which hybridises to (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence of on cancer in a cell or tissue type, for determining the presence of an acid surface, to identify a chromosome on which corresponding gene resides, and in tissue profilling, forensics, canalysis, mapping and diagnostic applications. (I) can be used to

06:25:14 2004

nd to screen for peptide analogues and antagonists

BP; 100 A; 80 C; 61 G; 138 T; 0 U; 21 Other;

Gaps ; DB 6; Length 400; 0.32; 0; Indels 1.8%; Score 25; DB 100.0%; Pred. No. 0.3 cive 0; Mismatches onservative

°;

25 69 CATTGTTAGACTTTGAAATTT CATTGTTAGACTTTGAAATTT

93

dard; cDNA; 626 BP.

(first entry)

novel human diagnostic protein #230.

some mapping; gene mapping; gene therapy; forensic; nt; medical imaging; diagnostic; genetic disorder; ss.

2001WO-US008631.

2000US-00540217 2000US-00649167

XI; Tang Liu C,

362/73.

polymucleotide and encoded polypeptides, useful in forensics, gene mapping, identification of mutations or genetic disorders or other traits and to assess

NO 230; 103pp; English.

primers, oligomers, and for chromosome and gene mapping, nant production of (II). The polymucleotides are also used useful in gene therapy techniques to restore normal or to treat diseases states involving (II). (II) is brating antibodies against it, detecting or quantitating a tissue, as molecular weight markers and as a food of tissue, as molecular weight markers and as a food of the binding partners are useful in medical imaging sising (II). (I) are useful in medical imaging rant, protein expression or biological activity. The relates to isolated polynucleotide (I) and polypeptide (II) nences. AAS64197-AAS94564 represent nevel human diagnostic ses of the invention. Note: The sequence data for this appear in the printed specification, but was obtained in until directly from WIPO at hub/published\_pct\_sequences orensics, gene mapping, identification of mutations or genetic disorders or other traits to assess biodiversity other types of data and products dependent on DNA and polynucleotide sequences have applications in rant id pol

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.,
Sequence 626 BP; 173 A; 126 C; 157 G; 170 T; 0 U; 0 Other;
                         Length 626;
                                              0; Indels
                       DB 5;
                                              Mismatches
                       Score 25;
Pred. No.
                                                                                    542 ATGTCATTGTTAGACTTTGAAATTT 566
                                                                      25
                                                                     1 ATGTCATTGTTAGACTTTGAAATTT
            1.8%; Scor.
100.0%; Pred
0; N
                                              Conservative
                  Query Match
Best Local Similarity
Matches 25; Conserv
g
                                                                     δ
                                                                                          d
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RESULT 59 AAX23451/

AAX23451 standard; DNA; 24

AAX23451;

18-JUN-1999

Human TNRL3 RACE primer 2.

Tumour necrosis factor receptor; signal transducer molecule, TNF; developmental abnormality; gestational abnormalitity; prostate ca APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; cytoplasmic domain; immunogen; antibody preparation; breast carci apoptosis; human; primer; ss.

Homo sapiens. Synthetic.

11-MAR-1999.

98WO-US018393, 04-SEP-1998;

97US-00924634. 05-SEP-1997;

UNIW ) UNIV WASHINGTON.

Chaudhary PM;

WPI; 1999-205191/17.

New Tumor Necrosis Factor family receptor polypeptides and ligand useful for diagnosis and treatment of prostate cancer and develop gestational abnormalities. 

Example VII; Page 121; 156pp; English.

This invention describes isolated Tumor Necrosis Factor (TNF) fam receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands I and 3 (TNRL1 and TN their active fragments. APO4 is useful for diagnosing prostate ca determining levels of APO4 is useful for diagnosing prostate cancer can created using APO4 selective binding agents linked to a therapeut moiety. APO4 polypeptides are also useful for identifying selectivity agents, useful in diagnosis/treatment of disease by binding agents to the polypeptide/active fragment which is extracellular. Expressed on the cell surface. The binding are preferably performently on the cell surface. The binding are also useful for scripty expressed on the cell surface. The binding and observing the changer for agonists and antagonists by binding and observing the changer cartivity. Effective pharmacological agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/ifragments and APO4 signal transducer molecules that specifically with a cytoplasmic domain of APO4 and detecting a change in level are all useful as immunogens for preparing antibodies. APO8 was transfected to human breast carcinoma cell and indicational MCF-7, and induced apoptosis

Sequence 24 BP; 7 A; 9 C; 3 G; 5 T; 0 U; 0 Other;

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ö
               Gaps
              0;
 Length 24;
              0; Indels
DB 2;
1.1;
   100.0%; Pred. no.
Score 24;
Pred. No.
1.78;
              Conservative
       larity
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GATGAGGGAAGGCTGTCTAC 633 GATGAGGGAAGGCTGTCTAC 1

ndard; DNA; 24 BP

(first entry)

RACE primer 1.

sis factor receptor; signal transducer molecule; TNF; APO4; l abnormality; gestational abnormalitity; prostate cancer; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease; domain; immunogen; antibody preparation; breast carcinoma; uman; primer; ss.

98WO-US018393.

97US-00924634.

WASHINGTON

crosis Factor family receptor polypeptides and ligands - aganosis and treatment of prostate cancer and developmental al abnormalities.

Page 121; 156pp; English.

on describes isolated Tumor Necrosis Factor (TNF) family peptides: APO4, APO6, aPO8 and APO9 or their active of isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or fragments. APO4 is useful for diagnosing prostate cancer by levels of APO4 in an individual. Prostate cancer can also be 3 APO4 selective binding agents linked to a therapeutic polypeptides are also useful for identifying selective is, useful in diagnosis/treatment of disease by binding of polypeptide/active fragment which is extracellular, or the call surface. The binding is preferably performed in olypeptides/ active fragments are also useful for screening and antagonists by binding and observing the changer in APO4 effective pharmacological agents useful in diagnosis or disease are also iseful in diagnosis or disease are also useful in diagnosis or disease are also useful in diagnosis or disease are also iseful in diagnosis or disease are also useful in diagnosis or disease are also disease lasmic domain of APO4 and detecting a change in level of APO4 method is performed in vivo or in vitro. APO polypeptides als as immunogens for preparing antibodies. APO4 is also agnosis/treatment of developmental or gestational and APO8 was transfected to human breast carcinoma cell line fective pharmacological agents useful in diagnosis or disease are also identified using APO4 polypeptides/active APO4 signal transducer molecules that specifically interact

3P; 7 A; 2 C; 13 G; 2 T; 0 U; 0 Other;

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Human; tumour necrosis factor; Apo-3 ligand; lymphotoxin; apopto NF-kappaB-dependent transcription; JNK/SAPK-dependent response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has cytostatic activity. Apo-3 ligand can be used to induce apoptosi mammalian cancer cells, to induce NF-kappaB-dependent transcript to induce JNK/SAFK-dependent responses in mammalian cells. The p sequence represents an Apo-3 ligand PCR primer, which is used in example from the present invention
                                                                                                                                                                                                                          Human tumour necrosis factor Apo-3 ligand PCR primer SEQ ID NO:5
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a human tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human Apo3- ligand (a tumor necrosis factor) homologue.
  Length 24;
                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe for gene amplification analysis of human PRO207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 40 BP; 9 A; 13 C; 13 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
 1.7%; Score 24; DB
100.0%; Pred. No. 1.1
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%, Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.7%; Score 24;
                                                   812 CTGCCCCTTCCTCACCTTCG 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pitti R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 CGGGCATCGCTGTCCGCCCAGGAG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 CGGGCATCGCTGTCCGCCCAGGAG 40
                                                                  24 CTGCCCCTTCCTCACCTACTTCG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 37; 74pp; English.
                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK40355 standard; DNA; 23 BP.
                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US021407.
                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0062037P.
97US-0069862P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marsters SA,
                                                                                                                                              AAX56003 standard; DNA; 40
                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                          24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-287982/24.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                               PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                              WO9919490-A1
                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                        22-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                      AAX56003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK40355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 62
                                                                                                                               AAX56003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABK40355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                       à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXXXXXX
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enign tumour; malignant tumour; lymphoid malignancy; uronal disorder; stromal disorder; blastocoelic disorder; disorder; lmmune disorder; angiogenic disorder; cytostatic; ve; probe; ss.

2000WO-US003565

99WO-US005028

99US-0123972P 99US-0133459P 99US-0140650P 99US-0140653P 99US-0144758P

99US-0146222P. 99US-0149395P. 99US-0151689P. 99WO-US028313. 99WO-US020111 99WO-US021090

ECH INC.

99WO-US028634

Hillan KJ; Stone DM; Gurney AL, Smith V, d A, Godowski PJ, Pitti RM, Roy MA, Goddard A, Pan J, P Wood WI;

567/26.

soleic acids encoding PRO polypeptides, useful for treating ignant tumors, leukemias and lymphoid malignancies, angiogenic and immunologic disorders.

ige 140; 302pp; English.

Ü

0;

0; Indels

1.6%; Score 22; DB 2; Length 38; 00.0%; Pred. No. 8.9;

Query Match Best Local Similarity

Sequence 38 BP; 9 A; 11 C; 12 G; 6 T; 0 U; 0 Other;

Wention relates to the isolation of novel human PRO (AAU86128-AAU86162) and the polynucleotide sequences. The PRO POLYpeptides, agonists, antagonists or anti-PRO bladder, breast, etc), leukaemias and lymphoid other disorders such as neuronal, glial, astrocytal, glandular, macrophagal, stromal and blastocoelic disorders, immune and angiogenic disorders. The polynucleotide also useful in gene therapy. The present sequence brobe used in the methods of the present invention

'; 1 A; 7 C; 7 G; 8 T; 0 U; 0 Other;

ò Score 23; DB 6; Length 23; Pred. No. 3.1; 0; Indels 100.0%; Pred. No. 3.1 ive 0; Mismatches 1.78; nservative

·;

Gaps

TGGGCCTGTTCACGTGTT 1003 TGGGCCTGTTCACGTGTT 23

lard; DNA; 38

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The present invention describes a human tumour necrosis factor (T lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has eytostatic activity. Apo-3 ligand can be used to induce apoptosis mammalian cancer cells, to induce NF-kappaB-dependent transcripti to induce JNK/SAFK-dependent responses in mammalian cells. The pr sequence represents an Apo-3 ligand PCR primer, which is used in example from the present invention
                                                                Human; tumour necrosis factor; Apo-3 ligand; lymphotoxin; apoptos NF-kappaB-dependent transcription; JNK/SAPK-dependent response; c
                                         Human tumour necrosis factor Apo-3 ligand PCR primer SEQ ID NO:6
                                                                                                                                                                                                                                                                                                                                                                    New human Apo3- ligand (a tumor necrosis factor) homologue.
                                                                                                                                                                                                                                                                                                                  Marsters SA, Pitti R;
                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 37; 74pp; English.
                                                                                                                                                                                                                       98WO-US021407.
                                                                                                                                                                                                                                               97US-0062037P
            15-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                            WPI; 1999-287982/24.
                                                                                            PCR primer; ss.
                                                                                                                                                                                                                                                                                                               Ashkenazi AJ,
                                                                                                                                                               WO9919490-A1.
                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                    09-OCT-1998;
                                                                                                                                                                                                                                               10-OCT-1997;
                                                                                                                                                                                                                                                            17-DEC-1997;
                                                                                                                                                                                         22-APR-1999
                                                                                                                       Synthetic
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Human breast cancer expressed polynucleotide 10722. Human; breast cancer; cell marker; cytostatic; ss. 100.0%; Pred. ... 0; Mismatches 834 CGGACTCTTCCAGGTTCACTGA 855 38 ccarcircacacricación 17 AAL18265 standard; cDNA; 223 BP 14-JAN-2000; 2000US-0176077P. 14-MAR-2000; 2000US-0189167P. 24-MAR-2000; 2000US-0192099P. 10-JAN-2001; 2001WO-US000798 22; Conservative 07-DEC-2001 (first entry) WO200151628-A2 Homo sapiens. 19-JUL-2001 AAL18265; Matches RESULT 64 **AA**L18265 à 셤

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The invention relates to recombinant carcinoma associated (CA) n acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. invention also encompasses expression vectors and host cells com CA nucleic acid, a polypeptide (sepecially an antibody) that specialise to the protein, and a biochip comprising CA nucleic acid of fragments thereof. The sequences of the invention were identified oncogenic retrovituses, which insert into the genome of the host at random. Many of these do not carry transduced host oncogenes can parting viral genes, meaning that cancer inciden direct consequence of the effects of proviral integration into he protonocogenes. The CA nucleic acid sequences can be used to dia carcinoma despecially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the cof a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also usefi
                       The invention relates to human breast cancer expressed polynucle (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation betwee expression of certain markers and the cancerous state of breast. The polynucleotides and encoded polypeptides are potential mark detecting, diagnosing, monitoring, characterising treating and polypeptides are also useful for isolating compounds with cytost activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant nucleic acid encoding carcinoma associated prote useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Sept9 carcinoma associated coding sequence, SEQ ID NO:1513
                                                                                                                                                                                                                                                                           Score 22; DB 4; Length 263; Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                  Sequence 263 BP; 52 A; 63 C; 63 G; 85 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                      100.0%; Pred. w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1513; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                         1330 AGATATTTTTTATTATT 1351
                                                                                                                                                                                                                                                                                                                                                                                   137 AGATATTATTTTTATTATT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA02995 standard; cDNA; 1005 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2002; 2002WO-US041414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2001; 2001US-00035832.
                                                                                                                                                                                                                                                                           1.68:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-587068/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003057146-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morris DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA02995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene; ss.
                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp.
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA02995
      X888888888888X8
                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               o;
                                                                                                                                                                                                                                                                                                       on relates to human breast cancer expressed polynucleotides L26789) and methods of assessing whether a patient is the breast cancer by examining the correlation between the fertain markers and the cancerous state of breast cells.
                                                                                                                                                                                                                                                                                                                                                                                          eotides and encoded polypeptides are potential markers for liagnosing, monitoring, characterising treating and preventing breast cancer. The polymucleotides and encoded are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                          useful as a marker for the diagnosis of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iseful as a marker for the diagnosis of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 46 A; 51 C; 48 G; 78 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer expressed polynucleotide 1278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; cell marker; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.6%; Score 22; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.1;
                                                                                                 ENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                 e 1912-1913; 3695pp; English.
                                                                                                                                            Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JY, Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTATTATTATTA 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rarrarrirarrarrarr 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278; 3695pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ndard; cDNA; 263 BP
                   2000US-0205230P.
2000US-0211315P.
2000US-0193480P.
                                                          2000US-0220534P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0192099P.
2000US-0193480P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0176077P
2000US-0189167P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0205230P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-US000798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0211315P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0220534P
                                                                                                                                          u Y, Wang Y,
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42.

(first entry)

Conservative

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06:25:14 2004
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ogents and in screening and evaluating drug candidates. The moc represents a specifically claimed murine CA nucleic acid the invention. Note: The complete sequence data for this soft form part of the printed specification, but was obtained tobb/published_pct_sequences.
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RESULT 68

BP; 285 A; 268 C; 273 G; 179 T; 0 U; 0 Other;

Gaps ·; 1.6%; Score 22; DB 8; Length 1005; 100.0%; Pred. No. 7.6; 0; Indels 100.0%; Pred. arity 100. onservative

. 0

CCCATTATGAAGTTCATC 448 CCCATTATGAAGTTCATC 396

BP dard; cDNA; 1005

(first entry)

tostatic; gene therapy; vaccine; carcinoma; lymphomas; asm; adenocarcinoma; sarcoma; gene.

A2.

2001WO-US051291. 2001US-00798586

2001US-00004113. 2001US-00052482. 2001US-00997722

2001US-00034650

3 DISCOVERY

gelhard EK;

337/23

nucleic acid, useful for treating carcinomas, lymphomas, Lasm, adenocarcinoma, or sarcomas. Ħ,

(D NO 561; 2304pp; English.

relates to a novel recombinant nucleic acid comprising a quence selected from any of the 660 sequences fully defined location. A polymucleotide of the invention has cytostatic may have a use in gene therapy, or in a vaccine. The scheic acids and polypeptides are useful for treating 9. lymphomas, cancers, neoplasm, adenocarcinoma, and present sequence represents a mouse cDNA of the invention.

BP; 285 A; 268 C; 273 G; 179 T; 0 U; 0 Other;

Gaps . 0 1.6%; Score 22; DB 9; Length 1005; 100.0%; Pred. No. 7.6; ive 0; Mismatches 0; Indels nservative arity

CCATTATGAAGTICATC 448 ccarrargagricare 396

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New recombinant nucleic acid comprising a nucleotide sequence of the carcinoma-associated (CA) genes, useful for screening for dru candidates for diagnosing or treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide sequence selected from any of the fully defined carcing associated (CA) genes from the 50 tables given in the specification of proteins are secreted, transmembrane or intracellular proteins recombinant nucleic acids are useful for screening for drug candifor diagnosing or treating carcinomas. Sequences given in ADC85514 represent CA genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to a recombinant nucleic acid comprising a
                                                                                                                                Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated secreted; transmembrane; intracellular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1005 BP; 285 A; 268 C; 273 G; 179 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 261; 983pp; English.
             ADC85475 standard; DNA; 1005 BP.
                                                                                                   Mouse Sept19 coding sequence.
                                                                                                                                                                                                                                                                  02-DEC-2002; 2002WO-US038582.
                                                                                                                                                                                                                                                                                              30-NOV-2001; 2001US-00997722
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                         Engelhard EK;
                                                                                                                                                                                                                                                                                                                           (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-513603/48.
                                                                                                                                                                                                       WO2003045230-A2.
                                                                       01-JAN-2004
                                                                                                                                                                                                                                      05-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                       Morris DW,
                                         ADC85475;
                                                                                                                                                                             Mus sp.
ADC85475
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375 GCAGCCCATTATGAAGTTCATC 396 AAS84907 standard; cDNA; 1778 BP RESULT 69 AAS84907 셤

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Indels

; 0

100.0%; Pred. ...

1.68;

Query Match Best Local Similarity 100.0 Matches 22, Conservative

427 GCAGCCCATTATGAAGTTCATC 448

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Score 22; DB 9; Length 1005; Pred. No. 7.6;

(first entry) 13-FEB-2002 AAS84907; 

DNA encoding novel human diagnostic protein #20711.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; s;

Homo sapiens.

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WO200175067-A2

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n relates to isolated polynucleotide (I) and polypeptide (II) is useful as hybridisation probes, polymerase chain R) primers, oligomeras, and for chromosome and gene mapping, binant production of (II). The polynucleotides are also used as as expressed sequence tags for identifying expressed used to the production of (II) and disease states involving (II). (II) is enerating antibodies against it, detecting or quantitating a in tissue, as molecular weight markers and as a food (II) and its binding partners are useful in medical imaging ressing (II). (II) and (II) are useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             errant protein expression or biological activity. The and polynucleotide sequences have applications in forensics, gene mapping, identification of mutations for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e other types of data and products dependent on DNA and equences. AAS64197-AAS94564 represent novel human diagnostic noes of the invention. Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ot appear in the printed specification, but was obtained in prmat directly from WIPO at 'pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide and encoded polypeptides, useful in forensics, gene mapping, identification of mutations for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO 20711; 103pp; English.
2001WO-US008631.
                                                                                                                                                                                                                                                                                Tang YT;
                                                                           2000US-00540217.
2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                       9362/73.
                                                                                                                                                                                                                                                                                Liu C,
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0
                                                     Gaps
                                                  0;
3 BP; 472 A; 408 C; 371 G; 527 T; 0 U; 0 Other;
                         Score 22; DB 5; Length 1778;
                                                  0; Indels
                                     7.3;
                                       100.0%; Pred. No. 7.3 ive 0; Mismatches
                                                                          84
                          1.6%;
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scarcececececicaes 205 SGATGGGGGGGGGGTGAGG

Conservative

dard; cDNA; 2942 BP.

(first entry)

varcinoma associated cDNA, SEQ ID NO:1512.

?: carcinoma associated; oncogene; carcinoma; cancer; breast; nphoma; leukaemia; cytostatic; gene therapy; drug screening;

A2.

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The invention relates to recombinant carcinoma associated (CA) n acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. invention also encompasses expression vectors and host cells compise to the protein, and a biochip comprising CA nucleic acid of binds to the protein, and a biochip comprising CA nucleic acid of fragments thereof. The sequences of the invention were identified oncogenic retroviruses, which insert into the genome of the host oncogenic retroviruses, which insert into the genome of the host oncogenic retroviruses, which insert into the genome of the host oncogenic ransacting viral genes, meaning that cancer inciden direct consequence of the effects of proviral integration into he protoncogenes. The CA nucleic acid sequences can be used to dia carcinoma despecially breast cancer, prostate cancer, lymphoma of leukaemia) or a propensity to carcinoma by determination of the of a CA gene, or by determination of CA gene expression in particities and in screening and evaluating drug candidat present sequence represents a specifically claimed murine CA nucleic sequence of the invention. Note: The complete sequence data for sequence of the invention.
                                                                                                                                                                                                  New recombinant nucleic acid encoding carcinoma associated prote useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of the invention. Note: The complete sequence data for patent did not form part of the printed specification, but was on a electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse; ss; cytostatic; gene therapy; vaccine; carcinoma; lymphom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8; Length 2942; 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2942 BP; 702 A; 837 C; 780 G; 623 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.6%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; neoplasm; adenocarcinoma; sarcoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1512; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 GCAGCCCATTATGAAGTTCATC 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         552 GCAGCCCATTATGAAGTTCATC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB72732 standard; mRNA; 2942 BP.
               26-DEC-2002; 2002WO-US041414.
                                                   26-DEC-2001; 2001US-00035832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2001; 2001US-00798586.
23-OCT-2001; 2001US-00004113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2001; 2001WO-US051291,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-DEC-2003 (first entry)
                                                                                     (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Conservative
                                                                                                                                                                WPI; 2003-587068/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse Sept9 mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003008583-A2.
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ADB72732
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ngelhard EK; DISCOVERY.

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The invention relates to recombinant carcinoma associated (CA) nu acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. Invention also encompasses expression vectors and host cells composed to a polypeptide (especially an antibody) that specific binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified oncogenic retroviruses, which insert into the genome of the host concogenic retroviruses, which insert into the genome of the host oncogenic retroviruses, which insert into the genome of the host oncogenic retroviruses, which insert into the genome of the distribution of the gathogenic trans-acting viral genes, meaning that cancer incidence direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagraction a propensity to carcinoma by determination of the second consequence acids, protecting and antibodies are also useful therapeutic agents and in screening and evaluating drug candidates between sequence represents a specifically claimed murine CA nucleic sequence of the invention. Note: The complete sequence data for the patent did not form part of the printed specification, but was obt in electronic format directly from MIPO at the printed pot sequences.
        recombinant nucleic acids are useful for screening for drug candifor diagnosing or treating carcinomas. Sequences given in ADC8521 ADC85514 represent CA genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse, murine, carcinoma associated, oncogene, carcinoma, cancer, prostate, lymphoma, leukaemia, cytostatic, gene therapy, drug scr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant nucleic acid encoding carcinoma associated proteiuseful for preparing compositions for treating carcinomas.
                                                                                             Sequence 2942 BP; 702 A; 837 C; 780 G; 623 T; 0 U; 0 Other;
                                                                                                                                         1.6%; Score 22; DB 9; Length 2942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Sept9 carcinoma associated gene, SEQ ID NO:1511.
                                                                                                                                                  100.0%; Prec. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1511; 245pp; English.
                                                                                                                                                                                                                         427 GCAGCCCATTATGAAGTTCATC 448
                                                                                                                                                                                                                                                                 552 GCAGCCCATTATGAAGTTCATC 573
                                                                                                                                                                                                                                                                                                                                                                          ADA02993 standard; DNA; 50295 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-DEC-2002; 2002WO-US041414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2001; 2001US-00035832
                                                                                                               Query Match
Best Local Similarity 100.0%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-587068/55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morris DW;
                                                                                                                                                                                                                                                                                                                                                                                                                  ADA02993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus sp
                                                                                                                                                                                                                                                                                                                                RESULT 73
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                                                                                                                                                                                                                                                                                                                  relates to a novel recombinant nucleic acid comprising a quence selected from any of the 660 sequences fully defined ication. A polynucleotide of the invention has cytostatic may have a use in gene therapy, or in a vaccine. The ucleic acids and polypeptides are useful for treating 9. lymphomas, cancers, neoplasm, adenocarcinoma, and present sequence represents a mouse mRNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the therapy; vaccine; cancer; carcinoma-associated gene; CA; smembrane; intracellular; ds.
                                                                                                                                                                                                            nt nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    It nucleic acid comprising a nucleotide sequence of any of associated (CA) genes, useful for screening for drug diagnosing or treating carcinomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 702 A; 837 C; 780 G; 623 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22; DB 9; Length 2942;
Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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100.0%; Pred. No. '...
                                                                                                                                                                                                                                                                          ID NO 560; 2304pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCATTATGAAGTICATC 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCCATTATGAAGTTCATC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lard; DNA; 2942 BP.
2001US-00052482.
2001US-00997722.
                                          2001US-00034650.
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onservative

(first entry)

The

relates to a recombinant nucleic acid comprising a [uence selected from any of the fully defined carcinoma-) genes from the 50 tables given in the specification. The escreted, transmembrane or intracellular proteins. The

NO 260; 983pp; English.

DISCOVERY. gelhard EK; 03/48.

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·; 95 BP; 10891 A; 12938 C; 13611 G; 12237 T; 0 U; 618 Other; Gaps ; 0 Length 50295; 0; Indels DB 8; 1.6%; Score 22; DB 8; 100.0%; Pred. No. 6.2; live 0; Mismatches larity 100. Conservative

GCCCATTATGAAGTTCATC 31093 GCCCATTATGAAGTTCATC 448

ndard; DNA; 50295 BP

(first entry)

ytostatic; gene therapy; vaccine; carcinoma; lymphomas; lasm; adenocarcinoma; sarcoma; gene.

-A2.

2001WO-US051291

2001US-00004113. 2001US-00052482. 2001US-00997722. 2001US-00798586

DISCOVERY.

2001US-00034650

Sngelhard EK;

3337/23.

unt nucleic acid, useful for treating carcinomas, lymphomas, olasm, adenocarcinoma, or sarcomas.

ID NO 559; 2304pp; English.

Trelates to a novel recombinant nucleic acid comprising a squance selected from any of the 660 sequences fully defined lication. A polymucleotide of the invention has cytostatic in may have a use in gene therapy, or in a vaccine. The nucleic acids and polypeptides are useful for treating and polypeptides are useful for treating by.g. lymphomas, cancers, neoplasm, adenocarcinoma, and present sequence represents a mouse gene of the invention.

BP; 10891 A; 12938 C; 13611 G; 12237 T; 0 U; 618 Other;

Gaps ö 1.6%; Score 22; DB 9; Length 50295; 00.0%; Pred. No. 6.2; 0; Indels 100.0%; Pred. No. Conservative arity

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SCCATTAIGAAGTICAIC 448

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dard; DNA; 50295 BP

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The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carci associated (CA) genes from the 50 tables given in the specificat CA proteins are secreted, transmembrane or intracellular protein recombinant nucleic acids are useful for screening for drug cand for diagnosing or treating carcinomas. Sequences given in ADC852 ADC85514 represent CA genes of the invention.
                                                                          Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated secreted; transmembrane; intracellular; ds.
                                                                                                                                                                                                                                                                                                                                                               New recombinant nucleic acid comprising a nucleotide sequence the carcinoma-associated (CA) genes, useful for screening for candidates for diagnosing or treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 259; 983pp; English
                                            Mouse Sept19 genomic sequence.
                                                                                                                                                                                                                                          30-NOV-2001; 2001US-00997722.
                                                                                                                                                                                                             02-DEC-2002; 2002WO-US038582
              01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                       Engelhard EK;
                                                                                                                                                                                                                                                                         (SAGR-) SAGRES DISCOVERY
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                                                                                                                                                   WO2003045230-A2.
                                                                                                                                                                               05-JUN-2003.
                                                                                                                                                                                                                                                                                                      Morris DW,
                                                                                                                      Mus sp.
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of dr

427 GCAGCCCATTATGAAGTTCATC 448 ð d

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1.6%; Score 22; DB 9; Length 50295; 100.0%; Pred. No. 6.2; ive 0; Mismatches 0; Indels (

Query Match Best Local Similarity 100.0 Matches 22; Conservative

Sequence 50295 BP; 10891 A; 12938 C; 13611 G; 12237 T; 0 U; 618

31072 GCAGCCCATTATGAAGTTCATC 31093

Search completed: April 8, 2004, 21:02:41 Job time : 662 secs time : 662 secs

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T27519 I52290 E30552	T37116 A71217 T08734	S31078 T02664 A75567	E75530 S59925 DWEG17	D90651	T24937 T31173	S76920 S44789	D87638 LGGT LGSH	B60738 G85343	S72567 AH0692	E90921	C86665 S60767	AB0273	G65056 I64174 A86387	H70866 G83208	C64124 T25942	A46066 B32352	C85592	A13154	F82439	A10566	AG0007	F71801 A64718	G75518 A97396	AB2614	S23780	AE3466	D70328	A31846 C75208	A46489	AD3295	C95927 R72604	C36718	B90172	
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5.1.6 Compugen Ltd.		Search time 20 Seconds (without alignments) 1365.920 Million cell undates/sec		PWAHLKAAPFLTYFGLFQVH 284		rs.		eters: 283366						licted by chance to have a	stributi		Description	hypothetical prote	photosystem I P700 protamine I-1 - pa	hypothetical prote hypothetical prote	bicyclomycin resis	hypothetical prote	probable cysteine formate dehydrogen	conserved hypothet hypothet	hypothetical prote	Sperm-binding glyc hypothetical prote	probable membrane	probable transport probable ATP-bindi	gamma-glutamyltran protamine II-3 - n	protamine 1 - Sagu	procamine - North hypothetical prote	protein 2C334.3 [i Ig heavy chain V r	conserved hypothet hypothet hypothetical prote	Orf51 [bacteriopha conserved hypothet
GenCore version Copyright (c) 1993 - 2004	in search, using sw model	ril 7, 2004, 17:54:48 ; S. (1	09-245-198A-4	4 MSLLDFEISARRLPLPRSLG	IGO pop 60.0 , Gapext 60.0	6 seqs, 96191526		ts satisfying chosen parameters	gth: 0 gth: 2000000000	isting first 100 summaries	IR 78:*	Diri	pir3:* pir4:*	ne number of than or equa	ı by analysis	SUMMARIES	try ch Length DB ID	111 2	733 2 58 2	143 2 197 2	220 2 278 2	339 2	379 2	387 2	397 2	443 2	465 2	576 2	586 45 2	50 2	86 2	.5 102 2 F87993 .5 115 2 PH1560	115 2	118 2

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Length 58;

DB 2;

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hypothetical protein Vng0080h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Fe
C;Accession: G84168
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shu
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. US.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt,
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E72374
hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju.
C;Date: 81-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju.
C;Accession: E72374
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.;
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB: AE004437; NID: 910579733; PIDN: AAG18715.1; GSPD C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-197 <ARN>
A;Cross-references: GB:AE001724; GB:AE000512; NID:g4980966; PIDN:AAD35
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Evidence for lateral gene transfer between Archaea and Bacter
A,Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.8%; Score 8; DB 2;
100.0%; Pred. No. 7.6;
ative 0; Mismatches
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100.0%; Pred. No. 3.5
tive 0; Mismatches
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2.8%; Score 8; DB 2;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity luu..
Best Sconservative
                                                                                                                                                                                                             8; Conservative
                                  A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-58 < HUN-
C;Superfamily: sperm histone
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                                                                                                                                                                                                                                                                                                               35 ORRRGRRG 42
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                                                                                                                                                                                   Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-143 <STO>
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          A; Accession: A58208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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G84168
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urce: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                     unkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
ck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
                                                                                                                 ein 23516 [imported] - Bscherichia coli (strain 0157:H7, substrain EDL9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U. Rep. 13, 336-342, 1995 coplast Genome of a chlorophyll a+c- containing Alga, Odontella sinensi
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Plast; electron transfer; membrane protein; membrane-associated comple
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s of reptiles.
RASB208; MUID:96394458; PMID:8798564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: EMBL:Z67753; NID:g1185127; PIDN:CAA91749.1; PID:g1185266
offide sequence was submitted to the EMBL Data Library, November 1995
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                                                                                                                                                                01 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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plast Odontella sinensis
98 #sequence_revision 26-Peb-1998 #text_change 20-Jun-2000
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6 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                          equence of enterohemorrhagic Escherichia coli O157:H7.
E: A85480; MUID:21074935; PMID:11206551
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0. 0.074;
0; Indels
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arity 100.0%; Pred. No. 3.3;
Onservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.07
:ive 0; Mismatches
ALIGNMENTS
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probable cysteine synthase - Mycobacterium tuberculosis (strain H³7RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-7u1-1998 #sequence_revision 17-7u1-1998 #text_change 20-7un
C;Accession: H70813
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Har; Connor, R.; Davies, R.; Davinh, K.; Feltwell, T.; Genles, S.; Haml: Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squ. A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barre A;Title: Deciphering the biology of Mycobacterium tuberculosis from the A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Status: preliminary; nucleic acid sequence not shown; translation not A;Residues: 1-372 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Methanococcus januaschi Cipate Landococcus Januaschi C; Species: Methanococcus januaschi C; Date: 13-Sep-1996 #text_change 21-Jul-C; Accession: E64300
R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutt ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurs Science 273, 1058-1073, 1996
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smit A; Title: Complete genome sequence of the methanogenic archaeon, Methano A; Reference number: A64300; MUID:96337999; PMID:8688087
A; Accession: E64300
A; Accession: E64300
A; Molecule type: DNA
A; Residues: 1-379 -8UL2.
A/Accession: C71132
A/Status: preliminary; nucleic acid sequence not shown; translation nc
A/Molecule type: DNA
A/Molecule type: DNA
A/Esidues: 1-339 «KAM»
A/Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29917.1; PID:g3
A/Experimental source: strain OT3
A/OCE: this accession replaces an interim accession for a sequence re
C/Genetics:
A/Genetics:
A/Genetics:
C/Superfamily: conserved hypothetical protein WTH900
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C,Genetics:
A;Map position: REV7250-6111
C;Superfamily: formate dehydrogenase chain B; ferredoxin 2[4Fe-4S] homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAA170
A;Experimental source: strain H37Rv
C;Genetics:
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C;Superfamily: threonine dehydratase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 LGLGLALA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 LGLLLAVV 77
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                                                                                                                                                                                                                                     ; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Sman, E.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Sci. U.S.A. 99, 443, 2002
sequence of the facultative intracellular pathogen Brucella melitens AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            m, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A82950; MUID:20437337; PMID:10984043
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nahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     equence and gene organization of the genome of a hyper-thermophilic A71000; MUID:98344137; PMID:9679194
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                                                                                                             cance protein [imported] - Brucella melitensis (strain 16M) a melitensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n PA4521 [imported] - Pseudomonas aeruginosa (strain PAO1) nas aeruginosa
                                                                                                                                                                           #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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100.0%; Pred. No. 11;
tive 0; Mismatches
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100.0%; Pred. No. 13;
ive 0; Mismatches
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probable ATP-binding transport protein Hill56 - Haemophilus influenzae C; Species: Haemophilus influenzae C; Species: Haemophilus influenzae C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 02-Peb C; Accession: E64186
R; Pleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, i Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Ge Science 269, 496-512, 1995
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smi A;Reference numbers: Ad4000; MUID:95350630; PMID:7542800
A;Accession: E64186
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma-glutamyltransferase (EC 2.3.2.2) related protein - human N.Alternate names: gamma-glutamyltransferase-like activity 1; GCT-REL G.Species: Homo sapiens (man.)

C.Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 18-Jun C.Accession: A41125

R.Heisterkamp, N.; Rajpert-De Meyts, B.; Uribe, L.; Forman, H.J.; Grof: Proc. Natl. Acad. Sci. U.S.A. 88, 6303-6307, 1991

A.Title: Identification of a human gamma-glutamyl cleaving enzyme relat A.Reference number: A41125, MUID:91296809; PMID:1676842

A.Recession: A41125

A.Recession: A81125

A.Recession: A81125

A.Recession: A81125

A.Recession: A81125
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A/Cross-references: GB:U32795; GB:L42023; NID:g1574708; PIDN:AAC22811.
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding c
C;Keywords: ATP; nuclectide binding; P-loop
F;355-550/Domain: ATP-binding cassette homology cABC>
F;372-379/Region: nucleotide-binding motif A (P-loop)
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C;Species: Chrysemys picta (painted turtle)
C;Date: 08-Nov-1996 #sequence_revision 08-Nov-1996 #text_change 07-May-
C;Accession: D58208
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C;Genetics:
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C;Keywords: aminoacyltransferase; glycoprotein; transmembrane protein
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100.0%; Pred. No. 25;
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A;Cross-references: GDB:134033
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                                   366 ALGLGLAL 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
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C.; Ma
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ce: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uence of the radioresistant bacterium Deinococcus radiodurans R1. A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, athewan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, nter, J.C.; Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #sequence_revision 02-Nov-2001 #text_change 17-May-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quence of Yersinia pestis, the causative agent of plague. AB0001; MUID:21470413; PMID:11586360
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                                                                                                                                                                                        Length 443;
                                                                                                                                                                                                                                          0; Indels
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                                                    rce: fetal kidney; clone DKFZp5660011
                                                                                                                                                                                2.8%; Score 8; DB 2;
arity 100.0%; Pred. No. 20;
onservative 0; Mismatches
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5. 21;
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100.0%; Pred. No. 21;
iive 0; Mismatches
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100.0%; Pred. No. 21;
vative 0; Mismatches
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<BLU>: EMBL:AL117414
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hypothetical protein CC2870 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-Ma
C;Accession: P87993
R;Anonymous, The C: elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C: elegans: a platform for i
A;Reference number: A70500, MUID: 99069613; PMID: 9851916
A;Note: see websites genome.wustl.edu/gsc/C elegans/ and www sanger.a
A;Note: published errata appeared in Science 283, 35, 1999; Science 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region (clone VH32) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 21-Jar
C;Accession: PH1560
R;Rassenti, L.Z.; Kipps, T.J.
J; Exp. Med. 177, 1039-1046, 1993
A;Title: Lack of extensive mutations in the VH5 genes used in common I A;Reference number: PH1557; MUID:93210459; PMID:7681468
A;Accession: PH1550
                                                                                                                                                                  Giocession: F87604
Ribierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, B.; Mierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L., J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Preference number: A87249; MUID:21173698; PMID:11259647
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AE005673; NID: 913424486; PIDN: AAK24834.1; GSPI C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:chr 1; PIDN:CAB04964.1; PID:g3881432; GSPDB:GN A;Note: predicted using Genefinder C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein ZC334.3 [imported] - Caenorhabditis elegans
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2.5%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches
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100.0%; Pred. No. 52;
tive 0; Mismatches
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA A;Residues: 1-102 <STO>
                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-86 <STO>
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A; Status: preliminary
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A, Map position: 1
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. 19, 5786, 1991
e 1 gene sequence from the primate Saguinus imperator isolated with PCR
r: S22582; MUID:92051332; PMID:1840669
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iis virginiana, Didelphis marsupialis virginiana (North American opossu
35 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115, 63-72, 1993
ization of a marsupial sperm protamine gene and its transcripts from
:: $34045; MUID:93345500; PMID:8344286
insky, H.E.; Elsey, R.M.; Wright, C.L.; Rice, P.; Bell, J.E.; Sharp,
1, 23547-23557, 1996
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93 #sequence_revision 12-Apr-1996 #text_change 21-Jul-2000
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                                                             :: A58208; MUID:96394458; PMID:8798564
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100.0%; Pred. No. 28;
ative 0; Mismatches
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100.0%; Pred. No.
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3GRR 24
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Orf51 [bacteriophage bIL285] homolog lin2570 [imported] - Listeria inn C; Species: Listeria innocua C; Species: Listeria innocua C; Species: Insteria innocua C; Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov C; Accession: AE1753
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Be.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A; Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; A; Atltle: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
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A;Cross-references: GB:ALS92022; PIDN:CAC97797.1; PID:g16415092; GSPDB
A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Karp, P.; Romero, P.; Zhang, S. Gience 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry,
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Africle: The Genome of the Natural Genetic Engineer Agrobacterium tume
A; Accession: AB2577; MUID:21608550; PMID:11743193
A; Accession: AH2707
A; Accession: AL7707
A; Retaus: pre-liminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein Atul065 [imported] - Agrobacterium tume
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov
C,Accession: AH2707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE008688; PIDN:AAL42078.1; PID:g17739458; GSPDB A;Experimental source: strain CS8 (Dupont)
C;Genetics:
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hypothetical protein ZC334.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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100.0%; Pred. No. 61;
ive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
                                         107 DGGAVRO 113
23 DGGAVRQ 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SLLDFEI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: AE1753
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                                                                                                                RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                am, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jenome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
: A82950; WUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : GB:AE004776; GB:AE004091; NID:g9949701; PIDN:AAG06945.1; GSPDB:GN001
ce: strain PA01
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                                                                                                                                                                                                                                                                                                                                                                                   ical protein PA3557 [imported] - Pseudomonas aeruginosa (strain PAO1) nas aeruginosa ) #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                                                                                                                                                  Gaps
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                             inoglobulin V region; immunoglobulin homology :etramer; immunoglobulin mmunoglobulin homology <IMM>
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                                                                                                                                 Length 115;
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100.0%; Pred. No. 59;
ive 0; Mismatches
                                                                                                                               2.5%; Score 7; DB 2;
100.0%; Pred. No. 58;
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100.0%; Pred. No. 58;
iive 0; Mismatches
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ive 0; Mismatches
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T37116
probable transposase, truncated (imported) - Streptomyces coelicolor C,Species Streptomyces coelicolor C,Species Streptomyces coelicolor C,Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 15-Sej C,Accession: T37116
E,Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B submitted to the EMBL Data Library, August 1999
A,Reference number: Z21588
A,Reference number: T37116
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-146 <SAU>
A;Cross-references: EMBL:AL109950; PIDN:CAB52967.1; GSPDB:GN00070; SC(
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: A71217
R; Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Y
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; F
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hy
A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: GB:AP000007; GB:AP000001; NID:g3236134; NID:g32361
A,Experimental source: strain OT3
A,Note: this accession replaces an interim accession for a sequence re
A,Note: this sequence is split into two separate translations in GenBa
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jur
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C;Specias: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug
C;Accession: T08734
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C;Superfamily: Pyrococcus horikoshii hypothetical protein PH2001
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                   Indels
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A,Gene: SCOEDB.SCJ4.33c
C,Superfamily: Synechocystis transposase sll1710
                 Mismatches
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Best Local Similarity 100.0
Matches 7; Conservative
            7; Conservative
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                                                        65 LALACLG 71
                                                                                                     9 LALACLG 15
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79-687, 1989
of small inducible proteins secreted by leukocytes are members of a ne ation processes.
830552; MUID:89093958; PMID:2521353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Res. Commun. 197, 612-618, 1993

<sup>1</sup>f rat interleukin-13 (IL-13) cDNA and analysis of IL-13 gene expressic

<sup>1</sup>: 152290; MUID:94092138; PMID:7916615
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s: EMBL: 282082; PIDN: CAB04964.2; GSPDB:GN00019; CESP: 2C334.3
irce: clone 2C334
                      #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            norvegicus (Norway rat)

6 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
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. 62;
                                                                                           3MBL Data Library, November 1996
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100.0%; Pred. No. 62;
tive 0; Mismatches
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100.0%; Pred. No. 64;
cive 0; Mismatches
abditis elegans
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"LAL 39
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C;Species: Delnococcus radioducaus idlicain K1)
C;Species: Delnococcus radioducaus
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar
C;Accession: E7530
B;White, O.; Fisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.;
M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 266, 157-1577, 1999
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E7530
A;Accession: E7530
A;Accession: E7530
A;Status: preliminary
A;Molecule type: DMA
A;Residues: 1-157 <WHI>
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CiSpecies: Oryza sativa (rice)
CiSpecies: Oryza sativa (rice)
CiSpecies: Oryza sativa (rice)
CiSpace: IS-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 20-Jun-
CiAccession: S59925
RiAlvarez, A.M.; Adachi, T.; Nakase, M.; Aoki, N.; Nakamura, R.; Matsuc
Biochim. Biophys. Acta 1251, 201-204, 1995
A;Title: Classification of rice allergenic protein cDNAs belonging to t
A;Reference number: S59922; MUID:95399441; PMID:7669811
                                                                                                                             C; Accession: A75567
R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J. M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                A,Title: Genome sequence of the radioresistant bacterium Deinococcus r
A,Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75567
                                                                                                                                                                                                                                                                                                                             A Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-157 < WHI>
A; Cross-references: GB: AE001867; GB: AE000513; NID: g6457693; PIDN: AAF09
A; Experimental source: strain R1
C; Genetics:
                                                                                 C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar
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A;Experimental source: strain R1
C;Genetics:
                                                        conserved hypothetical protein - Deinococcus radiodurans (strain R1) C;Species: Deinococcus radiodurans
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100.0%; Pred. No. 75;
tive 0; Mismatches
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Best Local Similarity 100.0%; Pr
Conservative 0;
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Best Local Similarity 100.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sture and expression of rice seed allergenic proteins belonging to the S31078; MUID:93144699; PMID:7678765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l, H.; Yamada, T.; Tanaka, K.; Takeuchi, S.; Nakamura, R.; Matsuda, T.
L, 239–248, 1993
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; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.rotein Sequence Database, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
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BL Data Library, January 1998
eotide sequence of rice allergenic protein.
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                                                                                                                                                                      rce: fetal kidney; clone DKFZp566F0546
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NA
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. 72;
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100.0%; Pred. No. 75;
tive 0; Mismatches
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100.0%; Pred. No. 72;
iive 0; Mismatches
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100.0%; Pred. No. 75;
ative 0; Mismatches
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t alpha-amylase inhibitor
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VS 17
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histone-like protein HlpA [imported] - Escherichia coli (strain O157:) C;Species: Escherichia coli C;Date: 18-Uul-2001 #sequence_revision 18-Uul-2001 #text_change 03-Au C;Accession: D90651 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yoko gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shina, DNA Res. 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia co A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-161 <HAY>
A;Residues: 1-161 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33603.1; PID:g13359636; GSPDI
A;Experimental source: strain Ol57:H7, substrain RIMD 0509952
C;Genetics:
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A,Molecule type: DNA
A,Residues: 1-16: DNA
A,Residues: 1-16: STO>
A,Cross-references: GB:AB005174; NID:gl2512906; PIDN:AAG54480.1; GSPDE
A,Experimental source: strain O157:H7, substrain EDL933
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct
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    Pred. No. 77; ; Mismatches
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2.5%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches
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2.5%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: ECs0180
C;Superfamily: DNA-binding 17K protein
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C,Superfamily: DNA-binding 17K protein
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Best Local Similarity
Matches 7; Conserva
                                                                                                               9 GLGLALA 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and sequencing of the gene for the DNA-binding 17K protein of Escherich of JUS084; MUID:88329735; PMID:2843433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i: EMBL:X54797; NID:g41468; PIDN:CAA38567.1; PID:g41469
rrce: strain K-12, substrain MG1655
Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CG lau, B.; Shao, Y.
1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,16-148,'E',150-152,'I',154-161 <RES>
EMBL:X75465; NID:g432661; PIDN:CAA53207.1; PID:g432662
protein has been believed to be a histone-like constituent of bacter
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rrce: strain K12; substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ii, P.; Vaara, M.
1223-1229, 1991
gene of Yersinia enterocolitica: cloning, sequencing, expression, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d nucleotide sequence of the firA gene and the firA200(Ts) allele $13728; MUID:91100302; PMID:1987124
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                                                                 3: EMBL:D42142; NID:g1398917; PIDN:BAA07713.1; PID:g1398918
3at alpha-amylase inhibitor
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14; A38063; $\overline{5}$13728; B64742; I54944; $20426
19, K.
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                                                                                                                                                                                                                                                                                                                                                                                                >>tein hlpA precursor - Escherichia coli (strain K-12)
>> DNA-binding 17K protein; histone-like protein hlp
ichia coli
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A64720; MUID:97426617; PMID:9278503
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                                                                                                                                        Length 160;
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                                                                                                                                        DB 2;
. 76;
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100.0%; Pred. No. 76;
iive 0; Mismatches
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d nucleotide s
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Jonservative
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A;Molecule type: DNA
A;Residues: 1-164 «KAN»
A;Cross-references: EMEL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA18
A;Note: the nucleotide sequence was submitted to the EMBL Data Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cipate: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar Cipate: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar B: Favello, AD.

Cipatesion: S44789 #sequence_revision 12-May-1995 #text_change 23-Mar B: Favello, AD.

Cipatesion: S44789 #sequence of the C. elegans cosmid D2007.

A; Reference number: S44619

A; Status: preliminary

A; Mccession: S44789

A; Status: preliminary

A; Molecule type: DNA

A; Molecule type: DNA

A; Coss-references: EMBL:L16560; NID:g289666; PID:g289670

C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76920
A;Status: preliminary
                                                                                                                                                                                                                                                                                                  Query Match 2.5%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches
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100.0%; Pred. No. 80;
tive 0; Mismatches
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Best Local Similarity 100.0
Matches 7; Conservative
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A;Molecule type: DNA
A;Residues: 1-174 <STO>
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A;Introns: 43/2; 121/3
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ABL Data Library, July 1998
Mete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      malysis of the genome of the unicellular cyanobacterium Synechocystis
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Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : EMBL:Z66516; PIDN:CAA91361.1; GSPDB:GN00020; CESP:W03C9.4 rce: clone W03C9
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                                                                                                                                   ary; translated from GB/EMBL/DDBJ
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3. 77;
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MBL Data Library, October 1995
: Z20155
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100.0%; Pred. No. 77;
iive 0; Mismatches
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100.0%; Pred. No. 77;
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                       4BL Data Library, July 1995
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insulin-like growth factor II precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Apr.1993 #sequence_revision 30-Sep-1993 #text_change 13-Nov
C;Accession: S12614; B60738
R;Catchpole, I.R.; Engstroem, W.
Nucleic Acids Res. 18, 6430, 1990
A;Title: Nucleotide sequence of a porcine insulin-like growth factor 1
                                                                                                                                                                                                       A, Molecule type: DNA
A, Residues: 1-37, 'Y', 39-102, 'N', 104-180 <ALI2>
A; Cross references: GB:X07009
A; Cross references: GB:X07009
A; Experimental source: beta-lactoglobulin II
R; Harris, S.; Ali, S.; Anderson, S.; Archibald, A.L.; Clark, A.J.
Nucleic Acids Res. 16, 10379-10380, 1988
A; Title: Complete nucleotide sequence of the genomic ovine beta-lacto
A; Reference number: S02136; MUID:89057492; PMID:3194215
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A.Residues: 19-37,'Y',39-165,'Q',167-180 <ERH>
A.Residues: 19-37,'Y',39-165,'Q',167-180 <ERH>
C.Commental source: beta-lactoglobulin C
C.Comment: This protein is the major milk whey protein of ruminants a C.Comment: Under physiological conditions beta-lactoglobulin exists a
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A; Molecule type: protein
A; Residues: 19-37, 'Y', 39-180 < PRE>
A; Residues: 19-37, 'Y', 39-180 < PRE>
A; Exhardt, G.; Godovac-Zimmermann, J.; Conti, A.
Biol. Chem. Hoppe-Seyler 370, 757-762, 1989
A; Title: Isolabation and complete primary sequence of a new ovine wild-A; Reference number: S04955; MUID:89374823; PMID:2775495
A; Accession: S04955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X12817; NID:91313; PIDN:CAA31305.1; PID:9131 R;Gaye, P.; Hue-Delahaie, D.; Mercier, J.C.; Soulier, S.; Vilotte, J. Biochimie 68, 1097-1107, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: mRNA
A,Residues: 1-180 cGAY>
A,Cross-references: GB:X04520; NID:g1315; PIDN:CAA28204.1; PID:g1316
R,Preaux, G.; Braunitzer, G.; Kolde, H.J.
Arch. Int. Physiol. Biochim. 88, B45-B46, 1980
A,Title: Primary structure of ovine beta-lactoglobulin.
A,Reference number: A03221; MUID:80219294; PMID:6155855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Artitle: Ovine beta lactoglobulin messenger RNA: nucleotide sequence A;Reference number: A25136; MUID:87049827; PMID:3096387
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C;Superfamily: lipocalin; lipocalin homology
C;Keywords: milk; polymorphism
F;1-19/Domain: signal sequence #status predicted <SIG>
F;19-180/Product: beca-lactoglobulin #status experimental <MAT>
F;28-178/Domain: lipocalin homology <LIP>
F;84-178,124-137/Disulfide bonds: #status predicted
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A; Reference number: A92942; MUID: 88172489; PMID: 3351935
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100.0%; Pred. No. 84;
tive 0; Mismatches
                      A;Accession: A30011
A;Molecule type: DNA
A;Residues: 1-180 <ALI1>
A;Cross-references: GB:X14971
A;Experimental source: beta-lactoglobulin I
A;Accession: B30011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: translation not shown
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itation of the gene encoding ovine beta-lactoglobulin. Similarity to
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physiological conditions beta-lactoglobulin exists as an equilibrium
pocalin; lipocalin homology
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35 #sequence_revision 19-page #text_change 22-Jun-1999
19; JQ0748; A30011; B30011; S02136; A25136; A03221; S04955
19han, M.; Simons, J.P.; Clark, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isation of the alleles encoding ovine beta-lactoglobulins A and B. i JQ0748; MUID:91007276; PMID:1976573
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                                                                        n precursor - goat
85 seagagrus hircus (domestic goat)
85 #sequence revision 12-Apr-1996 #text_change 22-Jun-1999
20; $14507; $42800; $42801
unitzer, G.; $chrank, B.; $tangl, A.
Physiol Chem. 360, 1595-1604, 1979
o acid sequence of goat beta-lactoglobulin.
I: A91682; MUID:80070611; PMID:511095
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.00.0%; Pred. No. 84;
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beta-lactoglobulin #status predicted <MAT>
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EMBL Data Library, March 1991
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probable membrane protein ydgQ - Escherichia coli (strain K-12)
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar
C;Accession: B64920
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland,
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64920
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-231 <- Laboration of Securichia acid sequence not shown; translation not shown
A;Residues: 1-231 <- Laboration acid sequence not shown; translation not shown
A;Residues: 1-231 <- Laboration acid sequence not shown; translation not shown
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A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein ydg0 [imported] - Salmonella enterica s C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov
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A;Cross-references: GB:AL513382; PIDN:CAD01913.1; PID:g16502755; GSPDB C;Genetics:
                                    A,Map position: 3
A;Introns: 42/2; 88/3; 126/3; 176/3
A;Note: C35D10.8
C;Superfamily: Caenorhabditis elegans hypothetical protein C35D10.8
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A) Start codon: GTG
A) Start codon: GTG
C; Superfamily: conserved hypothetical protein H11688
C; Keywords: transmembrane protein
F;18-34/Domain: transmembrane #status predicted <TM01>F;38-4/Domain: transmembrane #status predicted <TM02>F;31-87/Domain: transmembrane #status predicted <TM03>F;97-113/Domain: transmembrane #status predicted <TM03>
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100.0%; Pred. No. 1e+02;
tive 0; Mismatches 0
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100.0%; Pred. No. 94;
tive 0; Mismatches
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Best Local Similarity 100.0
Matches 7, Conservative
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Best Local Similarity 100...
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A;Molecule type: DNA
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             C;Genetics:
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: A60738; MUID:90039035; PMID:2809477
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n., R.; Smaldon, N.; Smith, A.; Sonnhammer, E.; Staden, R.; Sulston, J
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irboxyl-terminal propeptide (E peptide) #status predicted <CTP>
i/Disulfide bonds: #status predicted
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.sis thaliana (mouse-ear cress)
! #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
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EMBL:U21324; NID:g687879; PID:g687888
ce: strain Bristol N2
: S12614; MUID:91057136; PMID:2243790
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bditis elegans
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100.0%; Pred. No. 85;
ive 0; Mismatches
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100.0%; Pred. No. 87;
ive 0; Mismatches
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probable membrane protein YPO2240 [imported] - Yersinia pestis (strain C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov C;Accession: AB0273
R;Parkhill, J: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davieill, M.T. deno-Tarraga, A.M.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitel Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of play.Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                         Ribolotin, A., Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Wei Genome Res. II., 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium La A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C8666
A;Status: preliminary
A;Molecule type: DNA
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A; Residues: 1-233 < ZUB>
A; Cross-references: EMBL:L27436; NID:g439870; PIDN:AAA69690.1; PID:g4
A; Cross-references: EMBL:L27436; NiD:g439870; PIDN:AAA69690.1; PID:g4
C; Superfamily: ribonuclease III; double-stranded RNA-binding repeat h
F;150-223/Domain: double-stranded RNA-binding repeat homology < DSR>
                                         amino acid ABC trasporter permease protein [imported] - Lactococcus ]
                                                                      C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-De
C;Accession: C86665
                                                                                                                                                                                                                                                                                                                                                                        A)Residues: 1-231 <STO>
A;Cross-references: GB:AE005176; PID:g12723189; PIDN:AAK04421.1; GSPD
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Coxiella burnetii
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 22-Ju
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A;Cross-references: GB:ALS90842; PIDN:CAC91046.1; PID:g15980240; GSPDE
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R; Zuber, M.; Hoover, T.A.; Powell, B.S.; Court, D.L.
Mol. Microbiol. 14, 291-300, 1994
A; Title: Analysis of the rnc locus of Coxiella burnetii.
A; Reference number: S60767; MUID:95131751; PMID:7830573
A; Accession: S60767
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A,Gene: ydcC
C,Superfamily: ABC transporter permease protein
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2k, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
33, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in ydgQ [imported] - Escherichia coli (strain 0157:H7, substrain EDL93
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irce: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han,
unaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
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urce: strain O157:H7, substrain RIMD 0509952
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transmembrane #status predicted <TM05>
transmembrane #status predicted <TM06>
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Kha A; Authors: Hunter, J.L.; Y.; Liu, X.; Liu, Z.K.; Liu, Z.A.; Liu, Z.A.; Mai Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis A; Accession: A86387
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P. adman, S.; Yaun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
probable cytochrome b-561 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-
C;Accession: A86387
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A.Experimental source: strain H37Rv
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 7; Conservative
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A, Molecule type: DNA
A, Residues: 1-236 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, ott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. 2, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , 1999
nd analysis of chromosome 4 of the plant Arabidopsis thaliana.
A85001; MUID:20083488; PMID:10617198
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                                                                                                                                                                                                                                                                                                                                                                                  synthase-like protein [imported] - Arabidopsis thaliana
is thaliana (mouse-ear cress)
#sequence_revision 16-Feb-2001 #text_change 17-May-2002
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                                                                                           Length 233;
                                                                                      2.5%; Score 7; DB 2; Length 233; rity 100.0%; Pred. No. 1e+02; aservative 0; Mismatches 0; Indels
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                                         erved hypothetical protein HI1688
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molybdopterin biosynthesis protein moeb - Escherichia coli (strain K-: molybdopterin-converting factor chlN N.Alternate names: molybdopterin-converting factor chlN C; Species: Escherichia coli (c; Species: Escherichia coli C; Species: Escherichia coli C; Species: Dann-1990 #sequence_revision 07-Jun-1990 #text_change 01-Ma: C; Accession: B32352; B64820
E; Nohno, T.; Kasai, Y.; Saito, T.
J. Bacteriol. 100, 4097-4102, 1988
A; Title: Cloning and sequencing of the Escherichia coli chlEN operon A; Reference number: A32352; MUID:88314906; PMID:3045084
A; Reference number: A32352; MUID:88314906; PMID:3045084
A; Reference number: A32352; MUID:9145538; PIDN:AAA23580.1; PID:9145
A; Cross-references: GB:M21151; NID:9145538; PIDN:AAA23580.1; PID:9145
A; Cross-references: GB:M21151; NID:9145538; PIDN:AAA23580.1; PID:9145
A; Cross-references: GB:M21151; NID:91426617; PMID:9278503
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Taccesion: Réad?
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A;Residues: 1-249 < BIAT>
A;Cross-references: GB:AE000185; GB:U00096; NID:g1787047; PIDN:AAC739
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: Å46066
R;Browning, J.L.; Ngam-ek, A.; Lawton, P.; DeMarinis, J.; Tizard, R.;
Cell 7.2, 847-856; 1939
A;Title: Lymphotoxin beta, a novel member of the TNF family that forms
A;Title: Lymphotoxin beta, a novel member of the TNF family that forms
A;Reference number: A46066; MUID:93208881; PMID:7916655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-244 <BRO>
A;Cross-references: GB:L11015; NID:g292276; PIDN:AAA36191.1; PID:g2922
A;Note: sequence extracted from NCBI backbone (NCBIN:128066; NCBIP:128
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C.Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul
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                                                                                 Query Match
2.5%; Score 7; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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C;Superfamily: molybdopterin biosynthesis protein moeB
C;Keywords: molybdenum; molybdopterin biosynthesis
A,Map position: 5
A;Introns: 41/1; 84/2; 144/3; 195/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA; protein
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                                                                                                                                                                                                                                  234 AASSLGP 240
                                                                                                                                                                                                                                                                                                  225 AASSLGP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphotoxin beta - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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       Jenome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                             GB:AE004770; GB:AE004091; NID:99949633; PIDN:AAG06882.1; GSPDB:GN001
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100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0; Indels
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served hypothetical protein HI1688

cce: strain PAO1

<STO>

ynthesis protein moeB - Haemophilus influenzae (strain Rd KW20) ilus influenzae

#sequence\_revision 18-Aug-1995 #text\_change 29-Sep-1999

.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, cott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. 12, 1995

C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, ome random sequencing and assembly of Haemophilus influenzae Rd. : A64000; MUID:95350630; PMID:7542800

acid sequence not shown; translation not shown

iybdopterin biosynthesis protein moeB lenum; molybdopterin biosynthesis pterin biosynthesis

Score 7; DB 2; Length 243; Pred. No. 1.16+02; 0; Mismatches 0; Indels 2.5%; ( iarity 100.0%; Conservative 0,

TROI 185

#sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999 ein ZC196.8 - Caenorhabditis elegans habditis elegans 99 #sequence\_revision 15-Oct-1999 #te

EMBL Data Library, April 1997 e sequence of C. elegans cosmid ZC196. nary; translated from GB/EMBL/DDBJ 220115

:s: EMBL:U97007; PIDN:AAB52299.1; GSPDB:GN00023; CESP:ZC196.8 arce: strain Bristol N2; clone ZC196

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C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov
C;Accession: Alfo602
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Gattung, S.; Miller, N.; Blanchard, M.; Quan, Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lapps Science 294, 2323-2328, 2001 (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accession (C)Accessio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E R;Wood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, J.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues; 1-252 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL45655.1; PID:g17743380; GSPD
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tum
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Cross-references: GB:AL513382; PIDN: CAD05291.1; PID:g16502055; GSPDE
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2.5%; Score 7; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: STY0884
C; Superfamily: molybdopterin biosynthesis protein moeB
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0;
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-249 < PAR>
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A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthesis [imported] - Escherichia coli (strain O157:H7, substrain EDL\mathfrak g
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urce: strain O157:H7, substrain EDL933
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: A99629; MUID:21156231; PMID:11258796
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naga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
2001
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rce: strain Ol57:H7, substrain RIMD 0509952
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92
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r: A85480; MUID:21074935; PMID:11206551
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.00.0%; Pred. No. 1.1e+02;
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larity 100.0%; Pred. No. 1.1e+02;
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2.5%; Score 7; DB 2; Length 254; Conservative 100.0%; Pred. No. 1.1e+02; Conservative 0; Mismatches 0; Indels NRQI 185 | | | | | | NRQI 18 | April 7, 2004, 17:59:25

lybdopterin biosynthesis protein moeB

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Ltd.		Search time 17 Seconds (without alignments) 869.878 Million cell updates/sec		.PWAHLKAAPFLTYFGLFQVH 284				31				results predicted by chance to have a to the score of the result being printed, of the total score distribution.		scription	homo	mus m esche	go odontella s q6 cyanidium c 44 gluconobect	73 brucella me	k4 pan troglod	91 mesocricetu	81 haemophilus 69 homo sapien	15 octopus vul	14 saguinus im	5 didelphis m 2 drosophila	8 escherichia	9 mus musculu 3 rattus norv	1 pyrococcus	v8 sus scrora 81 oryza sativ	457 escherichia 378 caenorhabdi 365 hubalua	755 bubalus bub 756 capra hircu 757 ovis aries	Q8efgl shewanella Q8g534 bifidobacte O8xex9 salmonella	58344 escherichia
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STANDARD;

O3L OR DR3LG.

(Human)

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This SWISS-PROT entry is copyright. It is produced through a collibration the Swiss Institute of Bioinformatics and the EMBL out the Bureopean Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in motified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMOR NECROSIS FACTOR LIGAND SUPERFY MEMBER 12, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 MAARRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARAIAAHYEVHPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 GAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 LLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLK?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 LLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytokine; Angiogenesis; Apoptosis; Transmembrane; Glycoprotein;
                      by proteolytic processing.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
-!- CAUTION: Ref. 3 sequence differs from that shown due to a frameshift in position 125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.7%; Score 249; DB 1; Length 249; 100.0%; Pred. No. 2.9e-232;
  PTM: The soluble form derives from the membrane form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                EMBL, AF030099; AAC51923.1; -.
EMBL, AF05872; AAC53724.1; -.
EMBL, BC019047; AAH19047.1; ALT_FRAME.
GENEW; HGNO:11927; TRNESF12.
GO:0005867; -.
GO:0005867; C:integral to plasma membrane; TAS.
GO: GO:0005102; F:receptor binding; TAS.
GO: GO:0005102; P:induction of apoptosis; TAS.
GO: GO:0007165; P:induction of apoptosis; TAS.
GO: GO:0007165; P:induction of apoptosis; TAS.
InterPro; IPR0066052; TNF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEMBER 12, SECRETED FORM. CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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1D TN12_MOUSE STANDARD;
1A C 054907; Q9CTP2;
DT 28-FEB-2003 (Rel. 41, Created)
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Matches 249; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00229; TNF; 1.
SMART; SM00207; TNF; 1
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93
139 13
249 AA;
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L., Feingold E.A., Grouse L.H., Derge J.G.,
collins F.S., Wagner L., Schamen C.M., Schuler G.D.,
Collins F.S., Wagner L., Schamen C.M., Schuler G.D.,
Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,
Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
quellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
ICBwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk.S.W.,
worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk.S.W.,
Morley K.C., Shevchenko Y., Bouffard G.G.,
J., Touchman U.W., Schen E.D., Dickson M.C.,
J., Grimwood J., Schmutz J., Myers R.M.,
S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schmutz J. Jones S.J.M., Marra M.A.,
und initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                            liver, and Tonsil;
11.5; PubMed=9405449;
1e Y., Bourdon P.R., Yu H., Hsu Y.-M., Scott H.,
1axcia I., Browning J.L.;
1 secreted ligand in the tumor necrosis factor family that
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Binds to FN14 and possibly also to TNRFSF12/APO3. Weak prospensis in some cell types. Mediates NP-KappaB n. May promote angiogenesis and the proliferation of ial cells.
                                                             Rel. 41, Created)
Rel. 41, Last sequence update)
Rel. 42, Last annotation update)
s factor last annotation update)
s factor last annotation update)
s factor last APO3 ligand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on of a ligand for the death-domain-containing receptor
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                                                                                                                                                                                                                                         tazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
.heria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sheridan J.P., Pitti R.M., Brush J., Goddard A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                     N.A., AND N-TERMINUS OF SOLUBLE FORM
                      249 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss apoptosis.";
n. 272:32401-32410(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355; PubMed=9560343;
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YFBW ECOLI
Q47377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ragawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Ira A., Fukudishi Y., Komon H., Adachi J., Fukuda S., wa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., aki Y., Gojobori T., Bono H., Kasukawa T., Saito R., suda H.A., Ashburner M., Batalov S., Casavant T., Gaasterland T., Gissi C., King B., Kochiwa H., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T., ol T., Puruno M., Aono H., Baldarelli R., Barsh G., elli D., Bojunga N., Carninci P., de Bonaldo M.F., Mall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., thomi L., Mashima J., Mazzarelli J., Mombaerts P., no R., Schoenbach C., Seya T., Shibata Y., Storch K.-F., o-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., o-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                          PY., Bourdon P.R., Xu H., Hsu Y.-M., Scott H., ircia I., Browning J.L.; secreted ligand in the tumor necrosis factor family that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Binds to FN14 and possibly also to TNRFSF12/APO3. Weak apoptosis in some cell types. Promotes angiogenesis and eration of endothelial cells. Mediates NF-KappaB
tel. 41, Last sequence update)
tel. 41, Last annotation update)
s factor ligand superfamily member 12 (TNF-related weak
)ptosis) (TWEAK) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (By similarity).
lomotrimer (Potential).
R LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                        azoa, Chordata, Craniata, Vertebrata, Buteleostomi, jeria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         motation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         soluble form is produced from the membrane form by c processing (By similarity). Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            logenesis; Apoptosis; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MCIFICITY: Widely expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                              apoptosis.";
272:32401-32410(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5J; TISSUE=Retina;
560; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251; TNF 1; FALSE NEG. 349; TNF 2; 1.
                                                                                                                                                                                                                                                                                                                       115; PubMed=9405449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              )06052; TNF family.
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); BAB32249.1; -.
                                                                                                                                                                                                                                                                                        leal macrophage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -225 FROM N.A.
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Blattner F.R., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collibetween the Swiss Institute of Bioinformatics and the EMBL out: the European Bioinformatics Institute. There are no restriction: use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centifies requires a license agreement (See http://www.isb-sib.ch/cor send an email to license@isb-sib.ch).
                              MEMBER 12, MEMBRANE FORM.
TUMON NECROSIS FACTOR LIGAND SUPERFA
MEMBER 12, SECRETED FORM (BY SIMILAR
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROT
                                                                                                                                                                                                                                                        Ö
              TUMOR NECROSIS FACTOR LIGAND SUPERFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                    .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                      Score 32; DB 1; Length 225;
Pred. No. 4.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  characterization of the menE gene from Escherichia coli."; Gene 168:43-48(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sharma V., Hudspeth M.E., Meganathan R.; "Menaquinone (vitamin K2) biosynthesis: localization and
                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000315; -; NOT ANNOTATED CDS.

EMBL; L35031; AAB04895.1; -.

ECGGEN; EC14344; yfbW.

InterPro; IRF000620; DUF6.

Pfam; PF00892; DUF6; 1.

Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                         -LINKED (GLCNAC. . .) (PC 90C412CC0480659B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 56 POTENTIAL.
62 82 POTENTIAL.
89 108 POTENTIAL.
111 AA; 12192 MW; 7CFA06D75DA33D69 CRC64;
                                                                                                                                 CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                    N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                          139 RRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-OEB-2003 (Rel. 41, Last annotation update)
19-PEB-2003 (Rel. 41, Last annotation update)
YFBW OR B2257.1.
                                                                                                                                                                                                           11.3%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                           80 RRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEE 111
                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 111 AA.
                                                                                                                   EXTRACELLULAR
                                                                                                    (POTENTIAL)
                                                                                                                                                     POTENTIAL.
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                                                                                                               225 EX
70 CL
186 PO
115 N-
24781 MW;
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                                                                                                                                                                                                                      Query Match 11.3
Best Local Similarity 100.
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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82
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225
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167
115
225 AA;
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뜊뿂윰뎙텉몷쎰뿀ਲ꽘뚕욵욳첑뜵쁉첉긂둮퍖닔잗팑팑군단광동타타난타다타다니다니다.

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                                                                                                                                                                                                                                                                                                                                                                                                            IRON-SULFUR (4FE-4S) (SHARED WITH DIMERIC PARTWER) (BY SIMILARITY).
MAGNESIUM (CHICOROPHYLL-A B1 AXIAL LIGAND; P700 SPECIAL PAIR) (BY SIMILARITY).
MAGNESIUM (CHLOROPHYLL-A B3 AXIAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                     IRON-SULFUR (4FE-4S) (SHARED WITH DIMERIC PARTNER) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inouchi S.; in the genes encoding the three-component membranedehydrogenase from Gluconobacter suboxydans and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ogenase 15 kDa subunit precursor (G3-ADH subunit III).
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eobacteria; Alphaproteobacteria; Rhodospirillales;
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                                                                                                                                                                                                 19; PHOTOSYZEM I PSAAB; 1.
CCTCON transport; Photosynthesis; Thylakoid;
Chlorophyll; Metal-bindding; Iron; Magnesium;
Fe-45; Transmembrane; Chloroplast.
6 69 I (POTENTIAL).
5 158 II (POTENTIAL).
7 291 IV (POTENTIAL).
9 353 VV (POTENTIAL).
9 355 VVI (POTENTIAL).
7 439 VII (POTENTIAL).
7 535 VII (POTENTIAL).
7 535 VII (POTENTIAL).
7 536 VII (POTENTIAL).
7 537 VII (POTENTIAL).
8 665 X (POTENTIAL).
9 777 XI (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
CHLOROPHYLL-A B3 (BY SIMILARITY).
PHYLLOQUINONE B (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.2%; Score 9; DB 1; Length 734;
100.0%; Pred. No. 1.8;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4496AA2AE59CA9B9 CRC64;
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Last annotation update)
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                                                                                                                             12; -; 1.
106244; PsaB.
101280; PSI_PsaA/B.
psaA_psaB; 1.
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                                                                                                      AAF12881.1; -.
                                                                                                                                                                            PHOTSYSPSAAB.
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DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Lo Varonva N., Anderson I., Bhattacharya A., Lykdish B., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsma Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R., "The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a coll. between the Swiss Institute of Bioinformatics and the EWBL out. the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contities requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Membrane; Periplasmic; Signal; Pyrrolidone carboxylic acid.
SIGMAL
24 POTENTIAL.
CHAIN
25 179 ALCOHOL DEHYDROGENASE 15 KDA SUBUNIT
MOD RES
25 25 PYRROLIDONE CARBOXYLIC ACID.
SEQÜENCE 179 AA; 19943 MM; F6AF243656B3CC66 CRC64;
                         Appl. Environ. Microbiol. 63:1131-1138 (1997).
-!- FUNCTION: NOT ESSENTIAL FOR ALCOHOL DEHYDROGENASE ACTIVITY.
-!- SUBUNIT: HETEROTRIMER (DEHYDROGENASE, CYTOCHROME AND PROTEIN ADHS), THAT FORMS THE ALCOHOL DEHYDROGENASE COMPLEX.
-!- SUBCELLULAR LOCATION: Membrane-bound, facing the periplasmic
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the UPF0191 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 2.8%; Score 8; DB 1; Length 179; Best Local Similarity 100.0%; Pred. No. 4.9; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FFB-2003 (Rel. 41, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
42-FFB-cal protein BMEII0304.
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expression in Acetobacter pasteurianus.";
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STRAIN-16M / ATCC 23456 / Biotype 1;
MEDLINE-20020109; PubMed=11756688;
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HAMAP, MF -01207; -; 1. InterPro; IPR00791; y DPF0191.
Pfam; PP05252; UPP0191; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D86440; BAA19756.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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Our entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial itses a license agreement (See http://www.isb-sib.ch/announce/ail to license@lab-sib.ch).
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L., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
Tettelin H., Gill S.R., White O., Salzberg S.L.,
Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,
suis genome reveals fundamental similarities between
                                                                                                                                                                                                                Gaps
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741; PubMed=12271122;
Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
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.cad. Sci. U.S.A. 99.13148 13153 (2002).
AM LOCATION: Integral membrane protein (Potential).
Y: Belongs to the UPF0191 family.
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100.0%; Pred. No. 5.8;
ve 0; Mismatches 0; Indels
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Transmembrane; Complete proteome. POTENTIAL.
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                                                                                                               POTENTIAL.
182C0244743B17FA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Rel. 43, Created)
Rel. 43, Last sequence update)
Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                220 AA
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POTENTIAL.
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Pred. No.
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                                                                                                                                  24815 MW;
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2007916; UPF0191.
2; UPF0191; 1.
                                                                                                                                                                                              100.08;
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104
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175
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protein;
20 39
54 72
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Fm. J. Phys. Anthropol. 121:67-80(2003).

-!- FUNCTION: Receptor for MSH (alpha, beta and gammA) and ACTH.

-creativity of this receptor is mediated by G proteins which act
adenylate cyclase (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: Belongs to family 1 of G-protein coupled recepto:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collibbetween the Swiss Institute of Bioinformatics and the EMBL out the Bursopean Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch, or send an email to license@isb.sh).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Rees J.L., Harding R.M., Healy E., Jackson I.J., Ray A.J., Ellis
Flanagan N., Todd C., Dixon C., Mathews J.N., Sajantila A.,
Birch-Machin M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Isolate 3; MEDLINE=22572539; PubMed=12687585; Mundy N.I., Kelly J.; "Evolution of a pigmentation gene, the melanocortin-1 receptor,
                                                                                                                                            MSHR PANTR STANDARD; PRT; 317 AA.

O9TUK4; O864L1;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Melanocyte stimulating hormone receptor (MSH-R) (Melanotropin receptor) (Melanocotrin-1 receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ245705; CAB53398.1; -.
EMBL; AZ205086; AAP879050.1; -.
InterPro; IPR060276; GPGR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR06237; GPGRRHODPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00274; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00274; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00274; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Chimpanzee melanocortin 1 sequence.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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118
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163
183
132 ALLVPLAL 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9598;
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280
301
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinloch R.A., Ruiz-Seller B., Wassarman P.M.;

"Genomic organization and polypeptide primary structure of zona pellucida glycoprotein hzp3, the hamster sperm receptor.";

Dev. Biol. 142:414-421(1990).

-!- FUNCTION: Functions as a sperm-receptor. It is responsible for sperm-adhesion to the zona pellucida, and may contribute to th sperm-adhesion to the insemination.

-!- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1-
-!- SUBCELLULAR LOCATION: Type I membrane protein. Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
ZONA PELLUCIDA SPERM-BINDING PROTEIN
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Zona pellucida sperm-binding protein 3 precursor (Zona pellucida glycoprotein ZP3) (Sperm receptor) (Zona pellucida protein C).
ZP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00682; ZP_DOMAIN; 1.
Glycoprotein; Signal; Sulfation; Sperm; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: Oocytes.
-!- DEVELOPMENTAL STAGES: GROWING OOCYTES.
-!- PTM: Sulfated glycoprotein with O-linked oligosaccharides.
-!- SIMILARITY: Contains 1 ZP domain.
                                                                                                                                     Length 379;
                                                                                  43014 MW; 9C257CCAD5547F5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                            IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
     IRON-SULFUR (4FE-4S)
                                                                                                                                        DB 1;
                                                                                                                                  2.8%; Score 8; DB 1;
100.0%; Pred. No. 9.4;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          422 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZP.
PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus auratus (Golden hamster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001507; Endoglin/CD105.
Pfam; PF00100; zona pellucida; 1.
PRINTS; PR00023; ZPELUCIDA.
SMART; SM00241; ZP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91078540; PubMed=2257975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M63629; AAA37079.1; -.
                                                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
     333
336
340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
386
386
4422
4407
158
                                                                                                                                                                                                                                              217 LVDGVLAL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extracellular matrix.
                                                                                                                                                                                                                                                                                                       LVDGVLAL 42
                            336 3
340 3
379 AA;
                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
23
387
408
45
1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ZP3 MESAU
                                                           METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                    35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
ZP3_MESAU
                                                                                                                                                                                           Matches
     FFF8
                                                                                                                                                                                                                                                                                                                                                                                                                                          HERET THE THE TENT OF THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND T
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                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199; PubMed=8688087; te O., Olsen G.J., Zhou L., Fleischmann R.D., Iake O., Olsen G.J., Zhou L., Fleischmann R.D., Gocayne J.D., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Irkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Oghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Oberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., raser C.M., Smith H.O., Woese C.R., Venter J.C.; me sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4S ferredoxins.
TO THE BETA SUBUNIT OF M.THERMOAUTOTROPHICUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
(BY SIMILARITY).
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(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The iron-sulfur centers are similar to those of
                                                                                                                                     ;
0
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98; 4FE4S FERREDOXIN; 2.
rotein; Oxidoreductame; NAD; Electron transport;
S-palmitoyl cysteine (Potential) 6615D2146E1D247F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       imer of alpha and beta chains (By similarity).
                                                                               DB 1; Length 317;
                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58-1073 (1996). ACTIVITY: Formate + NAD(+) = CO(2) + NADH. Binds 2 4Fe-4S clusters (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 43, Last annotation update) dehydrogenase beta chain (EC 1.2.1.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rchaeota; Methanococci; Methanococcales; occaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Complete proteome.
280 IRON-SULFUR (4FE-4S) (283 IRON-SULFUR (4FE-4S) (290 IRON-SULFUR (4FE-4S) (330 IRON-SULFUR (4FE-4S) (
                                                                                                                                                                                                                                                                                                                                                                                 379 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                            2.8%; Score 8; DB 1
100.0%; Pred. No. 8;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01450; 4Fe4S_ferredoxin.
07525; FrhB_FdhB_C.
07516; FrhB_FdhB_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .A.
DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                      AA; 34699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FrhB FdhB C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB97986.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4Fe-4S
                                                                                                                                  nservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jannaschii.
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type 4Fe-48

286 290 330

rotein; (Fe-4S; Co 280

64300.

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SETTTTTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Our entry is copyright. It is produced through a collaboration Swiss Institute of Bloinformatics and the EMBL outstation - Bloinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this statement is not removed. Usage by and for commercial lires a license agreement (See http://www.isb-sib.ch/announce/nail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ^{	ext{a}} ). 
 TY: Belongs to the ABC transporter family. MsbA subfamily.
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOMEHOW INVOLVED IN THE CYTOCHROME D BRANCH OF AEROBIC LON. SEEMS TO BE A COMPONENT OF A TRANSPORT SYSTEM JARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., R., Bult C.J., Tomb J.-F., Dougherty B.A., Merzick J.M., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., itchman J.L., Fuhrmann J.L., Geoghagen N.S.M., AcDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AR LOCATION: Integral membrane protein. Inner membrane
(GLCNAC. .) (POTENTIAL).
                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oteobacteria; Gammaproteobacteria; Pasteurellales;
                                                                                                                       DB 1; Length 422;
                                                                                                                                                                   0; Indels
                                                                    -LINKED (GLUNAC. . .) (PC DOF95BE7FF8E7E01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0929; ABC_TMIF; 1.
0211; ABC_TRANSPORTER 1; 1.
0893; ABC_TRANSPORTER_2; 1.
Transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
2-binding protein cydC.
                                                                                                                       Score 8; DB 1; Pred. No. 10; 0; Mismatches
                                                                                                                                               10;
               N-LINKED (
N-LINKED (
N-LINKED (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R003593; AAA ATPase.
R001140; ABC TM_transpt.
R003439; ABC_transporter.
H; ABC membrane; 1.
S; ABC_tran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0006; ABC transporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XW20 / ATCC 51907;
0630; PubMed=7542800;
                                                                             45827 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   Rel. 32, Created)
                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; AAC22811.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sae; Haemophilus.
                                                                                                                         2.8%;
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         influenzae.
                                                                                                                                                                                                                                   |||||
3LGLA 393
                                                                                                                                                                                                           SLGLA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E64186.
                                                                                 AA;
                                                                                                                                             arity
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뒢줨윾잂튑몆뚑쑚쯩믕쯩죵헕뀵긂혍첉줥첉첉첉첉첉첉첉퍞퍞퍞夫용용당당당당당당당뚕뚕픙퓩퓩퓩퓩퓩퓩퓩퓩퓩퓩퓩퓩

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MEDLINE=20057165; PubbMed=10591208;

MEDLINE=20057165; PubbMed=10591208;

Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,

Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark C. Concy D., Corbley V.E., Cole C.G., Collier R.E., Connor R.,

Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson J.

Bhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.

Brans K.L., Fey J.M., Fleming X., Freench L., Garner A.A.,

Gilbert J.G.R., Goward M.E., Graffman D.V., Griffiths M.N.D., Hall

R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,

Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,

Martyn I.D., Mashreshi-Mohammadi M., Matthews L.H., Mccann O.T.,

Mcclay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.

Mcclay J., Mclaren S., McMurray A.A., Milne S.A., Mortimore B.J.

Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rosers L., Ross

Scott C.E., Spragon L., Steward C.D., Smalley S., Smith M.L.,

Sott C.E., Spragon L., Steward C.D., Smalley S., Smith M.L.,

Wuldin M., Wall M., Walls J.M., Whiteley M.N., Willey D.L.,

Wright C.L., Hubbard T., Bentley D.R., Rogers J., Shimi:
                                                                                                                                                                                                                                                                                                                                                                     GGT5_HUMAN STANDARD; PRT; 586 AA.

93269; Q96FC1; Q9UFM5;
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 42, Last annotation update)
Gamma-glutamyltransferase 5 (Gamma-glutamyltransferase-1ike activi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a human gamma-glutamyl cleaving enzyme relate
but distinct from, gamma-glutamyl transpeptidase.",
Proc. Natl. Acad. Sci. U.S.A. 88:6303-6307(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann S., Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heisterkamp N., Rajpert-De Meyts E., Uribe L., Forman H.J.,
                                                                                                                                                                           DB 1; Length 576; . 14;
                                                                                                                                        64831 MW; A9ACD8B9B294B1B3 CRC64;
                                                                                    POTENTIAL.
ABC TRANSPORTER
                                                                                                                                                                           Score 8; DB 1; Pred. No. 14; 0; Mismatches
                                                                                                                         (POTENTIAL
                                                 POTENTIAL.
                    POTENTIAL
                                    POTENTIAL
                                                                                                                                                              2.8%; Scur
100.0%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91296809; PubMed=1676842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A. (ISOFORM 2).
TISSUE=Fetal kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                              Conservative
 36
153
175
264
301
574
                                                                                                                                                                                                                                                                                159 PLALGIGL 166
                                                                                                                                        576 AA;
                                                                                                                                                                                        Local Similarity
Les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               58 PLALGLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
   16
133
133
155
155
244
244
338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTLA1 OR GGT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Groffen J.
                                                                                                       DOMAIN
NP BIND
SEQUENCE
                                   TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
                                                                                      TRANSMEM
                                                                                                                                                                           Query Match
                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                        GGT5_HUMAN
                                                                                                                                                                                                                                                                                                                                        RESULT 13
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S

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Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S., To L., Crabtree J., Deschamps S., Do A., Do T., Ig F., Chu L., Crabtree J., Deschamps S., Lai H., Lao H.I., Is S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., Join Y., Ray L., Ran Q., Shaull S., Sloan D., Song L., Y., Wang Z., White J., Willingham D., Wu H., Yao Z., J., Chissoe S., Murray J., Milliam D., Wu H., Bourne S., Z., Fulton L., Goela D., Graves T., Hawkins J., Z., Fulton L., Golla D., Graves T., Hawkins J., Z., Fulton L., Goela D., Graves T., Hawkins J., Z., Hallier E., Layman D., Ozersky P., Rohffing T., Iker C., Wamsley A., Mohldaman P., Pepin K., Nelson J., Iker C., Wangley A., Mohldaman P., Pepin K., Nelson J., Iker C., Mansley H., Shanon A., Wong A.C., Morrow B.E., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Shank H., Simon M.I., Dumanski J.P., Adra D., Seroussi E., Fransson I., Tapia I., Bruder C.E., Wilhison P., Bodenteich A., Hartman K., Hu X., Pace C. L., Millann Chromosome 22.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9-495 (1999)
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## N.A. (ISOFORM 1).

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Collins F.S., Wagner L.H., Derge J.G.,
Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Caeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Narusina K., Farmer A.A., Rubin G.M., Hong L.,
Soares M.B., Bonaldo M.F., Caeavant T.L., Scheetz T.E.,
T., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Juellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Vorley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
Wazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
On E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Jon E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Jon E., Ketteman M., Schwutz J., Myers R.M.,
Grimwood J., Schwutz J., Myers R.M.,
S.N., Kzzywinski M.I., Skalska U., Smailus D.E.,
Schein J.E., Jones S.J.M., Marra M.A.;
Initial analysis of more than 15,000 full-length
Se CDNA sequences.";
Ind initial analysis of more than 15,000 full-length
Se CDNA sequences.";
Cleaves the gamma-glutamyl peptide bond of glutathione
S, but maybe not glutathione itself. Converts
Is C. (111) Land Landylleng M. (111) Landylleng A. Artvivy. (4-11-11) Length
Levelleng M. (111) Length Levelleng M. Artvivy. (4-11-11) Length Levelleng M. Artvivy. (4-11-11) Length Levelleng M. Artvivy. (4-11-11) Length Levelleng M. Artvivy. (4-11-11) Length Levelleng M. Artvivy.
257; PubMed=12477932;
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# srnative splicing; Named isoforms=2; 36269-1; Sequence=Displayed;

Jeukotrieme metabolism; second step.

Heterodimer composed of the light and heavy chains.

Site is located in the light chain (By similarity).

REDCATION: Type II membrane protein (By similarity).

REPRODUCTS:

ACTIVITY: (5-L-glutamyl)-peptide + an amino acid = 5-L-glutamyl-amino acid.

36269-2; Sequence=VSP 008146; experimental confirmation available; Y: Belongs to the gamma-glutamyltransferase family. Ref.2 sequence differs from that shown due to a c in position 446.

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M64099; AAA588503.1;	RMBL; M64099, AAA89503.1;   RMBL; M64099, AAA89503.1;   RMBL; AAA1125.1;   AA1125.1;   A	AAA58503.1; - ; CAB55910.1; ALT FRAME. ; -; NOT ANNOTATED CDS.	GTLA1.	ntegral to membrane; TAS. amma-glutamyltransferase activity; TAS. mino acid meraholiam: TAS	nutathione metabolism; TAS.; Peptidase T3.	u transpept; 1. TRANSPTASE.	esis, Transferașe;	Zymogen; G	GAMMA-GLUIX CHAIN (BY 5 GAMMA-GLUIX CHAIN (BY 5	LASMI L-ANC	586 EXTRACELLULAR (POTENTIAL) 98 N-LINKED (GLONAC. ) (POTENTIAL)	04 N-LINKED (GLCNAC )	(GLCNAC ) ( (GLCNAC ) (	50 N-LINKED (GLCNAC) (Missing (in isoform 2).	/FTId=VSP 008146. 330 R -> K (IM REF. 2 AND 4). 408 N -> Y (IN REF. 2). 437 W -> R (IN REF. 2 AND 4). 62319 MW, 1BE543CB0934B16B CRC64;	2.8%; Score 8; DB 1; Length 586; 100.0%; Pred. No. 14; ative 0; Mismatches 0; Indels 0; G	8	1	ANDARD; PRT; 24 AA.  41, Created) 41, Last sequence update) 41, Last annotation update) 30 (copy) 30 (box) (Fragment).  (Octopus) A) Mollusca; Cephalopoda; Coleoidea; Neocoleoide.  Cotopoda; Incirrata; Octopodidae; Octopus.  N, AND MASS SPECTROMETRY.  Y, H.B.; Chiva M.;  11 ing and protamines during spermiogenesis of Octopoda)  12 00 2001)  12 coloul
	EMBL; M64 EMBL; ALI EMBL; ALI EMBL; ALI EMBL; ALI EMBL; BA1 PIR; A411 PIR; A411 PIR; A411 PIR; A411 PIR; A411 PIR; A411 GO; GO: 00 FEB-20 SPER-20	440	25; A41125. (20; T17220. (03.002; NC:4260; GGT	.68; 16021; C:int 103840; F:gam 106520: P:ami	106749; P:glu IPR000101;	1019; G glu R01210; GGTR	PS00462, G G ne biosynthe	ferase, Signa. ve splicing.	<b>⊣</b> 88		Ŋ	01.0	ካጥư	אטיי	₹ '	arity onserva	GLGLALA 6	61	STAN (Rel. 4 (Rel. 4 (Rel. 4 (Rel. 4) (Rel. 4) (Rel. 6 (Rel. 4 (Rel. 6

A into a highly condensed, stable and inactive

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Monodelphis domestica (Short-tailed grey opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                          01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-CCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                    49 AA.
                                                                                                                                                                                                                              Sperm protamine P1 (Cysteine-rich protamine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR000221; Protamine Pl. Pfam; PF00260; protamine Pl; 1. PROSITE; PS00048; PROTAMINE Pl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X61678; CAA43853.1; -
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                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIDMA
                                                                                 HSP1_SAGIM
P24714;
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                              RESULT
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                                                                           36; C:nucleosome; NAS.
34; C:nucleus; NAS.
77; F:DNA binding; NAS.
71; F:DNA binding; NAS.
71; F:DNA binding; NAS.
72; F:DNA binding; NAS.
74; P:nultotic chromosome condensation; NAS.
74; P:nultotic chromosome condensation; NAS.
74; P:nultotic chromosome condensation; NAS.
75; P:nultotic chromosome condensation; NAS.
76; P:nultotic chromosome condensation; NAS.
77; P:ppermatogenesis; NAS.
78; P:ppermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Cinucleus; NAS.
77; F:DNA binding; NAS.
01; P:chromosome organization and biogenesis (sen. . .; NAS.
76; P:mitotic chromosome condensation; NAS.
34; P:nucleosome assembly; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    emodelling and protamines during spermiogenesis of Octopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protamines substitute for histones in the chromatin of ring the haploid phase of spermatogenesis. They compact A into a highly condensed, stable and inactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea, es; Octopoda, Incirrata, Octopodidae, Octopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fe P., Ribes E., Buesa C., Sautiere P., Kouach M., sinsky H.E., Chiva M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.5%; Score 7; DB 1; Length 30; 100.0%; Pred. No. 9.3; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 24;
                                                                                                                                                                                                                                                                                 protein; Nucleosome core; Spermatogenesis; DNA condensation; Nuclear protein.
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DNA condensation; Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                   AA; 3381 MW; 308E90ED9D2C9C9C CRC64;
JAR LOCATION: Nuclear.
PECIFICITY: Testis.
TROMETRY: MW=4389; METHOD=Electrospray.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAR LOCATION: Nuclear.
PECIFICITY: Testis.
CTROMETRY: MW=3941; METHOD=Electrospray.
86; C:nuclessome; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 41, Last sequence update)
1. 41, Last annotation update)
P5 (Po5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.5%; Score 7; DB 1
100.0%; Pred. No. 7.7
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCTION, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83; P:spermatogenesis; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-ARG.
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MEDLINE=92051332; PubMed=1840669; Queralt R., Oliva R.; Queralt R., Oliva R.; Protamine I gene sequence from the primate Saguinus imperator isolated with PCR using consensus oligonucleotides."; Nucleic Acids Res. 19:5786-5786(1991).
-! FUNCTION: Protamines substitute for histones in the chromati sperm during the haploid phase of spermatogenesis. They comp sperm DNA into a highly condensed, stable and inactive compliance. SUBUNIT: Cross-linked by interchain disulfide bonds around t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL on the Bursopean Bioinformatics Institute. There are no restrictiouse by non-profit institutions as long as its content is indiffered and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch or send an email to license@isb-sib.ch).
Saguinus imperator (Emperor tamarin).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Sagui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-bindi
Testis; DNA condensation; Nuclear protein.
INIT MET 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.5%; Score 7; DB 1; Length 49; Best Local Similarity 100.0%; Pred. No. 14; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-helix (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- ILSUE SPECIFICITY: Testis.
-!- SIMILARITY: Belongs to the protamine P1 family.
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STUDINGE STORM N. A.

STUDINGE STORM N. A.

RA GARMS M. D., Celniker S. B., Holt R. A., Evans C. A., Gocayne J. D., Adams M. D., Celniker S. B., Holt R. A., Evans C. A., Galle R. F., Adams M. D., Celniker S. B., Holt R. A., Ends G., Chen L. K., Adams M. D., Celniker S. B., Holt R. A., Change M., Ffeifer B. B. Stradon G. G., Wortman J. R., Yandell M. D., Zhang Q., Chen L. K., Bardell M. D., Change M., Ffeifer B. B. Brandon R. C., Rogers Y. H. C., Black B. R. B. Handon C. R., Miklos G. L. Abril J. F., Agbayani A., An H. J., Andrews-Pfannkoch C., Baldwin B. P. Barlew R. M., Baan A., Baxendale J., Bayrakranglu L., Beasley B. M. Beeson K. Y. Bernos P. V. Bernan B. P., Bhandari D., Bolshakov S., Burtis K. C., Busam D. A., Butler H., Cadjeu E., Davise P., Butlis K. D. Bottham M. R., Bouck J., Brokstein P., Brottier P., Burtis K. C. Busam D. A., Butler H., Cadjeu E., Davise P., D.

Burtis K. C., Busam D. A., Butler H., Cadjeu E., Davise P., Burtis K. C. Busam D. A., Butler H., Cadjeu E., Davise P., D. Borthaw B. C., Rerraz C., Ferriera S., Fleischman R. B. Burtis N. J. Burtis M., A Downes M., Dugan-Rocha S., Dunkov B. C., Dunn Dodson K., Doup L. E., Downes M., Dugan-Rocha S., Dunkov B. C., Dunn Dodson K., Doup L. E., Downes M., Dugan-Rocha S., Dunkov B. C., Dunn Dodson K., J. Warnell J. H., Gu Z., Guan P., Harris M., A Houston K. J. Howland T. C., Merraz C., Ferriera S., Fleischman Foaler F., Kodire C. D., Kraft C., Kravitz S., Kulp D., Laiz Z., Liang Y., Lin X. Mount S.M., Muthel B., McIncosh T. C., McIced M., M., Muthel B., McIncosh T. C., McIced M., Markel B., McIncosh T. C., McIced M., Markel B. M. Muthy B., Murphy L., Muzny D.M., Nelson D.I. Merkulov G., Milshina N. V., Mobarry C., Morris J., Mount S. M., Moy M., Murphy B., Murphy L., Muzny D.M., Durik J., Shen H., Shue B. C., Siden-Kiamos I., Simpson M., Strong R., Sun B., Shiek B. C., Scalleron C., Scheeler F., Shriek B. R., Tector C., Turner R., Vonner B., Mang Z.-Y., Wassarman D.A., Weinstock G. M., Weisserhead G., Shen H., Shieb B. C., Morris J., Woldage T., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collibetween the Swiss Institute of Bioinformatics and the EMBL out: the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centifies requires a license agreement (See http://www.isb-sib.ch/cor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ZIM62H-12C, ZIM62H-16C, ZIM62H-28C, ZIM62H-30C, ZIM62H-34C ZIM6ZI-5C, ZIM62I-10C, ZIM62I-17C, ZIM62I-1BC, and ZIM62I-53C; MEDLINE=20556153; PubMed=11102381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MATED FEMALE FLIES. MAY CONTRIBUTE TO THE TOXICITY OF SEMINAL FLUID AND THE DECREASED LIFE-SPAN OF MATED FEMALES. MAY ALSO AFFECT NEUROMUSCULAR EVENTS AFTER MATING CONCERNING SPERM STOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Begun D.J., Whitley P., Todd B.L., Waldrip-Dail H.M., Clark A.G., "Molecular population genetics of male accessory gland proteins i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics 156:1879-1888(2000).
-!- FUNCTION: RESPONSIBLE FOR PHYSIOLOGICAL AND BEHAVIORAL CHANGE:
  genes for male accessory gland proteins in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- TISSUE SPECIFICITY: Seminal fluid.
-!- SIMILARITY: SOME, TO P.NIGRIVENTER TX2-6.
                                                   nsect Biochem. Mol. Biol. 27:825-834(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003475; AAF47683.1; -.
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                                                                                                    SEQUENCE FROM N.A.
                           melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Of entry is copyright. It is produced through a collaboration wiss institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                              Cajewski C., Westerman M., Winkfein R.J., Dixon G.H.; (Cajewski C., Westerman M., Winkfein R.J., Dixon G.H.; Jogeny and evolution of marsupial protamine Pl genes."; Lond., B. Biol. Sci. 259:7-14(1995).
Protamines substitute for histones in the chromatin of ing the haploid phase of spermatogenesis. They compact into a highly condensed, stable and inactive complex. R. LOCATION: Nuclear.
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                                                                                                                       Nishikawa S., Connor W., Dixon G.H., ion of a marsupial sperm protamine gene and its com the North American opossum (Didelphis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lanogaster (Fruit fly).
.azoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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brosophilidae; Drosophila.
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100.0%; Pred. No. 16;
ive 0; Mismatches 0; Indels
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S; TISSUE=Male accessory gland;
20; PubMed=9474779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 0 BY SIMILARITY.
AA; 7810 MW; 283715B280214E52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (: Belongs to the protamine P1 family.

    40, Last sequence update)
    42, Last annotation update)
    protein Acp62F precursor.

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                                                                                                  500; PubMed=8344286;
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lel. 40, Last seque
lel. 42, Last annot
ld protein Acp62F I
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7, 13616;
                                                                            upialis;
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왕<sup>5</sup> 양<sup>5</sup> 인근틱보본본동왕으로요중동당중종종

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8; AAG35367.1; -.
9; AAG35368.1; -.
0; AAG35370.1; -.
1; AAG35370.1; -.
2; AAG35371.1; -.
3; AAG35372.1; -.
4; AAG35374.1; -.
5; AAG35375.1; -.
7; AAG35375.1; -.
7; AAG35375.1; -.
7; F. Serine protease inhibitor activity; IDA.
10020509; Acp62P.
17; F. Serine protease inhibitor activity; IDA.
107; F. Serine protease inhibitor activity; IDA.
17; F. Serine protease inhibitor activity; IDA.
17; F. Serine protease inhibitor activity; IDA.
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100.0%; Pred. No. 30;
ive 0; Mismatches 0; Indels
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#### 118 AA. PRT; STANDARD;

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steobacteria; Gammaproteobacteria; Enterobacteriales;
Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 41, Last annotation update)
(Ment ISS very hypothetical 12 kDa protein.
                                                                                                                                                                                                  aceae; Escherichia
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### sequence of IS5 from Escherichia coli."; 1653; PubMed=6269959; Cahn M.; 74 (1981). 1 N.A.

van Bree M.P.; de sequence and protein-coding capability of the element IS5."; PubMed=6269958; 63 (1981)

Duncan M., Allen E., Araujo R., Aparicio A., Chung E., lerspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Roberts D., 1 N.A.

P-1996) to the EMBL/GenBank/DDBJ databases.

Mori H., Murayama N., Kataoka K., Yano M., Itoh T., Inokuchi H., Miki T., Hatada E., Fukuda R., Mizuno T., Makino K., Nakata A., Yura T., Sampei G., B-1996) to the EMBL/GenBank/DDBJ databases

1 N.A.

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MEDLINE=89093958; PubMed=2521353;
Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast derived inflammatory agents, growth factors, and indicators of various activation processes."; J. Immunol. 142:679-687(1989).
J. Immunol. 142:679-687(1989).
SYNERGIZES WITH ILZ IN REGULATING INTERFERON-GAMMA SYNTHESIS. MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONK
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collibrate the Swiss Institute of Bloinformatics and the EMBL out the European Bloinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in wordified and this statement is not removed. Usage by and for emitties requires a license agreement (See http://www.isb-sib.ch, or send an email to license@isb-sib.ch).
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01-FEB-1991 (Rel. 17, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Interleukin-13 precursor (IL-13) (T-cell activation protein P600
IL13 OR IL-13.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi.
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
MEDLINE=97251357; PubMed=9097039;
Alba H., Baba T., Fulita K., Hayashi K., Inada T., Isono K.,
Itoh T., Kasai H., Kashimoto K., Ximura S., Kitakwa M.,
Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
Motomura K., Makade S., Nakamura Y., Nabhimoto H., Nishio Y.,
Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
Yamamoto Y., Horiuchi T.,
"A 570-kb DNA sequence of the Escherichia coli K-12 genome
orresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J01734; -; NOT ANNOTATED CDS.
EMBL; U70214; AAB08601; -
EMBL; U70214; AAB08601; -
EMBL; D90771; BAA14925.1; -
EMBL; D90772; BAA14935.1; -
EMBL; D90841; BAA15715.1; -
EMBL; D90841; BAA15958.1; -
EMBL; D90848; BAA15958.1; -
EMBL; D90848; BAA15963.1; -
EMBL; D90848; BAA15963.1; -
EMBL; D90848; BAA15963.1; -
EMBL; D90848; BAA15963.1; -
EMBL; D90848; BAA15963.1; -
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EMBL; D90848; BAA15963.1; -
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EMBL; B90848; BAA159648; -
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-!- SIMILARITY: Belongs to the IL-4 / IL-13 family.
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Matches 7; Conservative
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P20109;
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguch Aoki K.-I., Yoshizawa T., Nakamira Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;
Complete sequence and gene organization of the genome of a hyper thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
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Pyrococcus.
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N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

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N-LINKED (GLCNAC. . .) (POTENTIAL).
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TRANSMEM 41 61 POTENTIAL.
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14093 MW; E5008CAB8DE8C201 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein PH2001.
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100.0%; Pred. No. 34;
--ive 0; Mismatches
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BY SIMILARITY.
INTERLEUKIN-13
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                             Interpro; IPR003634; Interleukin 13.
InterPro; IPR001325; Interleukin 4 13.
Pfam; PF03487; Interleukin 13; 1.
ProDom; PP015887; Interleukin 13; 1.
                                                                                                                                                                       SMART; SM00190; IL4 13; 1.
PROSITE; PS00838; INTERLEUKIN 4 13; 1.
Cytokine; Glycoprotein; Signal.
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EMBL; AP000007; BAA31940.1; JOINED.
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Best Local Similarity 100..
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131 AA;
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   HSSP; P35225; 31TR
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CARBOHYD
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CYTOKINE INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
IN HILL IN REGULATING INTERFERON-GAMMA SYNTHESIS.
ITCAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES.
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sl. 36, Last annotation update)
precursor (IL-13) (T-cell activation protein P600)
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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BY SIMILARITY.
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100.0%; Pred. No. 34;
ive 0; Mismatches
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03634; Interleukin 13.
01325; Interleukin 4 13.
Interleukin 13; 1.
87; Interleukin 13; 1.
; IL4 13; 1.
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|38; INTERLEUKIN_4_13; 1.
|oprotein; Signal.
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Truet E.N.;
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E52290.
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2.5%; Score 7; DB 1; Length 147;

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                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine that binds to LTBR/TNFRSF3. May play a specific mmune response regulation. Provides the membrane anchor trachment of the heterotrimeric complex to the cell
                 Gaps
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Rel. 41, Last annotation update)
eta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heterotrimer of either two LTB and one LTA subunits or valent) two LTA and one LTB subunits. AR LOCATION: Type II membrane protein (By similarity). Y: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                               ogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,
                                                                                                                                                                                                                                                                  tazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
heria; Cetartiodactyla; Suina; Suidae; Sus.
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AA; 16423 MW; FE5C4CC657658B48 CRC64;
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  Pred. No.
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white; TISSUE=Fibroblast;
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                0;
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                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYC 200
                                        GLL 73
                                                                   dil 51
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ORIGEN MANANAN AN AND COULD COULD COULD COULD THE PRODUCE AND MANANAN AN AND COULD C

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MEDLINE=93144699; PubMed=7678765; MEDLINE=9314699; PubMed=7678765; Madchi T., Izumi H., Yamada T., Tanaka K., Takeuchi S., Adachi T., Izumi H., Yamada T., Tanaka K., Matsuda T.; Ramanura R., Matsuda T.; Research T., Tanaka T., Matsuda T.; "Gene structure and expression of rice seed allergenic proteins belonging to the alpha-amylase/trypsin inhibitor family."; Plant Mol. Biol. 21:239-248(1993).

-1- PTM: Five disulfide bonds are present (By similarity).
-1- ALLERGEN: Canaes an allergic reaction in human.
-1- SIMILARITY: Belongs to the cereal trypsin/alpha-amylase inhik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ö
                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enthartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a coll between the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is ir modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch. or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Histone-like protein HiP-1 precursor (DNA-binding 17 kDa protein)
HLPA OR SKP OR OMPH OR B0178 OR C0215 OR Z0190 OR ECS0180 OR SF01
OR S0171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
RA05_ORYSA STANDARD; PRT; 157 AA. 2018E1; 01-UN-1994 (Rel. 29, Created) 10-UN-1994 (Rel. 29, Last sequence update) 10-OCT_2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%; Score 7; DB 1; 00.0%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. ....
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                                                                                                                                             Seed allergenic protein RAS precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003612; AAI.
InterPro; IPR006106; Amylase inhib.
InterPro; IPR066106; Try/amyl inhib.
Pfam, PF00234; tryp_alpha_amyl; 1.
SMRAT; SM00499; AMIASEINHBTR.
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HSSP; P01085; 1HSS.
Gramene; Q01881; -.
                                                                                                                                                                                                     Oryza sativa (Rice).
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Escherichia coli 06,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4530;
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EMBL;
     N.A.
; STRAIN=K12 / W3110;
fori H., Murayama N., Kataoka K., Yano M., Itoh T.,
nokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S.,
ino K., Nakata A., Yura T., Sampei G., Mizobuchi K.;
quencing of the Escherichia coli genome: analysis of the (189,987 - 281,416pp) region.";
1-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "STRAIN=0157:H7 / RIMD 0509952;
31; PubMed=11258796;
Rino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., subo E., Nakayama K., Murata T., Tanaka M., Tobe T., i H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., ib T., Hattorii M., Shinagawa H.; me sequence of enterohemorrhagic Escherichia coli momic comparison with a laboratoxy strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ## STRAIN=O6:HI / LELVIN, | STRAIN=O6:HI / LELVIN, | STRAIN=O6:HI / LELVIN, | STRAIN=OF | STRAIN=OF | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | STRAIN | 
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12 / MG1655;
117; PubMed=9278503;
Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
ado-Vides G., Glasner J.D., Rode C.K., Maybew G.F.,
is N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                    sequencing of the gene for the DNA-binding 17K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ncan M., Allen E., Araujo R., Aparicio A., Chung E., rspiel N., Hyman R., Kalman S., Komp C., Kurdi O., ew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ice of enterohaemorrhagic Escherichia coli 0157:H7.";
)-533(2001).
                                                           eobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=0157:H7 / EDL933 / ATCC 700927;
US5; PubMed=11206551;
Unkett G. III, Burland V., Mau B., Glasner J.D.,
hew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
kett J., Klink S., Boutin A., Shao Y., Miller L.,
Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Antharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                      N.A., AND SEQUENCE OF 21-40.
                                                                                                                217992, 83334, 623;
                                                                                                                                                                                                                           35; PubMed=2843433;
                                                                                   Escherichia.
li 0157:H7, and
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FEBS Lett. 262:123-126 (1990).
-!- SUBGILLIA. Homotetramer.
-!- SUBGELLULAR LOCATION: BITHER IN THE NUCLEOID (CHROMATIN) OR II THE OUTER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE OMPH/HLPA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=E.coli; STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646;
Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties of proteins encoin the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collabrate the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for or entities requires a license agreement (See http://www.isb-sib.ch/eor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=S.flexneri; STRAIN=301 / Serotype 2a; MEDLINE=22272406; PubMed=12384590; Since Y. Yana Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liù H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S. Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of Shigella flexneri 2a: insights into pathogenic through comparison with genomes of Escherichia coli K12 and O157. Nucleic Acids Res. 30:4432-4441 (2002).
                                                                                                                                                                                                                                   the firA gene and the firA200
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SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed-12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Maybew G.F., Plunkett G. III, Rose D.J., Darling A.,
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.,
"Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T";
Infect. Immun. 71:2775-2786(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hirvas L., Coleman J., Koski P., Vaara M.;
"Bacterial 'histone-like protein I' (HLP-1) is an outer membrane
                                                                     SEQUENCE OF 72-161 FROM N.A.
SPECIES-E.coli; STRAIN=K12 / MG1655;
MEDLINE=91100302; PubMed=1987124;
                                                                                                                                                                                  Dicker I.B., Seetharam S.R.;
"Cloning and nucleotide sequence of
allele from Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90201355; PubMed=2318304;
                                                                                                                                                                                                                                                                                                                Bacteriol. 173:334-344(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE016755; AAN78707.1; -. AE005194; AAG54480.1; -. AP002550; BAB33603.1; -.
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X75465; CAA53207.1; -.
AE015054; AAN41830.1; -.
AE016978; AAP15711.1; -.
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EMBL; AE000127; AAC73289.1; -
EMBL; D8354; BAA77853.1; -.
EMBL; U70214; AAB08607.1; -.
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE016978; AAP1
PIR; D85502; D85502
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 21-32.
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180 AA

D90651

ALA 68 ALA 15

arity

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TISSUE=Mammary gland;
MEDLINE=99304500; PubMed=10376212;
Das P., Jain S., Nayak S., Apparao K.B.C., Totey S.M., Garg L.C.,
"Molecular cloning and sequence analysis of the cDNA encoding
beta-lactoglobulin in Bubalus bubalis.";
DNA Seq. 10:105-108(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kolde H.-J., Liberatori J., Braunitzer G.;
"The amino acid sequence of the water buffalo beta-lactoglobulin milchwiseanschaft 36:89-86[1981].

Milchwiseanschaft 36:89-86[1981].

Milchwiseanschaft J. Si8-86[1981].

Milchwiseanschaft J. Si8-86[1981].

Milchwiseanschaft J. Si8-86[1981].

Milchwiseanschaft J. Si8-86[1981].

Milchwiseanschaft J. Signature of that molecule as an equilibrium mixture of monomeric and dimeric forms.

SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch. or send an email to license@isb-sib.ch).
                                                                                                                                                                 Bubalus bubalis (Domestic water buffalo).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: Synthesized in mammary glound and secret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: Alternate disulfide bonds occur in equal amounts.
-!- SIMILARITY: Belongs to the lipocalin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transport; Lipocalin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5%; Score 7; DB 1; Length 180; 100.0%; Pred. No. 45; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6836C97B2C2E33CF CRC64;
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                                   P02755, 062822,
21-JUL-1986 (Rel. 01, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
18-FRA-2004 (Rel. 43, Last annotation update)
Beta-lactoglobulin precursor (Beta-LG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATE
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InterPro, IPR002345, Lipocalin.
InterPro, IPR000566, Lipocin_cytFABP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00061; lipocalin; 1.—"
PRINTS; PR00179; LIPOCALIN; 1.
PROSITE; P800213; LIPOCALIN; 1.
Milk; Whey; Retinol-binding; Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20023 MW;
                                                                                                                                                                                                                                    Bovidae; Bovinae; Bubalus.
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Best Local Similarity 100...
7; Conservative
                    STANDARD;
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SEQUENCE OF 19-180.
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                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      NCBI_TaxID=89462;
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ID LACB CAPHI
AC P02756;
                    LACE BUBBU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nscough R., Anderson K., Baynes C., Berks M.,
Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bear S., Du Z., Durbin R., Favello A., Fraser A.,
troher A., Green P., Hawkins T., Hillier L., Jier M.,
Jones M., Kershaw J., Kirsten J., Laisster N.,
Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
don N., Smith A., Saunders D., Shownkeen R.,
don N., Smith A., Smith M., Sonnhammer E., Staden R.,
hierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Matson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ntiguous nucleotide sequence from chromosome III of C.
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                                                                                                  HISTONE-LIKE PROTEIN HLP-1.
2A966BBD83F3E675 CRC64;
                                                          Outer membrane; Signal; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein D2007.4 in chromosome III.
                                                                                                                                                                 2.5%; Score 7; DB 1;
100.0%; Pred. No. 41;
tive 0; Mismatches
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Rel. 28, Last sequence update)
Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1718; PubMed=7906398;
                                                                                                                        AA; 17688 MW;
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               005632; OmpH.
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                                                                                                                                                                                                           onservative
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455; hlpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s elegans.
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RCL 100 RCL 227

protein.

844789

180 AA

N.A.

O

Goat).

N.A.

N.A.

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SPECIES=Sheep;
MEDLINE=91007276; PubMed=1976573;
Ali S., McClenaghan M., Simons J.P., Clark A.J.;
"Characterisation of the alleles encoding ovine beta-lactoglobuli; and B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=Sheep;
MEDLINE=89374823; PubMed=2775495;
Brhardt G., Godovac-Zimmermann J., Conti A.;
"Isolation and complete primary sequence of a new ovine wild-type beta-lactoglobulin C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harris S., Ali S., Anderson S., Archibald A.L., Clark A.J.; "Complete nucleotide sequence of the genomic ovine beta-lactoglob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Ovine beta-lactoglobulin messenger RNA: nucleotide sequence and levels during functional differentiation of the mammary gland."; Biochimie 68:1097-1107(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of the gene encoding ovine beta-lactoglobulin. Similarity to the genes for retinol binding protein and other secretory proteins.";
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0
                        Indels
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MEDLINE=80219294; PubMed=6155855;
Preaux G., Braunitzer G., Kolde H.-J.;
"Primary structure of ovine beta-lactoglobulin.";
Arch. Int. Physiol. Biochim. 88:845-846(1980).
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0
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100.0%; Prec. ....
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                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=Sheep;
MEDLINE=88172489; PubMed=3351935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89057492; PubMed=3194215;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (BLG 1 AND 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Mol. Biol. 199:415-426(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (BLG 1).
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SEQUENCE OF 19-180 (BLG B)
      Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                       STANDARD;
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                                                       63 LGLALAC 69
                                                                                   8 LGLALAC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ali S., Clark A.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or entry is copyright. It is produced through a collaboration wiss Institute of Bioinformatics and the EMBL outstation-Bioinformatics Institute. There are no restrictions on its profit institutions as its content is in no way this statement is not removed. Usage by and for commercial res a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Under physiological conditions beta-lactoglobulin exists librium mixture of monomeric and dimeric forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       •R LOCATION: Secreted.
SCIFICITY: Synthesized in mammary glound and secreted
                                                                                                      azoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Neria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unitzer G., Schrank B., Stangl A.;
d sequence of goat beta-lactoglobulin.";
7. Physiol Chem. 360:1595-1604(1979).
Primary component of whey, it binds retinol and is nvolved in the transport of that molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                         . A., Sanchez A.;
nence of the caparine beta-lactoglobulin gene.";
7:3483-3497(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nate disulfide bonds occur in equal amounts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               etinol-binding; Transport; Lipocalin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.5%; Score 7; DB 1; Length 180;
                                                                                                                                                                                                                                                                                                                                      , Kim J., Yu M.;
1-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                       >11 A., Sanchez A.;
sequencing of the cDNA encoding goat beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2449BB02A1A80F1 CRC64;
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   :el. 01, Created)
161. 22, Last sequence update)
161. 43, Last annotation update)
wlin precursor (Beta-LG).
                                                                                                                                                                                                        gagrus; TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          il to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              002345; Lipocalin.
                                                                                                                                                                                                                        59; PubMed=8226387;
                                                                                                                                                                                                                                                                                                                                                                                                                         151; PubMed=7699130;
                                                                                                                                                                                                                                                                                        71:2832-2832 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=511095;
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213; LIPOCALIN; 1.
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CAA79624.1; -.
CAA83946.1; -.
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lipocalin;

AAA31510.1 AAA31510.1

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CAA28204.1;

STANDARD;

2.5%;

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139 38

Conservative

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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wai Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K. Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C. Quall MA., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                SPECIES=S.typh; STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyiami V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strain
and CT18.";
J. Bacteriol. 185:2330-2337(2033).
-!-FINCTION: May be part of a membrane complex involved in elect
transport (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBDNIT: Composed of at least six subunits; rnfA, rnfB, rnfC, rnfD, rnfE and rnfG (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a coll between the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction web by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Electron transport, Transmembrane, Inner membrane, Complete prote
TRANSMEM 34 56 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24318 MW; E198B4CEA13F249E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
-:- SIMILARITY: Belongs to the nqrDE/rnfAE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Electron transport complex protein rnfE.
Escherichia coli 0157:H7.
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                    MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE008763; AAL20376.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE016838; AA068972.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            StyGene; SG????; rnfE.
HAMAP; MF 00478; -; 1.
InterPro; IPR003667; Rnf_Ngr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
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                                                                                                                                                                                                                                                               Nature 413:848-852(2001)
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183 2
230 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALGLGLA 44
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Best Local Similarity
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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RNFE ECO57
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      CSGNET
                                                                                                                                                                                                                                                                                                                       OT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation-Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial ires a license agreement (See http://www.isb-sib.ch/announce/ail to license@isb-sib.ch).
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                                                                                                                                                                                                                    ACTIVITY: Formyl-L-methionyl peptide + H(2)0 = formate +
                                             equence of Bifidobacterium longum reflects its adaptation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       948; PubMed=11677609; Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Iquyen C., Scott K., Holmes A., Grewal N., Mulvaney B., H., Florea L., Miller W., Stoneking T., Nhan M., Wilson R.K.; ome sequence of Salmonella enterica serovar Typhimurium
                                                                                                          Removes the formyl group from the N-terminal Met of thesized proteins. Requires at least a dipeptide for an rate of reaction. V-terminal L-methionine is a ite for activity but the enzyme has broad specificity at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               teobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                   f: Belongs to the polypeptide deformylase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       himurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.5%; Score 7; DB 1; Length 217;
100.0%; Pred. No. 53;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               844; Pep_deformylase; 1.
nthesis; Hydrolase; Iron; Complete proteome.
ilen M.-C., Desiere F., Bork P., Delley M.,
Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24443 MW; 52F5B469B6F47163 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
                                                                 Jastrointestinal tract.";
cad. Sci. U.S.A. 99:14422-14427(2002)
                                                                                                                                                                                                                                                               Binds 1 iron(II) ion (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rel. 41, Created)
Rel. 41, Last sequence update)
Rel. 42, Last annotation update)
sport complex protein rnfE.
54 OR STY1668 OR T1322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63; -; 1.
000181; Fmet_deformylase.
                                                                                                                                                                                             tions (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pep_deformylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; AAN24991.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76; PDEFORMYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phimurium, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   onservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2-856 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                        Arigoni
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ALA 68

N.A.

AA;

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231 AA

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MEDLINE=812 / JM109;

MEDLINE=99342054; PubMed=10411911;

MEDLINE=99342054; PubMed=10411911;

MEDLINE=99342054; PubMed=10411911;

Mallin E., von Heijne G.;

"Divergent evolution of membrane protein topology: the Escherich coli RnfA and RnfE homologues.";

"Divergent evolution of membrane complex;

-!- FUNCTION: May be part of a membrane complex involved in electransport (By similarity).

-!- SUBUNTION: May be part of a least six subunits; rnfA, rnfB, rnfC, rnfD, rnfE and rnfG (By similarity).

-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction when by non-profit institutions as long as its content is impositied and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Moromura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Y. Horiuchi T., Yamamoto Y., Horiuchi T., Yamamoto Y., Horiuchi T., Yamamoto B., Masamoto Y., Horiuchi T., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamoto S., Nasamo
                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                         MEDIJINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland
Kiley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Electron transport; Transmembrane; Inner membrane; Complete prot
DOMAIN 1 38 PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Potential).
-!- SIMILARITY: Belongs to the nqrDE/rnfAE family.
                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Electron transport complex protein rnfE.
RNFE OR B1632.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97251357; PubMed=9097039;
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HAMAP; MF 00478; -; 1.
InterPro; IPR003667; Rnf_Ngr.
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02508; Rnf-Ngr;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
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                                                                                                                                                                                                 Escherichia coli
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60
63
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     RNFE ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
TRANSMEM
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     NoT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial lires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAXIO K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., tsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., inh H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., inba T., Hattori M., Shinagawa H.; some sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            May be part of a membrane complex involved in electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                slattner F.R.;
snce of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                           Slunkett G. III, Burland V., Mau B., Glasner J.D., sybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., ickett J., Klink S., Boutin A., Shao Y., Miller L., Davis N.W., Lim A., Dianlanta E.T., Potamousis K., Mantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : (By similarity).
Composed of at least six subunits; rnfA, rnfB, rnfC,
Es and rnfG (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comparison with a laboratory strain K-12.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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CYTOPLASMIC (POTENTIAL).
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PERIPLASMIC (POTENTIAL).
POTENTIAL.
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                                                                                                                  EDL933 / ATCC 700927;
                                                                               1 N.A.
17 / EDL933 / ATCC 7009
1935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 / RIMD USUSSE,
5231, PubMed=11258796,
  aceae; Escherichia.
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2003667; Rnf Ngr.
3; Rnf-Ngr; ī.
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LGLA 66

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38 59 62

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MEDLINE=21470413; PubMed=11586360; MEDLINE=21470413; PubMed=11586360; MEDLINE=214704113; PubMed=11586360; MEDLINE=214704113; Withouson N.E., Titball R.W., Holden M.T.G. Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L. Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M. Chillingworth T., Cronin A., Davies R.W., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Genome sequence of Yersinia pestis, the causative agent of plagu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                          2.5%; Score 7; DB 1; Length 233;
100.0%; Pred. No. 56;
live 0; Mismatches 0; Indels
                                                                                                                                                                                    A -> T (IN REF. 1).
; IAllCB5FD960784F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., N
Berna N.T., Rose D.J., Mau B., Zhou S., Schwartz /
Fetherston J.D., Lindler L.E., Brubaker R.R., Pla
Straley S.C., McDonough K.A., Nilles M.L., Matsor
Perry R.D.; Adenome sequence of Yersinia pestis KIM.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 184:4601-4611(2002).
-!- FUNCTION: May be part of a membrane completransport (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: Composed of at least six subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Belctron transport complex protein rnfE.
RNFE OR YFO2240 OR Y2081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rnfD, rnfE and rnfG (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane ?

    -!- SIMILARITY: Belongs to the ngrDE/rnfAE <sup>f</sup>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is
Pfam; PF00035; dsrm; 1.
Pfam; PF00636; Ribonuclease_3; 1.
                                                                                                                                                                    204 220 D
116 116 A
233 AA; 26199 MW;
                                                                                                                                                                                                                            Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                164 ARRLPLP 170
                                                                                                                                                                                                                                                                                                                            10 ARRLPLP 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              YERPE
                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8ZED4;
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                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Off entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation-Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial ires a license agreement (See http://www.isb-sib.ch/announce/ail to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jad. Sci. U.S.A. 100:5455-5460(2003).
Digests double-stranded RNA. Involved in the processing nal RNA precursors and of some mRNAS (By similarity).
ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR LOCATION: Cytoplasmic.

Y: Contains 1 DRBM (double-stranded RNA-binding) domain.

Y: Contains 1 RNase III domain.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paulsen I.T., Bisen J.A., Read T.D., Nelson K.E., Vard N.L., Tettelin H., Davidsen T.M., Beanan M.J., augherty S.C., Brinkac L.M., Madupu R., Dodson R.J., Samuel J.B., Faraser C.M., Heidelberg J.F., ome sequence of the Q-fever pathogen, Coxiella
                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :eobacteria, Gammaproteobacteria, Legionellales;
Coxiella.
                                                                                                                                                                      DB 1; Length 231;
                                                                                                                                                                                                          0; Indels
                                                                                                                                  CFA37A2D292604C3 CRC64;
                                                                        PERIPLASMIC (POTENTIAL).
PERIPLASMIC (POTENTIAL)
                                    CYTOPLASMIC (POTENTIAL).
                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /51; PubMed=7830573;
/or TA., Powell B.S., Court D.L.;
ihe rnc locus of Coxiella burnetii.";
L. 14:291-300(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                          lel. 42, Last sequence update)
lel. 42, Last annotation update)
II (EC 3.1.26.3) (RNase III).
                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                    233 AA
                                                                                                                                                                    2.5%; Score 7; DB 1
100.0%; Pred. No. 56;
ive 0; Mismatches
                                                                                        POTENTIAL.
                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ile phase I / RSA 493;
557; PubMed=12704232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04; -; 1.
001159; DS_RBD.
000999; RNASe_III.
                                                                                                                                                                                                                                                                                                                                                                                                                          Rel. 34, Created)
                                                                                                                                24459 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; AAO91000.1;
S60767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA69690.1; -
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حح

pg 36

0

Conservative

LGLA 44 LGLA 66

148

554555556655666

STANDARD;

influenzae

KW20

I64174.

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MEDLINE=20165223; PubMed=10700230;
Tamada K., Shimozaki K., Chapoval A.I., Zhu G., Sica G., Flies C.
Boone T., Hsu H., Fu Y.-X., Nagata S., Ni J., Chen L.;
"Modulation of T-cell-mediated immunity in tumor and graft-versu disease models through the LIGHT co-stimulatory pathway.";
Nat. Med. 6:283-289(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal liver;

MEDLINE=20354998; PubMed=10894944;

Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;

Misawa I., Mosaka T., Kojima T., Hirai M., Kitamura T.;

"Molecular cloning and characterization of a mouse homolog of hu
TNFSF14, a member of the TNF superfamily.";

Cytogenet. Cell Genet. 89:89-91(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLOSOBLE DYMPHICATED TO THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS OF THE ADDRESS 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                      membrane; Complete prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteolytic processing.
-:- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \mbox{similarity}).
-!- PTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                  Length 235;
                                                                                                                                                                                                                                                            C054FE596647837A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tumor necrosis factor ligand superfamily member 14.
                                                                                                                                                                                                                                                                                                                     DB 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 AA.
                                                                                                                                                                                                                                                                                                                                                  57;
                                                                                                                                                                                                                                                                                                                  2.5%; Score 7; DB 1
100.0%; Pred. No. 57;
ative 0; Mismatches
                                                                                         Electron transport; Transmembrane; Inner
                                                                                                                   POTENTIAL.
                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                            25845 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
HAMAP; MF_00478; -; 1.
InterPro; IPR003667; Rnf_Ngr.
Pfam; PF02508; Rnf-Ngr; I.
                                                                                                                                                                                                                                                                                                                                                                             7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                     60 ALGLGLA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 ALGLGLA 68
                                                                                                                                                                                                                                                            235 AA;
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFSF14 OR LIGHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lymphoma;
                                                                                                                                                                                                 152
206
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                                                                                                                                              TRANSMEM
                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                TRANSMEM
                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        090YH9;
                                                                                                                                                                                                                                                                                                                                                                             Matches
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     DR RY ET TT TE SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation-Bioinformatics Institute. There are no restrictions on its -profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial uires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                random sequencing and assembly of Haemophilus influenzae
                                                                                                                      Aborn...
300367; Rnf Ngr.
9; Rnf-Ngr; 1.
1sport; Transmembrane; Inner membrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., R., Bult C.J., Tomb J.-F., Dougherty B.A., Marrick J.M., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Phillips C.A., Sprigs T., Hedblom E., Cotton M.D., R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496-512(1995).

May be part of a membrane complex involved in electron t (By similarity).

Composed of at least six subunits; rnfA, rnfB, rnfC, fE and rnfG (By similarity).
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oteobacteria; Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
491E18F335E8CB90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TY: Belongs to the ngrDE/rnfAE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
nsport complex protein rnfB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7; DB 1; ; Pred. No. 56; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mail to license@isb-sib.ch).
nail to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0630; PubMed=7542800;
                                                     51; CAC91046.1; -. 10; AAM85645.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                  24587 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / ATCC 51907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.5%; £
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; AAC23334.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAINER / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soctt J.D., Shirliey R., Lu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a coll between the Swiss Institute of Bioinformatics and the EMBL out the Buropean Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centities requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 269:496-512(1995)
-!- PUNCTION: INVOLVED IN BIOSYNTHESIS OF A DEMOLYBDO COFACTOR (MOLYBDOPTERIN), MECESSARY FOR MOLYBDOBNZYMES. PLAYS A ROLE I ACTIVATION OF THE SMALL SUBUNIT OF THE MOLYBDOPTERIN CONVERTI FACTOR (MOLD) (BY SIMILARITY).
-!- PATHWAY: MOLYBDOPM COFACTOR biosynthesis.
-!- SIMILARITY: BELONGS TO THE HESA/MOEB/THIF FAMILY.
                                                                                                                                                                                                                                                          Electron transport; Transmembrane; Inner membrane; Complete prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole-genome random sequencing and assembly of Haemophilus influ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                 2.5%; Score 7; DB 1; Length 240; 100.0%; Pred. No. 58; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                          25794 MW; 3D90687ED462D8B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Molybotperin biosynthesis protein moeB.
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 AA
                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                          EMBL; AE004770; AAG06882.1; -.
                                                                                                                                                                                                 HAMAP, MF 00478; -; 1.
InterPro; IPR003667; Rnf Ngr.
Pfam; PF02508; Rnf-Ngr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                 115
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
T; Conserve
                                                                                                                                                                               G83208; G83208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 ALGLGLA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 ALGLGLA 46
                                                                                                                                                                                                                                                                                                                                                                          240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOEB HAEIN
                                                                                                                                                                                                                                                                                                                                       TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOEB_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 40
    8
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0
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                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                   MEMBER 14, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   May be part of a membrane complex involved in electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composed of at least six subunits; rnfA, rnfB, rnfC, E and rnfG (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ceobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.5%; Score 7; DB 1; Length 239;
100.0%; Pred. No. 58;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217874AC71AD6BE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          MEMBER 14, SOLUBLE FORM.
                                                                                                                                                                                                                                                                                             asmembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLEAVAGE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1). Y: Belongs to the ngrDE/rnfAE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rel. 41, Created)
Rel. 41, Last sequence update)
Rel. 41, Last annotation update)
sport complex protein rnfE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                        251; TNF 1; FALSE NEG. 049; TNF 2; 1
                                                                                           006053; TNF abc.
006052; TNF family.
008983; TNF like.
003636; TNF subf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By Bimilarity).
  5; AAF76453.1; -. 5; BAA88559.1; -. 3; AAF36722.1; -.
                                                                                                                                                                                           34; INECROSISFCT.
012; INF subf; 1.
7; INF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26338 MW;
                                                                             Tnfsf14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathogen.";
9-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N.A.
5692 / PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  onservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                                                                                        239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eruqinosa.
                                                                                                                                                                                                                                                                                                                                                                                            37
                                                                                                                                                                               ; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AA;
                                                                                                                                                                                                                                                                                                                                                      32
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Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung Miyamoto K.E., Nguyen C.P., Nguyen D.A., Pool C.L., Robertson P. Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Cytokine that binds to LTBK/TRERSF3. May play a sprola in immune response regulation. Provides the membrane and for the attachment of the heterotrimeric complex to the cell surface. Isoform 2 is probably non-functional.

-!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits (less prevalent) one LTB and two LTA subunits.

-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL ou the European Bioinformatics Institute. There are no restrictio week by non-profit institutions as long as its content is i modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELULAR (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
GLVTETADPGAQAQGLGFQKLPEE -> GLGFRS
                                                                                   Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL-ANCHOR (TYPE-II MEMBRANE PRO
[6] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS GLU-70 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q06643-2; Sequence=VSP_006441, VSP_006442; -: TISSUE SPECIFICITY: Spleen and thymus. -: SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Glycoprotein; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing, Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 600978; -
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0005102; F:roxin activity; NAS.
GO; GO:0007267; F:toxin activity; NAS.
GO; GO:0007267; F:toxin activity; NAS.
GO; GO:0007165; F:signal transduction; TAS.
InterPro; IPR006053; TNF_anci.
InterPro; IPR008983; TNF_anci.
InterPro; IPR008983; TNF_ike.
InterPro; IPR008983; TNF_ike.
Fram; PF00229; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF subf; 1.
SWART; SW00207; TNF; 1.
PROSITE; PS00251; TNF 1, 1.
PROSITE; PS00251; TNF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q06643-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, L11016; AAA99888.1; -
EMBL, U89922; AA651769.1; -
EMBL, U79029; AAB37342.1; -
EMBL, L11015; AAA36191.1; -
EMBL, X14768; CAA75069.1; -
EMBL, X470656; AAD108089.1; -
EMBL, AX070219; AAL49955.1; -
EMBL, AX070219; AAL49955.1; -
EMBL, AX070219; AAL49955.1; -
EMBL, AX070219; AAC93134.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A46066; A46066.
PIR; JC5645; JC5645.
HSSP; P01374; ITNR.
Genew; HGNC:6711; LTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
222
53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytokine;
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CARBOHYD
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amiya G., Oka A., Inoko H.;
s 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
EP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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(Rel. 29, Last sequence update)
(Rel. 43, Last annotation update)
seta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor cor ligand superfamily member 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ion of two lymphotoxin beta isoforms expressed in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stazoa, Chordata, Craniata, Vertebrata, Euteleostomi, .heria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Ngam-Ek A., Lawton P., Demarinis J., Tizard R., sssion C., O'Brine-Greco B., Foley S.F., Ware C.F.; beta, a novel member of the TNF family that forms a complex with lymphotoxin on the cell surface."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M N.A. (ISOFORM 1).
dan A., Qin S., Shaffer T., James R., Ratcliffe A.,
ickhoff R., Loretz C., Madan A., Dors M., Young J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Renard N., Charlot C., Bienvenu J., Coiffier B.,
                                                                                                                                                                                                                                                                                                                                                                                                2.5%; Score 7; DB 1; Length 243; 100.0%; Pred. No. 59; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                         ofactor biosynthesis; Complete proteome.
13 AA; 26996 MW; 218A3382A975BDBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l lines and non-Hodgkin's lymphomas.";
phys. Res. Commun. 238:273-276(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3881; PubMed=7916655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5965; PubMed=9299492;
                                                                                                                                                 1007901; Moez MoeB. 1000205; NAD BS. 1000594; ThiF domair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                     7; MoeZ MoeB; 1.
                                                                                                                    1009036; MoeB.
                             AAC23099.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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356 (1993)

큝죮똣둮뭄FFF속속똣틍몽뚕풒핇옰첉줥꿡돲턽닕엹쿒췙쒔꿦붎뉥뵱곒뿂췠퍖첉톴뷺쉆뀰교횬궾뮫뮫뮫셛쮼뀵욛묜

(Human)

AA; 0

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STRAIN=ATCC 33913 / NCPPB 528;

STRAIN=ATCC 33913 / NCPPB 528;

MEDLINE=2202145; PubMed=12024217;

MEDLINE=2202145; PubMed=12024217;

MEDLINE=2202145; PubMed=12024217;

A Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N. Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A lowes L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.P.,

A caractic G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.

Cicarelli R.M.B., Coutinho L.L., Cureino-Santos J.R., El-Dorry H.

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.

Locali E.C., Medhado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martine E.C., Meidanis J., Menor C.F.M., Miyaki C.T., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.D.,

"Comparison of the genomes of two Xanthomonas pathogens with diffi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 417.459-463 (2002).

-!- FUNCTION: Functions in the N-end rule pathway of protein degradation where it conjugates Leu, Phe and, less efficientl. Met from aminoacyl-RRMs to the N-termini of proteins contain an N-terminal arginine or lysine (By similarity).

-!- CATALYTIC ACTIVITY: L-leucyl-tRNA + protein = tRNA + L-leucyl
                                                                                                                                                                                                                                                                                          coprotein, Signal-anchor.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: L-phenylalanyl-tRNA + protein = tRNA + L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
1cucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6) (L/F-transferase) (Leucyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.5%; Score 7; DB 1; Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. ) (PC
                                                                                                                                                                                                                                                                                                                                                                                    49 244 EXTRACELLULAR (POTENTIAL).
222 222 N-LINKED (GLCNAC. .) (PC
244 AA; 25420 MW; A4047858335D5B97 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 59; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                          Cytokine; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                EMBL, AB054536; BAB83881.1; -.
EMBL, AB100082; BAC78156.1; -.
InterPro, IPR006053; TNF_abc.
InterPro, IRR006052; TNF_family.
InterPro, IPR008983; TNF_IRM.
                                                                                                                                                   Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
PRODOM; PD002012; TNF subf; 1.
SMART; SM00207; TNF 1; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.5
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 GLYYLYC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 GLYYLYC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       host specificities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT OR XCC1969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XANCP
                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ad. Sci. U.S.A. 100:7708-7713(2003).
Cytokine that binds to LTBR/TMFRSER3. May play a specific
mmune response requiation. Provides the membrane anchor
stachment of the heterotrimeric complex to the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .na T., Kimura N., Yanagiya K., Kohara S., Shigenari A., Culski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y., Jashiro H., Iwamoto C., Umehara Y., Imanishi T., S., Gojobori T., Bahram S., Inoko H., sequencing of human and chimpanzee MHC class I regions
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3y similarity).

Jeterotrimer of either two LTB and one LTA subunits or valent) two LTA and one LTB subunits (By similarity).

AR LOCATION: Type II membrane protein (Potential).

F: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tel. 43, Last annotation update)
sta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Not; PubMed=12493009; Shiina I., Anzai I., Kohara S., Inoko H.; penomic analysis of the MHC: the evolution of class I cocks, diversity and complexity from shark to man."; 190:95-122(2002).
                                                                                                                                                                                                                                             /FTId=VAR 013026.
DPGAQAQQGL -> GLSAPGSGRT (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss (Chimpanzee).
.azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cions/deletions as the major path to genomic
KQISAPGSQLPTS (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                  F41569459830ED4C CRC64;
                     'FTId=VSP 006441.
Aissing (in isoform 2).
                                                                  FTIG=VSP_006442.
                                                                                       3 -> E.
/FTId=VAR_013025.
                                                                                                                                    S -> R.
/FTId=VAR_016331.
                                                                                                                                                                                                  FTId=VAR_016332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or ligand superfamily member 3).
                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                                                                                                                                                             2.5%; Score 7; DB 1
100.0%; Pred. No. 59;
iive 0; Mismatches
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                                             Missing
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                                                                                                                                                                                                                                                                                                                    25390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tel. 43, Created)
                                                                                                                                                                                                                                                                                                                                                                                                              nservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                  3; Leu Phe_trans; 1.
3R00667; aat; 1.
Acyltransferase; Complete protecume.
19 AA; 27404 MW; E4584D8A464EDB54 CRC64;
iny-protein.
AR LOCATION: Cytoplasmic (By similarity).
Y: Belongs to the L/F-transferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prea. ....
                                                                                                                                                                                                                                                        nail to license@igb-sib.ch).
                                                                                                                                                                                                                                                                                                           1; AAM41258.1; -.
                                                                                                                                                                                                                                                                                                                                                               1004616; Aat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30DG 116
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(MOLYBDOPTERIN), NECESSARY FOR MOLYBDOENZYMES. PLAYS A ROLE ACTIVATION OF THE SMALL SUBUNIT OF THE MOLYBDOPTERIN CONVERT FACTOR (MOAD).

-!- PATHWAY: Molybdenum cofactor biosynthesis. -!- SIMILARITY: BELONGS TO THE HESA/MOEB/THIF FAMILY.

InterPro; IPR00205; MDD BS.
InterPro; IPR00205; ThiF\_domain.
Pfam; PF05237; MoeZ\_MoeB; 1.
Pfam; PF00899; ThiF; 1.
Molybdenum cofactor biosynthesis; Complete proteome; 3D-structur: SEQUENCE 249 AA; 26719 MW; 12C77082B3F39D7D CRC64;

EcoGene; EG10154; moeB. InterPro; IPR009036; MoeB. InterPro; IPR007901; MoeZ MoeB.

EMBL, AE000185, AAC73913.1; -.
EMBL, D90720; BAA35514.1; -.
EMBL, D90721; BAA3551.1; -.
PIR, B32352; B32352.

PDB; 1JW9; 21-NOV-01. PDB; 1JWA; 21-NOV-01.

PDB; 1JWB; 21-NOV-01

EMBL; M21151; AAA23580.1; -.

sequencing of the Escherichia coli chlEN operon involved srin biosynthesis."; 5617; PubMed=9278503;
., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Llado-Vides J., Glanner J.D., Rode C.K., Mayhew G.F., avis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., oteobacteria, Gammaproteobacteria, Enterobacteriales, iaceae, Escherichia.  $_{\rm 3}$  genome sequence of Escherichia coli K-12."; 1453-1474(1997). (Rel. 12, Created) (Rel. 12, Last sequence update) (Rel. 42, Last annotation update) 1 biosynthesis protein moeB. 170:4097-4102(1988). 1906; PubMed=3045084; sai Y., Saito T.; STANDARD; OR B0826. 4 N.A. MG1655;

1202; PubMed=8905232; iba H., Baba T., Fujita K., Hayashi K., Honjo A., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., itagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., omura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., eki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,

N.A.

A sequence of the Escherichia coli K-12 genome 3 to the 12.7-28.0 min region on the linkage map."; 37-155(1996).
INVOLVED IN BIOSYNTHESIS OF A DEMOLYBDO COFACTOR

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SEQUENCE FROM N.A.
STRAIN=LIZ / SGSC1412 / ATCC 700720;
MEDLINE=15194948; PubMed=11677609;
MCClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreill, Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Laym. Lieonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney:
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Watersfron R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimu:
                                                                                                                                                                                                                                                                                                                        Bacteria; Profeobacteria; Gammaproteobacteria; Enterobacteriales
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001).
-:- FUNCTION: INVOLVED IN BIOSYNTHESIS OF A DEMOLYBDO COFACTOR (MOLYBDOPTERIN), NECESSARY FOR MOLYBDOENZYMES. PLAYS A ROLE
                                                  .,
                  DB 1; Length 249;
                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=LT2;
Wong K.K., Kwan H.S.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Molybdopterin biosynthesis protein moeB. MOEB OR STMO845.
                                                                                                                                                                                                 249 AA.
                2.5%; Score 7; DB 1, 100.0%; Pred. No. 60; tive 0; Mismatches
                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
Query Match
Query Match
Best Local Similarity 100...
                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                            Salmonella typhimurium.
                                                                                179 LRYNRQI 185
                                                                                                                  10 LRYNROI 16
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                                                                                                                                                                                               SALTY
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                                                                                                                                                                                MOEB_SALTY
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TISSUB-Brain, and Lung;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.L., Mang J., Hsieh F., Diatchenko L., Marushna K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T. Brownstein M.J., Usdin T.B., Torshyuki S., Carninci P., Prange C. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H. Richards S., Worley K.C., Hale S., Garcia A.M., Gay, L.J., Hulyk S. Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schertich G., Schmutz J., Marra M.A.; Stelin J.E., Jones S.J.M., Marra M.A.; Rodriguez A. Schein J.E., Jones S.J.M., Marra M.A.; Rodriguez M.A., Schein J.E., Jones S.J.M., Marra M.A.; Rodriguez M.A.; Rodriguez M.A.; Rodriguez M.A.; Rodriguez M.A.; Rodriguez M.A.; Rodriguez M.A.; Rodriguez M.A.; Rodriguez M.A.; Rodriguez M.A.; Rodriguez M.A.; Rodriguez M.A.; Rodriguez M.A.; Marra M.A.; Rodriguez M.A.; Rodriguez M.A.; Marra M.A.; Rodriguez M.A.; Rodriguez M.A.; Marra M.A.; Marra M.A.; Rodriguez M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Marra M.A.; Ma
                                                 InterPro; IPR001173; Glydo_trans_2.
Plan; PF00535; Glydos_transf_2; 1.
Lipopolysaccharide blosynthesis; Transferase; Glycosyltransferase
SEQUENCE 257 AA; 29233 WW; D40D7B57E002F990 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Testis;
Ottenwaelder B., Obermaier B., Mewes H.-W., Gassenhuber J.,
                                                                                                                                                                                 2.5%; Score 7; DB 1; Length 257;
100.0%; Pred. No. 62;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Neuroblastoma, and T-cell;
Li W. B., Gruber C., Jessee J., Polayes D.;
"Full-length CDNA libraries and normalization.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Note=No experimental confirmation available;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNO9_HUMAN STANDARD; PRT; 277 AA. Q86T03; Q86T09; Q8WUC0; Q9BUG7; Q9NSU8; 10-0CT-2003 (Rel. 42, created) 15-CT-2003 (Rel. 42, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein C14orf9.
                              EMBL; U52844; AAC44433.1;
                                                                                                                                                                                                       Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                    229 GLLLAUV 235
                                                                                                                                                                                                                                                                                             71 GLLLAVV 77
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                                                                                                                               Off entry is copyright. It is produced through a collaboration was Institute of Bioinformatics and the BMBL outstation aloinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial test a license agreement (See http://www.isb-sib.ch/announce/il to license@isb-sib.ch).
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Y: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2. WAAE/KDTX
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OF THE SMALL SUBUNIT OF THE MOLYBDOPTERIN CONVERTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :eobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rel. 39, Created)
xel. 39, Last sequence update)
xel. 41, Last annotation update)
xride core biosynthesis glycosyl transferase kdtX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 249;
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G -> R (IN REF. 1).

S -> A (IN REF. 1).

S -> T (IN REF. 1).

G -> E (IN REF. 1).

G -> E (IN REF. 1).
                                                 Olybdenum cofactor biosynthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           actor biosynthesis; Complete
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100594; ThiF domain.
                                                                                                                                                                                                                                                                                                                                                                                                                          009036; MoeB.
007901; MoeZ MoeB.
000205; NAD_BS.
                                                                                                                                                                                                                                                                                                                                                  AAA96530.1; -.
; AAL19781.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26903 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sceae; Serratia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%;
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                                                            Not entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial lizes a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine that binds to LTBR/TNFRSF3. May play a specific immune response regulation. Provides the membrane anchor attachment of the heterotrimeric complex to the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVICCHCKNTFLWTEFIDRTLARCPHCRKVSSIGRRÝPRKR
CICCFLLGLLLAV -> GKHAPPQGKPGRVRGAPRGTLKAG
EGAGPRAEAGPSRQVRDCCTCDWARLPSLRNRDHSLGTEGG
                                                                                                                                                                                                                                                                                                                                                                                                           AFPPFPEGHPAVLPGEDPPPYSPLTSPDSGSAPMITCRVCQ
                                                                                                                                                                                                                                                                                                                                                                                                                           SLINVEGKMHQHVVKCGVCNEATPIKNAPPGKKYVRCPCNC
LLICKVTSQRIACPRPYCKRIINLGPVHPGPLSPEPQPMGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQPDRSANYEKPSELGQRVEDQKDFPTTVEHQWGCK (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1748; PubMed=10721723;
311 E.A., Brown C.L., Cullen J.M.;
/mphotoxin-alpha, -beta and tumor necrosis factor genes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 41, Last sequence update)
(Rel. 43, Last annotation update)
seta (LT-beta) (Tumor necrosis factor C) (TNF-C) (Tumor or ligand superfamily member 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Sheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VSP 007817.
P -> T (IN REF. 3; AAH20947).
A85FE1F736366CBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                        -> AGKHAPPQ (in isoform 2).
                                                                                                                                                                                                                                                                                                                      protein, Transmembrane, Alternative splicing.
112 234 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
               ?86T03-3; Sequence=VSP_007816, VSP_007817;
y be due to intron retention.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VSP 007816.
Missing (in isoform 3).
"T-A-VSP 007817.
                                                                                                                                                                                                                                                                                                                                                                                         FTId=VSP 007815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7; DB 1; Pred. No. 66; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                      nail to license@isb-sib.ch).
                                                                                                                                                                                                 )0; CAD61939.1; -.
5; CAD6347.1; ALT_INIT.
7; CAB70896.1; ALT_INIT.
7; AAH20847.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .soform 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 41, Created)
(Rel. 41, Last seque
(Rel. 43, Last annol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29469 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.5%; £
                                                                                                                                                                                                                                                                                                         C14orf9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             k (Woodchuck)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                          T46382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                        .9299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               995;
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da Silva A.C.R., Ferror J.A., Reinach F.C., Farah C.S., Furlan L.I. Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N. Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., Camarocte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P. Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H. Faria J.B., Ferreira R.C., Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A., Lemos M.V., Machado M.A., Madeira A.M., Matrinez-Rossi N.M. Martins E.C., Machado M.A., Madeira A.M., Mayaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., oliveira V. Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collibetween the Swiss Institute of Bioinformatics and the EMBL out the Buropean Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch, or send an email to license@isb-sib.ch).
-!- SUBUNIT: Heterotrimer of either two LTB and one LTA subunits (less prevalent) two LTA and one LTB subunits (By similarity. -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential). -!- SIMILARITY: Belongs to the tumor necrosis factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PRO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
4-bydroxy-3-methylbut_2-enyl diphosphate reductase (EC 1.17.1.2)
1SPH OR LYTB OR XCC1157,
Xanthomoras campestris (py. campestris).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D -> H (IN REF. 1; AAF34865).
73B354EFC8B3B3BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. . .) (PO'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1234; TNECROSISECT.
ProDom; PD002012; TNF subf; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF; 1.
PROSITE; PS50049; TNF 2; 1.
Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; DB 1;
Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.5%; Scor.
100.0%; Prec
0; M
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006053; TNF abc.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR003336; TNF subf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 310 EX
272 272 N-1
280 280 D
310 AA; 32644 MW;
                                                                                                                                                                                                                                                                                             EMBL; AF096268; AAF34866.1; -. EMBL; AF095587; AAF34865.1; -. HSSP; P01374; ITNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 GLYYLYC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GLYYLYC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
Les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISPH_XANCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8PBG4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISPH_XANCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
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fastidiosa.";
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ID ODPB BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 51
      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                           Tentry is copyright. It is produced through a collaboration wiss Institute of Bioinformatics and the BMBL outstation-ioinformatics Institute. There are no restrictions on its rofit institutions as long as its content is in no way his statement is not removed. Usage by and for commercial res a license agreement (See http://www.isb-sib.ch/announce/iltolicense@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alves L.M.C., Arruda P., Baia G.S., Baptista C.S., Onaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Canargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Ferreira A.J.S., Ferreira V.C.A., Ferro A., Gones S.C., Franco M.C., Frohme M., Furlan L.R., Indian G.H., Goldman M.H.S., Gones S.L., Kitajima J.P., Kuramae E.E., Lambais M.R., Laite L.C.C., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Martins E.A.L., Mattins E.M.F., Mattins B.A.L., Mattins E.M.F., Mattins C.L., Mixacca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., ticos M., Truffi D., Tsai S.M., White F.F.,
                                              the genomes of two Xanthomonas pathogens with differing
                                                                                                                          y similarity).

ACTIVITY: Isopentenyl diphosphate + NAD(P)(+) + H(2)0 = oxy-3-methylbut-2-en-1-yl diphosphate + NAD(P)H.

ommevalonate terpenoid biosynthesis pathway; seventh
                                                                                               Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate ntenyl diphosphate (IPP) and dimethylallyl diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          el. 41, Last sequence update)
1. 42, Last annotation update)
thylbut-2-enyl diphosphate reductase (EC 1.17.1.2)
R XF2416 OR PD1435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Complete proteome; Oxidoreductase; NADP.
34641 MW; 6BF5A272A4CA1E4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 316; . 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      iosa, and
iosa (strain Temeculal / ATCC 700964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.5%; Score 7; DB 1
100.0%; Pred. No. 74;
live 0; Mismatches
                                                                                                                                                                                                              Belongs to the ispH family
                                                                                                                                                                                                                                                                                                                                                                                                                                             00216; ispH_lytB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                            ; AAM40456.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            el. 41, Created)
                 antos M., Trufí
Kitajima J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ae; Xylella.
1, 183190;
                                                                                                                                                                                                                                                                                                                                                                                                         03451; LytB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                -463(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              nthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LA 223
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An Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
A publication of Coliveira M.C., Monteiro-Vitorello C.B.,
Miyaki C.Y., Furlan L.R., Camargo L.B.A., da Silva A.C.R., Moon D.
A Takita M.A., Lemos B.C.B.M., Machado M.A., Ferro M.I.T., da Silva F.
Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.
Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siquejra W.
Coutinho L.L., Kimura B.T., Ferro B.S., Harakava R., Kuramae E.E.,
Marino C.L., Gigliori E., Abreu I.L., Alves I.M.C., do Amaral A.M.
Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
A da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi I.
Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.I.
A de Souza A.A., Trufff D., Tsukuno F., Yanai G.M., Zaros L.G.,
Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
Kitajima J.P.,
Comparative analyses of the complete genome sequences of Pierce's
disease and citrus variegated chlorosis strains of Xylella
A Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
A Mhani A. Ur., Nobrega F.G., Nunes L.R., Oilveira M.A.,
de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
A Peixoto B.R., Pereira G.A.G., Pereira H.A. Ur., Pesquero J.B.,
A Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
de Rosa V.E. Ur., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A da Silveira J.F., Sllvestri M.L.Z., Squeira W.J., de Souza A.A.,
A da Silveira J.F., Sllvestri M.L.Z., Squeira W.J., Tsuhako M.H.,
A Ullada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Zago M.A., Zatz M., Meidanis J., Setubal J.C.,
The genome sequence of the plant pathogen Xylella fastidiosa.";
In Nature 406:151-159(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 185:1018-1026(2003).
-!- FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosph into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a colle between the Swiss Institute of Bioinformatics and the EMBL outs the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centities requires a license agreement (See http://www.isb-sib.ch/e or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: Isopentenyl diphosphate + NAD(P)(+) + H(2)(E)-4-hydroxy-3-methylbut-2-en-1-yl diphosphate + NAD(P)H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAWAP; MF 00191; -; 1.

InterPro; IPR003451; LytB.

Pfam; PF02401; LXTB; 1.

TIGRFAMs; TIGR00216; ispH lytB; 1.

Isoprene blosynthesis; Complete proteome; Oxidoreductase; NADP. SEQUENCE 316 AA; 34704 MW; 1A2E80B9A98D334A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (last) step.
-!- SIMILARITY: Belongs to the ispH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.5%; Score 7; DB 1
100.0%; Pred. No. 74;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Temeculal / ATCC 700964;
MEDLINE=22421331; PubMed=12533478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004050; AAF85215.1; -.
EMBL; AE012558; AAC29279.1; -.
PIR; C82561; C82561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 LVDGVLA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 LVDGVLA 282
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Pfam; PF02779; transket pyr; 1.
Pfam; PF02780; transketolase C; 1.
Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a coll between the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch. or send an email to license@isb-sib.ch).
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Rhabditidae, Peloderinae, Caenorhabditis.
lipoamide dehydrogenase (E3).
-!- FUNCTION: THE B.SUBTILIS PDH COMPLEX POSSESSES ALSO BRANCHED-
2-OXOACID DEHYDROGENASE (BCDH) ACTIVITY.
-!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
acetyldihydrolipoamide + CD(2).
-!- COFACTOR: Thiamine pyrophosphate.
-!- SUBUNIT: Heterodimer of an alpha and a beta chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jassal B.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-!- SIMILARITY: BELONGS TO THE C.ELEGANS RECEPTOR-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.5%; Score 7; DB 1; Length 324; 100.0%; Pred. No. 75; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 AA; 35343 MW; D2A7C9B32DED0F0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-Nov-1995 (Rel. 32, Created)
01-Nov-1995 (Rel. 32, Last sequence update)
28-F88-2003 (Rel. 41, Last amotation update)
Serpentine receptor class alpha 6 (Sra-6 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P09061, 1QS0.
Subtilist, BG10208; pdhB.
InterPro; IPR009014; Transketo_C_like.
InterPro; IPR005476; Transketolase_C.
InterPro; IPR005475; Transketolase_CR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, M57435; AAA62682.1; -.
EMBL, AF012285; AAC4933.1; -.
EMBL, Z99111; CAB1332.1; -.
PIR, C36718; C36718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z48009; CAA88083.1; -. PIR; T18619; T18619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100..
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : The pyruvate dehydrogenase complex catalyzes the overall no f pyruvate to acetyl-CoA and CO(2). It contains copies of three enzymatic components: pyruvate nasse (E1), dihydrolipoamide acetyltransferase (E2) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Ferrari E.; lysis of the mobA-ampS region of the Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  558; PubMed=1697575;
Lva A., Paulin L., Arvidson S., Palva I.;
complex of Bacillus subtilis: sequence analysis and
yruvate dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taldwell R., Enfield L., Ferrari E.,
E (124 degrees-127 degrees) region of the Bacillus chromosome: sequencing of a 27 kb segment and nof several genes in the area.";
                                           Rel. 18, Created)
Rel. 18, Last sequence update)
Rel. 42, Last annotation update)
drogenase El component, beta subunit (EC 1.2.4.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                          micutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172:5052-5063(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           033; PubMed=9384377;
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                                                                                                                                                                                   Da Subunit).
OR BSU14590.
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RR 140 JRR 303

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RESULT 55

ID43 DEIRA

AC Q9RTH9,

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 38-FEB-2003 (Rel. 41, Last annotation update)

DF 3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydroges)

DE (IMDH) (3-IPM-DH).
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-2003 (Rel. 41, Last annotation update)
3-isopropylmale dehydrogenase (EC 1.1.1.85) (Beta-IPM dehydroge (IMDH) (3-IPM-DH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a coll. between the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centicies requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biochem. 109:852-857(1991).
-!- FUNCTION: Catalyzes the oxidation of 3-carboxy-2-hydroxy-4-methylpentanoate (3-isopropylmalate) to 3-carboxy-4-methyl-2-oxopentanoate. The product decarboxylates to 4-methyl-2-oxopentanoate.
                                                                                                                                                                                                                                                                                      Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oxopentanoate. CATALYTIC ACTIVITY: 3-carboxy-2-hydroxy-4-methylpentanoate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kirino H., Oshima T.;
"Molecular cloning and nucleotide sequence of 3-isopropylmalate
dehydrogenase gene (leuB) from an extreme thermophile, Thermus
aquaticus YF-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the isocitrate and isopropylmalate dehydrogenases family. LeuB subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAD(+) = 3-carboxy-4-methyl-2-oxopentanoate + NADH.
-!- PATHWAY: Leucine biosynthesis; third step.
-!- SUBUNIT: Homodimer.
-!- SUBCELIULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00180; isodh, 1.
TIGREMMS; TIGREMMS; TIGREMMS; TSO0470; IDH IMDH; 1.
OXIGOTED: PS00470; IDH IMDH; 1.
OXIGOTEDERSE; Leucine biosynthesis; NAD.
SEQUENCE 344 AA; 36949 MW; 4F31A9444EB26408 CRC64;
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1XAA.

(Mouse)

ALR 254 arity

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(EC 3.1.8.1) (PON 1)

(Rat)

-Dawley;

19;

N.A.

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CHARACTERIZATION, AND SEQUENCE OF 1-20.

MEDLINE-92031444; PubMed=1718413;

MEDLINE-92031444; PubMed=1718413;

Turlong C.E., Richter R.J., Chapline C., Crabb J.W.;

Purification of rabbit and human serum paraoxonase.";

Biochemistry 30:10133-10140(1991).

-!- FUNCTION: Hydrolyzes the toxic metabolites of a variety of organophosphora insecticides. Capable of hydrolyzing a broad spectrum of organophosphate substrates and a number of aromat: carboxylic acid esters. Mediates an enzymatic protection of 1c density lipoproteins against oxidative modification.

-!- CATALYTIC ACTIVITY: Aryl dialkyl phosphate + H(2)O = dialkyl phosphate + an aryl alcohol.

-!- CHALVITC ACTIVITY: A phenyl acetate + H(2)O = a phenol + acet

-!- SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=93345100; PubMed=8393745;
Furlong C.E., Costa L.G., Hassett C., Richter R.J.,
Sundstrom J.A., Adler D.A., Disteche C.M., Omiecinski C.J.,
Chapline C., Crabb J.W.;
Human and rabbit paraoxonases: purification, cloning, sequencing
mapping and role of polymorphism in organophosphate detoxification
Chem. Biol. Interact. 87:35-48(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: Glycosylated.

PTM: The signal sequence is not cleaved.

PTM: The signal sequence is not cleaved.

POLYMORPHISM: There are two allelic forms, allozyme A and B, v differ in their embstrate specificity. Both forms have similar arylesterage activity but allozyme B possesses greater paraox activity. Allozyme A is better at protecting LDL from oxidatic SIMILARITY: Belongs to the paraoxonase family.

CAUTION: Ref. 3 (ARC6398) sequence differs from that shown due a stop codon in position 355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., FUNCTION, AND VARIANTS SER-81; GLU-92 AND GLY.
STRAIN=New Zealand white; TISSUE=Liver;
MEDLINE=21163843; PubMed=11266077;
                                                                                                                                                                                                                                                                                                                                                                                                               (Serum aryldialkylphosphatase 1) (A-esterase 1) (Aromatic esteras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of cDNA clones encoding rabbit and human serum paraoxonase: the mature protein retains its signal sequence."; Biochemistry 30:10141-10149(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE=92031445; PubMed=1657140;
Hassett C., Richter R.J., Humbert R., Chapline C., Crabb J.W.,
Omiecinski C.J., Furlong C.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watson C.E., Draganov D.I., Billecke S.S., Bisgaier C.L., "Rabbits possess a serum paraoxonase polymorphism similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                        PONI_RABIT STANDARD, PRT, 358 AA. P27170; Q9BGN1; Q9BGN2; Q9BGN3; 01-AUG-1992 (Rel. 23, Created) 01-AUG-1992 (Rel. 23, Last sequence update) 01-AUG-2003 (Rel. 42, Last annotation update) Serum paraoxonase/arylesterase 1 (EC 3.1.1.2)
100.0%; Pred. No. 82; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pharmacogenetics 11:123-134(2001).
                             7; Conservative
                                                                                                                            269 LGLGLAL 275
                                                                           61 LGLGLAL 67
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                      T entry is copyright. It is produced through a collaboration wiss Institute of Bioinformatics and the EMBL outstation-ioinformatics Institute. There are no restrictions on its roff institutions as long as its content is in no way nois statement is not removed. Usage by and for commercial res a license agreement (See http://www.isb-sib.ch/announce/il to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  May be a single membrane channel protein acting both as e and a translocase. It is the key enzyme in homeostatic of blood glucose levels.

ACTIVITY: D-glucose 6-phosphate + H(2)O = D-glucose +
                                                                                              azoa; Chordata; Craniata; Vertebrata; Buteleostomi; eria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a cDNA for the catalytic subunit of rat liver phatase: regulation of gene expression in FAO hepatoma in, dexamethasone and cAMP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (BY SIMILARITY). PREVENT SECRETION FROM ER (POTENTIAL).
                                                                                                                                                                                                                                                                             in S., Chuang E., Bulkuisen W., Naji A., Taub R.A.; f glucose-6-phosphatase gene and protein expression prive response in proliferating liver and diabetes."; c. 95:832-041(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Auconeogenesis and glycogenolysis; last step. R LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50; PubMod=8865366;

ajima H., Horikawa Y., Hamaguchi T., Yamasaki T.,

lamba M., Hanatusa T., Matebuzawa Y.;

d distribution of glucose-6-phospharase catalytic

ger RNA and its changes in the diabetic state.";

[ol. Pathol. Pharmacol. 93:13-24(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nthesis; Hydrolase; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gaud D.M., El-Maghrabi M.R., Pan W., Subir M.,
el. 41, Last annotation update)
phatase (EC 3.1.3.9) (G6Pase) (G-6-Pase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C44960E102F4244D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ys. Res. Commun. 201:302-309(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08934; AcPase_VanPerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -Dawley; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA74381.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=8198588;
                                                                                                                                                                                                                                                           PubMed=7860767;
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Du B

t Pa

DB 1; Length 357;

2.5%; Score 7;

40555 MW;

Æ;

00326; PA\_PTPase.

acidPPc; 1

ticulum

75

BAA24348.1; -

sequence of the gene cluster and thermostable properties of the

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OT entry is copyright. It is produced through a collaboration Swiss Institute of Baloinformatics and the BYMEL outstation—Bloinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial ires a license agreement (See http://www.isb-sib.ch/amnounce/ail to license@isb-sib.ch).
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Rel. 43, Last annotation update)
oxidoreductase chain 8 (EC 1.6.99.5) (NADH dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
P -> S (IN ALLELE A).
K -> E (IN ALLELE A).
S -> G (IN ALLELE A).
A -> S (IN REF 3).
A -> V (IN REF 3).
A -> V (IN REF 3).
A -> V (IN REF 3).
A -> V (IN REF 3).
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ATCC 27634;
%490; PubMed=9020134;
%5.S., Subd' V.D., Ohnishi T., Yagi T.;
xranslocating NADH-quinone oxidoreductase (NDH-1) obacterium Thermus thermophilus HB-8. Complete DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tioxidant; Glycoprotein; Signal; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 358;
5.82;
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                                                                                                                                                                                                                                                                                                                                     9; F:antioxidant activity; IDA.
3; F:aryldialkylphosphatase activity; NAS.
4; F:arylesterase activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)

    P:response to organophosphorus; IDA.
002640; Arylesterase.

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.00.0%; Pred. No. 82;
.ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
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                                                                                                                                                                                                                         1; AAK06398.1; ALT_TERM.
2; AAK06399.1; -.
                                                                                                                                                                                                                                                                                                                  C:extracellular; NAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      008363; Paraoxonasel.
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100.0%; Pre-
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                                                                                                                                                                                                                                                                    3; AAK06400.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39878 MW;
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                                                                                                                                                                               AAA31452.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85; PARAOXONASE.
                                                                                                                                                                                                       AAB27713.2;
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expressed NGO2 submit...;

Ly Biol. Chem. 272:4201-4211(1997).

Ly Biol. Chem. 272:4201-4211(1997).

Ly Biol. Chem. Subtities electrons from NADH, via FMN and irc sulfur (Re-S) centers, to quinones in the respiratory chain. Immediate electron acceptor for the enzyme in this species is believed to be menaquinone. Couples the redox reaction to protor translocation (for every two electrons transferred, four hydrons are translocated across the cytoplasmic membrane), and to conserves the redox energy in a proton gradient.

-!- CATALYTIC ACTIVITY: NADHH + quinone = NAD(+) + quinol.

-!- SUBUNIT: COMPOSED OF 14 DIFFERENT SUBUNITS. SUBUNITS NGO7-14

CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX.

-!- SUBMITY: Belongs to the complex I submit 1 family.
                                                                                                                                                                                                                                    This SMISS-FROT entry is copyright. It is produced through a coll between the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-gib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Nucleotide sequences of the Acinetobacter calcoaceticus benABC g
for benzoate 1,2-dioxygenase reveal evolutionary relationships am
multicomponent oxygenases.";
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Moraxellaceae; Acinetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neidle E.L., Hartnett C., Ornston N.L., Bairoch A., Rekik M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.5%; Score 7; DB 1; Length 365;
100.0%; Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41008 MW; AE920CC029333C09 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00667; COMPLEXI ND1 1; 1.
PROSITE; PS00668; COMPLEXI ND1 2; 1.
Oxidoreductase; NAD; Quinone; Transmembrane.
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InterPro; IPR001694; Resp_NADH_dhl.
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MEDLINE=91358314; PubMed=1885518;
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U52917; AAA97945.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acinetobacter calcoaceticus.
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nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00146; NADHdh;
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310 3
336 3
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P07775;
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of the protein activity to the cell surface. The N-product is active species in both local and long-range signaling, whereas C-product has no signaling activity (By similarity). SIMILARITY: Belongs to the hedgehog family.
                                                                                      This SWISS-PROT entry is copyright. It is produced through a collibetween the Swiss Institute of Bioinformatics and the EMBL out: the Buropean Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for centities requires a license agreement (See http://www.isb-sib.ch/cor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS, PRO0632; SONICHHOG.
ProDom, PD003042; HH signal; 1.
ProDom, PD00305; HintC; 1.
SMART; SM00305; HintC; 1.
PROSITE; PS50817; INTEIN TER; 1.
Developmental protein; Autocatalytic cleavage; Hydrolase; Protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-palmitoyl cysteine (By similarity)
Cholesterol glycine ester (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
DESERT HEDGEHOG PROTEIN 1.
DESERT HEDGEHOG PROTEIN 1 N-PRODUCT.
DESERT HEDGEHOG PROTEIN 1 C-PRODUCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Desert hedgehog protein precursor 2 (DHH-2) (Hedgehog protein 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLEAVAGE (AUTO-) (BY SIMILARITY). INVOLVED IN AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
ESSENTIAL FOR AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 396; . 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
774A3EC2268A5EE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                InterPro; IPR009045; Hedgehog/DD_pept.
InterPro; IPR003587; Hedgehog hint N.
InterPro; IPR003586; Hedgehog_hintC.
InterPro; IPR00320; HH signal.
InterPro; IPR006141; InTein_S.
InterPro; IPR001767; Pept C46 hint.
InterPro; IPR001657; Pept C46 hint.
Pfan; PF01085; HH signal; I.
Pfan; PF01085; HH signal; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 AA; 44087 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.5%; £
100.0%;
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HSSP; Q62226; 1VHH.
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279
198
267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                   MEROPS; C46.UPW;
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197
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NCBI_TaxID=8355;
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23
198
276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T entry is copyright. It is produced through a collaboration wiss Institute of Bioinformatics and the EMBL outstation ioinformatics Institute. There are no restrictions on its rofit institutions as long as its content is in no way his statement is not removed. Usage by and for commercial res a license agreement (See http://www.isb-sib.ch/announce/il to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALECTOBERM, NERVOUS SYSTEM AND SOMITES. INDUCES ECTOPIC AL ECTODERM, NERVOUS SYSTEM AND SOMITES. INDUCES ECTOPIC ND FORMATION IN EMBRYOS.

R LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE E THE N-TERMINAL PEPTIDE BEFUSES FROM THE C.E. HENGEHOG FROTEIN IS ALSO SECRETED IN EITHER CLEAVED THE FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terminal domain displays an autoproteolysis activity esterol transferase activity. Both activities result in ge of the full-length protein and covalent attachment of rol moiety to the C-terminal of the newly generated N-ragment (N-product). This covalent modification appears essential role in restricting the spatial distribution
                                   R LOCATION: Integral membrane protein.
OUS: THE BEN OPERON ENCODE THE PROTEINS RESPONSIBLE FOR
ATION OF BENZOATE TO CATECHOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ession and shared activities of members of the hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE STACE: DETECTABLE WITHIN THE BARLY GASTRULA. IN PRESSION BECOMES RESTRICTED TO ANTERIOR STRUCTURES, NG BOTH NEURAL PLATE AND ENDODERMAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   azoa, Chordata, Craniata, Vertebrata, Euteleostomi, achia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grew L.L., Lai C.-J., Lee J.J., von Kessler D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .. 38, Last sequence update)
.. 42, Last annotation update)
protein precursor 1 (DHH-1) (Cephalic hedgehog
               PROBABLY INVOLVED IN THE TRANSPORT OF BENZOATE.
                                                                                                                                                                                                                                                                                                                                                                         matic hydrocarbons catabolism; Transmembrane. AA; 42288 MW; 5466C4D460784BB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    2.5%; Score 7; DB 1; Length 394;
100.0%; Pred. No. 90;
rative 0; Mismatches n. T-3-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (African clawed frog).
173:5385-5395(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52; PubMed=7671800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis.";
1:2337-2347(1995).
                                                                                                                                                                                                                                                             AAC46440.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                      53; BenE; 1.
00843; benE; 1.
                                                                                                                                                                                                                                                                                          04711; BenE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   el. 42,
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(H).
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852; PubMed=7671800;

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0
                                                                                                                                           SIGNAL INVOLVED IN THE BARLY INDUCTION AND PATTERNING OF ASAL ECTOPER, NERVOUS SYSTEM AND SOMITES. INDUCES ECTOPIC AND FORMATION IN EMBRYOS.
AR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE TERMINAL PEPTIDE BERMAINS ASSOCIATED WITH THE ACE. HEIGHEN PROPRIED IN EITHER CLEAVED WED FORM TO MEDIATE SIGNALING TO OTHER CHILS (BY
                                                                                                                                                                                                                                                                                                                                                                                    C-terminal domain displays an autoproteolysis activity lesterol transferase activity. Both activities result in age of the full-length protein and covalent attachment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erol moiety to the C-terminal of the newly generated N-fragment (N-product). This covalent modification appears un essential role in restricting the spatial distribution otein activity to the cell surface. The N-product is the ceins in both local and long-range signaling, whereas the has no signaling activity (By similarity).

Y: Belongs to the hedgehog family.
                                                              ression and shared activities of members of the hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; Autocatalytic cleavage; Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-palmitoyl cysteine (By similarity).
Cholesterol glycine ester (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESERT HEDGEHOG PROTEIN 2.
DESERT HEDGEHOG PROTEIN 2 N-PRODUCT.
DESERT HEDGEHOG PROTEIN 2 C-PRODUCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
L.L., Lai C.-J., Lee J.J., von Kessler D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN AUTO-CLEAVAGE (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.5%; Score 7; DB 1; Length 398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JPW; -. 1009045; Hedgehog/DD pept. 2003587; Hedgehog hint N. 2003586; Hedgehog hintC. 2000320; HH_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1000320; HH signal.
1001767; Pept C46 hint.
1001657; Peptidase_C46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       042; HH signal; 1.)5; HintC; 1.)6; HintN; 1.
                                                                                             f Xenopus laevis."
21:2337-2347(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palmitate
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9; Hint; 1.
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                                  achy P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398
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   CGrew
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TISSUB=Cerebellum,

BEDLINE=25564621, PubMed=7637580,

SaijOh K., SaitOl N., Lee M.J., Fujii M., Kobayashi T., Sumino K.

"Molecular cloning of cDNA encoding a bovine selenoprotein P-likk

"Molecular containing 12 selenocysteines and a (His-Pro) rich domain

protein containing 12 selenocysteines and a (His-Pro) rich domain

insertion, and its regional expression.";

Brain Res. Mol. Brain Res. 30:301-311(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a col. between the Swiss Institute of Bioinformatics and the EMBL out the buropean Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch. or send an email to license@isb-sib.ch).
                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi.
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Selenium; Selenocysteine; Repeat.

BY SIMILARITY.

SELENOPROTEIN P-LIKE PROTEIN.
                                 P49907; 019003;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Selenoprotein P-like protein precursor.
SEPPI OR SELP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H-P REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D25220; BAA04949.2; --
EMBL; D88033; BAA23414.1; --
EMBL; D88031; BAA23414.1; JOINED.
EMBL; D88032; BAA23414.1; JOINED.
InterPro; IPR007672; SelP_C.
InterPro; IPR007671; SelP_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF04593; SelP C; 1.
Pfam; PF04592; SelP N; 1
                     STANDARD;
                                                                                                                                                                                                                        Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal; SIGNAL 1
                                                                                                                                                           Bos taurus (Bovine).
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         NCBI_TaxID=9913;
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399
204
                     SELP BOVIN
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SELP BOVIN
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STRAIN=HI6 / DSM 428 / ATCC 17699;

MEDLINE=95283415; PubMed=7763137;

Schaeferfohann J., Yoo J.-G., Bowien B.;

Schaeferfohann J., Yoo J.-G., Bowien B.;

"Analysis of the genes forming the distal parts of the two cbb CO:
fixation operons from Alcaligenes eutrophus.";

Arch. Microbiol. 163:291-2951.

-! CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceroyl phosphate.

-! PATHMAX: Calvin cycle.

-! PATHMAX: Calvin cycle.

-! SUBUNIT: Monomer (By similarity).

-! SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics and the EMBL out: the Buropean Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for \alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoid
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Bogan A., Maina C.V., Yamamoto K., Cohen F., Sluder A.E.;

"Caenorhabditis elegans nuclear receptor sequences exhibit biophy compatibility with the ligand-binding domain fold.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a coll:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/. or send an email to license@isb-sib.ch)
                                                                                                                                            Alcaligenes eutrophus (Ralstonia eutropha).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the phosphoglycerate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.5%; Score 7; DB 1; Length 413; 100.0%; Pred. No. 93; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Phosphoglycerate kinase, chromosomal (EC 2.7.2.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NH59_CAEEL STANDARD; PRT; 416 AA. O9TXZI, Q9GTPZ; 1, Q9GTPZ; 29-FBB-2003 (Rel. 41, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) NHR-59 OR T27B7.1.
             413 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U12422; AAC43444.1; -. PIR; I39551; I39551.
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InterPro; IPR001576; PGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100...
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 EFSATAA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 EFSATAA 294
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                       NCBI_TaxID=510;
             PGKC ALCEU
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NH59 CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UE; PubMed=7763137;
1J., Yoo J.-G., Bowien B.;
he genes forming the distal parts of the two cbb CO2
ns from Alcaligenes eutrophus.";
J. 163:291-2991(1995).
ACTIVITY: AFF + 3-phospho-D-glycerate = ADP + 3-
glyceroyl phosphate.
Jalvin cycle.
Incomer (By similarity).
R. LOCATION: Cycoplasmic.
R. LOCATION: Cycoplasmic.
R. Belongs to the phosphoglycerate kinase family.
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eobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                           2.5%; Score 7; DB 1; Length 402;
100.0%; Pred. No. 91;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .11; PGLYCERATE KINASE; 1.
(inase; Calvin cycle; Plasmid.
2 AA; 42298 MW; 9E84C666859E7274 CRC64;
             181 SRPQ -> KALE (IN REF. 2).
256 T -> P (IN REF. 2).
282 L -> V (IN REF. 2).
312 Y -> D (IN REF. 2).
45018 MW, B7CF18751FB0E8FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           cel. 34, Last sequence update)
cel. 41, Last annotation update)
te kinase, plasmid (BC 2.7.2.3)
                                                                                                                                                                                                                                                                                                                                      412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trophus (Ralstonia eutropha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93;
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100.0%; Pred. No.
POLY-HIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ae; Ralstonia.
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)01576; PGK.
PGK; 1.
                                                                                                                                                                  nservative
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                                                                                                                                                                                                                                                                                                                                      STANDARD;
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AA 293

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8ZYE7;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phosphoglycerate hydro-lyase)
                                                                                                                                                                                                                                                                                                 -!- INDUCTION: By acute inflammation.
-!- SIMILARITY: Belongs to the serpin family.
-!- CAUTION: It is uncertain whether Met-1 or Met-11 is the initi
MEDLINE=90306038; PubMed=1694763;
Pages G., Rouayrenc J.F., le Cam G., Mariller M., le Cam A.;
"Molecular characterization of three rat liver serine-protease
inhibitors affected by inflammation and hypophysectomy. Protein
mRNA analysis and cDNA cloning.";
Eur. J. Biochem. 190:385-391(1990).
                                                                                                                              SEQUENCE OF 203-408 FROM N.A. MEDLINE=8114617; PubMed=3493437; Hill R.E., Hastie N.D.; "Accelerated evolution in the reactive centre regions of serine protease inhibitors:"; Nature 326:96-99(1987).
-!- FUNCTION: INHIBITS TRYPSIN, BUT NOT CHYMOTRYPSIN OR BLASTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serpin; Serine protease inhibitor; Glycoprotein; Signal.
SIGNAL 29 BY SIMILARITY.
CHAIN 30 418 CONTRAPSIN-LIKE PROTEASE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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100.0%; Pred. No. 94;
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C -> S (IN REF. 2).
D -> S (IN REF. 2).
N -> S (IN REF. 2).
E -> S (IN REF. 3).
V -> A (IN REF. 3).
O -> F (IN REF. 3).
O -> F (IN REF. 3).
O -> F (IN REF. 3).
O -> F (IN REF. 3).
O -> F (IN REF. 3).
O -> F (IN REF. 3).
O -> F (IN REF. 3).
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                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: Liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46651 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D00753; BAA00650.1; --
EMBL; X16359; CAA34408.1; --
EMBL; X13150; CAA31548.1; --
HSSP; P01011; 2ACH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00284; SERPIN;
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354
381
418 AA;
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CARBOHYD
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ENO PYRAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Or entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation—Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial itself a license alreement (See http://www.isb-sib.ch/announce/ailto license@ibb-sib.ch).
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heria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nscription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rel. 35, Last sequence update)
Rel. 35, Last annotation update)
ke protease inhibitor 6 precursor (CPI-26) (Serine bitor 3) (SPI-3) (SPI-2.2).
                                                                                                                                                                                                                               Belongs to the nuclear hormone receptor family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 416; . 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
       to the EMBL/GenBank/DDBJ databases.
                                                          1 N2;
sley P., O'Brien D.;
G-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                      N-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D4A21CA587ED96D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEAR RECEPTOR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR RECEPTOR; FALSE NEG.
                                                                                                                                                                                        Orphan nuclear receptor.
R LOCATION: Nuclear (Potential)
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100.0%; Pred. No. 2...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       001628; Znf_C4steroid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of C4steroid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 7; AAG15156.1; -. 5; AAF02172.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47721 MW;
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ZnF

1A6Y

요큐크되짓것같라면요요요리라라밤까까용이상용상상용상상등맞습통도통요요료료

AA;

ISA 177

1 N.A.

116;

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Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Signier P., Tebebult P., Wahlen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
In Nature 415:497-502(2002).
--- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
phospho-D-glyceroyl phosphate.
--- phospho-D-glyceroyl phosphate.
--- SUBLIMIT: Monomer (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collibetween the Swiss Institute of Bioinformatics and the EMBL outs the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for ce entities requires a license agreement (See http://www.isb-sib/ch/cor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huang M. E., Manus V., Chuat J.-C., Galibert F., reveals 36 open "Analysis of a 62 kb DNA sequence of chromosome X reveals 36 open reading frames and a gene cluster with a counterpart on chromosom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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01-FEB-1996 (Rel. 33, Last sequence update)
01-07-1996 (Rel. 34, Last annotation update)
Hypothetical 49.5 kDa protein in MIRI-STEI8 intergenic region.
VJR0084W OR J1860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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PROSITE; PSO0111; PGLYCERATE KINASE; 1.
Transferase; Kinase; Glycolysis; Complete proteome.
SEQUENCE 419 Aa; 43268 MW; 82192410852E3D81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.5%; Score 7; DB 1
100.0%; Pred. No. 95;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288c;
MEDLINE=96437976; PubMed=8840504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL646060; CAD14101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z49584; CAA89611.1; -. EMBL; L47993; AAB39307.1; -.
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InterPro; IPR001576; PGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
Les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00162; PGK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 EFSATAA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 EFSATAA 295
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P47130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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           셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tentry is copyright. It is produced through a collaboration wiss Institute of Bioinformatics and the EMBL outstation-sichiformatics Institute. There are no restrictions on its right institutions as long as its content is in no way his statement is not removed. Usage by and for commercial res a license agreement (See http://www.isb-sib.ch/announce/il to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                      Magnesium is required for catalysis and for stabilizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                        ad. Sci. U.S.A. 99:984-989(2002).
ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate
                                                                                                                                                                                                                                             ce of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                   T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genin S., Artiguenave F., Gouzy J., Mangenot S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.5%; Score 7; DB 1; Length 419; 100.0%; Pred. No. 95; vative 0; Mismatches 0; Indels
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BY SIMILARITY.

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                lomodiner (By similarity).
R LOCATION: Cytoplasmic (By similarity).
Belongs to the enolase family.
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                            rophilum.
rchaeota; Thermoprotei; Thermoproteales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lel. 41, Last sequence update)
lel. 41, Last annotation update)
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                                                                                                                                                         TCC 51768 / DSM 7523;
97; PubMed=11792869;
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                                                                                                                                                                                                                                                                                                                                                                            similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'sis; Magnesium;
                                                                           ae; Pyrobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02; Enolase; 1.
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8; ENOLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enolase; 1.
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이 불 이 당 본 단 본 쁨 왜 왜 온 은 % 뭐 될 싶 점 없

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-!- TISSUE SPECIFICITY: Oocytes.
-!- DEVELOPMENTAL STAGE: Expressed during the 2-week growth phase oogenesis, prior to ovulation.
-!- PTM: Sulfated glycoprotein with 0-linked oligosaccharides.
-!- PTM: Sulfated glycoprotein with 0-linked oligosaccharides.
-!- SIMILARITY: Contains 1 ZP domain.
                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a coll between the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is ir modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
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STRAIN=MoPn / Nigg;
MREDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZONA PELLUCIDA SPERM-BINDING PROTEIN EXTRACELLULAR (POTENTIAL).
SUBCELLULAR LOCATION: Type I membrane protein. Extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO0682; ZP_DOMAIN; 1.
Glycoprotein; Signal; Sulfation; Sperm; Receptor; Transmembrane;
Extracellular matrix.
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LINKED (GLCNAC. . .) (POTENTIAL)
LINKED (GLCNAC. . .) (POTENTIAL)
LINKED (GLCNAC. . .) (POTENTIAL)
LINKED (GLCNAC. . .) (POTENTIAL)
9089903PBD268365 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 424;
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100.0%; Pred. No. 96;
tive 0; Mismatches
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EMBL; X14376; CAA32550.1; --
FIR, A30334; A30334.
MCD; MGI:99215; Zp3.
InterPro; IPR001507; Endoglin/CD105.
FFAM; PF00100; Zona_Dellucida; 1.
FRINTS; PR00023; ZPELLUCIDA.
SMART; SM00241; ZP; 1.
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424 AA;
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                                                                               ; VIROB4W.
0; C:signalosome complex; IDA.
4; P:adaptation to pheromone during conjugation . . .; IMP.
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equence of the gene encoding zona pellucida glycoprotein % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Functions as a sperm-receptor. It is responsible for lession to the zona pellucida, and may contribute to the specificity of the insemination.
ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Chamberlin M.E., Baur A.W., Sobieski D.A., Dean J.; alysis of cDNA coding for ZP3, a sperm binding protein zona pellucida.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rel. 35, Last sequence update)
Rel. 39, Last annotation update)
a sperm-binding protein 3 precursor (Zona pellucida ZP3) (Sperm receptor) (Zona pellucida protein C).
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                                                                                                                                                                                                                                                                                                      AA; 49482 MW; 750CDA631916A621 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .cad. Sci. U.S.A. 85:6409-6413(1988).
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                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                              Score 7; DB 1;
Pred. No. 95;
0; Mismatches
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Res. 17:2861-2863(1989)
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100.0%; Pred
0; N
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048; PubMed=2541416;
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Rel. 35, Last seqn
Rel. 39, Last anno
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This SWISS-PROT entry is copyright. It is produced through a collèbetween the Swiss Institute of Bioinformatics and the EMBL outs the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contities requires a license agreement (See http://www.isb-sib.ch/cor send an email to license@isb-sib.ch).
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MEDIINE=89359127; PubMed=2549005;
Tichy H.V., Oberle B., Stiehle H., Schiltz E., Drews G.;
"Genes downstream from pucB and pucA are essential for formation of the B800-850 complex of Rhodobacter capsulatus.";
J. Bacteriol. 171:4914-4922(1989).
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Tichy H.V., Albien K.-U., Gad'On N., Drews G.,;
"Analysis of the Rhodobacter capsulatus puc operon: the pucC gene
plays a central role in the regulation of LHII (8800-850 complex)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00875; DNA photolyase; I.
Pfam; PF03441; FAD binding 7; 1.
PRINTS; PR00147; DNAPHOTLYASE:
PROSITE; P8001399; FAD binding N; 1.
PROSITE; P800394; DNA_PHOTOLYASES_1_1; 1.
PROSITE; P800691; DNA_PHOTOLYASES_1_2; 1.
Lyase; Chromophore; Flavoprotein; FAD; DNA repair; DNA-binding.
DNA_BIND 300 319 H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Protecbacteria; Alphaprotecbacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
-!- SIMILARITY: Belongs to the DNA photolyase class-1 family.
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100.0%; Pred. No. 1e+02;
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01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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InterPro; IPR002081; DNA_photolyase_1.
InterPro; IPR006050; DNA_photolyase_N.
InterPro; IPR005101; FAD_binding_N.
InterPro; IPR006101; FAD_binding_N.
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                                                                                                                                                                                                                                                                                                                 EMBL; X15060; CAA33161.1; -.
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Matches 7; Conservative
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PUCC_RHOCA
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                                                                                                                                                                                                           Tentry is copyright. It is produced through a collaboration wiss Institute of Bioinformatics and the EMBL outstation-ioinformatics Institute. There are no restrictions on its rofit institutions as long as its content is in no way his statement is not removed. Usage by and for commercial res a license agreement (See http://www.isb-sib.ch/announce/ilto license@isb-sib.ch).
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This enzyme catalyzes the light-dependent monomerization lM) of cyclobuty1 pyrimidine dimers (in cis-syn ion), which are formed between adjacent bases on the strand, upon exposure to ultraviolet radiation.
ACTIVITY: Cyclobutadipyrimidine (in DNA) = 2 pyrimidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contains 2 chromophores: a reduced flavin (FADH2) and an 3-hydroxy-5-deazaflavin (F420). Both chromophores are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2), At TRNA LIGASE II; 1.
synthetase, Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                       Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ion-covalent interactions.
SOUS: THIS PROTEIN BELONGS TO THE "LONG WAVELENGTH-TYPE
IS" WITH AN ABSORPTION MAXIMUM AT ABOUT 440 NM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  el. 12, Last sequence update)
el. 31, Last annotation update)
imidine photolyase (EC 4.1.99.3) (DNA photolyase)
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                   ACTIVITY: ATP + L-histidine + tRNA(His) = AMP e + L-histidyl-tRNA(His).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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100.0%; Pred. No. 96;
ive 0; Mismatches
                                                                                            omodimer (By similarity).
                                                                                                                            Cytoplasmic.
Res. 28:1397-1406(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02314; tRNA-synt_2b.
06195; tRNA_ligase_II.
HGTP_anticodon; 1.
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81660.
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00442; hiss; 1.
62; AA TRNA LIGA
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                                                                                                                            LOCATION:
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                     OT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the BMBL outstation - Bioinformatics Institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial iters a license agreement (See http://www.isb-sib.ch/announce/ailto license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KW20 / ATCC 51907;
3630; PubMed=7542800;
3.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
3., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oteobacteria; Gammaproteobacteria; Pasteurellales;
sae; Haemophilus.
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BFC7A8A0C549875A CRC64;
AR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                   PERIPLASMIC (PROBABLE).
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                                                                                                                                                                                           CYTOPLASMIC (PROBABLE)
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CYTOPLASMIC (PROBABLE)
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100.0%; Pred. No. 1e+02;
tive 0, Mismatches 0
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                           AAA26163.1; ALT_INIT.
                                                                                                                                                                               ex; Transmembrane.
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376
394
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Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.(
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR01898; Na/sul symport.
Pfam; PF00939; Na sulph symp; 1.
TIGRPAMs; TIGROPS5; dass; 1.
PROSITE; PS01271; NA SULPATE; 1.
Hypothetical protein; Transmembrane; Transport; Complete proteom
                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a coll between the Swiss Institute of Bioinformatics and the EMBL out the Buropean Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.ch. or send an email to license@isb-sib.ch).
                                                                                "Whole-genome random sequencing and assembly of Haemophilus infl
                                                                                                                                             -i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5%; Score 7; DB 1; Length 461; 100.0%; Pred. No. 1e+02; ative 0; Mismatches 0; Indels
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PIR; I64080; I64080.
TIGR; H10608; -.
                                                                                                                            Science 269:496-512(1995).
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Best Local Similarity
7; Conserve
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439
461 AA;
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2.8 193 10 QBL4K2 2.8 211 5 Q9WYU 2.8 211 5 Q9WYO 2.8 211 5 Q8XH4 2.8 220 16 QBFVS9	232 16 8 278 16 8 278 16 9 279 11	8 306 5 8 317 6 8 317 6	.8 317 6 .8 317 6 .8 317 6	.8 317 6 .8 317 6 .8 317 6	.8 317 6 .8 317 6 .8 317 6 .8 317 6	.8 317 6 .8 317 6 8 317 6	.8 339 17 .8 342 4 .8 343 4	.8 370 17 .8 372 16 .8 372 16	.8 375 1 .8 377 16 .8 387 10	.8 431 16 .8 435 16 .8 465 16	.8 472 4 .8 473 11 .8 473 11	.8 522 10 .8 535 2 .8 537 16	.8 564 12 .8 568 12 .8 568 12	.8 656 5 .8 1523 5	.5. .5. .3. .5. .4. .2.	.5 54 16 .5 67 2 .5 69 10	.5 86 16 .5 94 4 .5 97 16	.5 98 10 .5 100 5	.5 104 16 .5 108 9
17 18 19 19 19 10 10 10 10 10 10 10 10 10 10 10 10 10																			
	updates/sec	QVH 284										-		!	en ulu la	la hia hia	E C	onas rell teri	ativ ote cocc
5.1.6 Compugen Ltd.	Search time 45 Seconds (without alignments) 1991.270 Million cell	. PWAHLKAAPFLTYFGLFQ			satisfying chosen parameters: 1017041 :: 0 :: 2000000000							archeap:*  number of results predicted by chance to have a  t or equal to the score of the result being printed  analysis of the total score distribution.		Description	Q8izk7 homo sapien Q8bxs2 mus muscul O7vvb7 bordetella	Q7w7f2 bordetel Q8x4j8 escheric	Q7uc61 shigella Q98ij0 rhizobiu	QBppzB xanthomonas Q7ulk4 rhodopirell Q9hst7 halobacteri	Q94811 oryza sztrv Q848k4 gamma-prote Q86569 streptococc Q8džk5 streptococc

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	Nath EME PIR GO;	DR GO; GO: 0006955; P: immune response; IEA.  DR InterPro; IPR006052; TNF family.  DR INTERPO; IPR0060983; TNF-like.  DR SMART; SM00207; TNF; 2.  DR PROSITE; PS000251; TNF 1; 1.  DR PROSITE; PS00049; TNF 2; 2.  SQ SEQUENCE 410 AA; 4581 MW; S90A4B74C33FB8D4 CRC64;	Similarity 2; Conserva	AIAAHYEVHPRPGQDGA 	RESULT 3 Q7VVB7  ID Q7VVB7  AC (Q7VVB7)  DT 01-0CT-2003 (TrEMBLrel. 25, Created) DT 01-0CT-2003 (TrEMBLrel. 25, Last sequence update) DT 01-0CT-2003 (TrEMBLrel. 25, Last sequence update) DT 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) DE Putative chloride-channel protein.		ROUGENCE FROM N.A.  REQUENCE FROM N.A.  RY STRAIN=Tohana I / Arcc BAA-589 / NCTC 13251;  RX MEDLINE=22827954; PubMed=12910271;  RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,  RA HARTIS D.E., Holdem M.T.G., Churcher C.M., Bentley S.D., Murgall  RA HARTIS D.E., Holdem M.T.G., Churcher C.M., Bentley S.D., Murgall  RA HARTIS D.E., Holdem M.T.G., Churcher C.M., Bentley S.D., Murgall	RA Achtman M., Atkin R., Benjare D., Damme D., Bason N., Cherevach I RA Achtman M., Atkin R., Basham D., Bason N., Cherevach I RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels I RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price RA Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., RA Sharb S., Simmond M., Skelton J., Squares R., Straver	RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.; RT "Comparative analysis of the genome sequences of Bordetella perturers and Bordetella bronchiseptica."; RL Nat. Genet. 35:32-40(2003). DR EMBL; BX640419; CAE43035.1; COMPLEE Protecome XW Complete protecome SQ SEQUENCE 438 AA; 45402 MW; AD51A65B595D99D8 CRC64;	Query Match 4.2%; Score 12; DB 16; Length 438; Best Local Similarity 100.0%; Pred. No. 0.0062; Matches 12; Conservative 0; Mismatches 0; Indels 0;
Q9hy60 pseudomonas Q928f7 pseudomonas Q928g5 listeria in Q941x6 euphorbia t Q84pv3 oryza sativ Q84fpv3 oryza sativ Q8eff2 shewanella Q8ugh2 agrobacteri Q7n8Z3 synechococc Q7xx77 oryza sativ		odate) update)	rata; Euteleostomi; nidae; Homo.	Lozano J.C., rcia-Sanz J.A.,	PRIL, a functional cell surface receptor binding; IEA.	B CRC64;	Length 330; 55; Indels 0; Gaps 0; 1. LatvVsLGSRASLSAQEPAQEEL 95	LLAVVSLGSRASLSAQEPAQEEL 60 GRKTRARRAIAAHYEVHPRPGQD 155 GRKTRARRAIAAHYEVHPRPGQD 120	AGLYYLYCQ 201           	te) date)
2.5 115 16 Q9HY60 2.5 118 2 Q93.9F7 2.5 118 16 Q928G5 2.5 119 10 Q94LX6 2.5 121 10 Q8WM1 2.5 122 10 Q8FG2 2.5 122 16 Q8FG2 2.5 123 16 Q7GR23 2.5 123 16 Q7GRZ3 2.5 124 10 Q7XRX7 2.5 125 5 Q9U1P6	SNME	RELIMINARY; PRT; 330 AA. TYEMBLYEL. 23, Created) TYEMBLYEL. 23, Last sequence update TYEMBLYEL. 25, Last annotation update (Human).	stazoa; Chordata; Craniata; Vertebrata; But sheria; Primates; Catarrhini; Hominidae; Ho	1 N.A. 1924; PubMed=12411489; 1 B., Medema J.P., Lopez-Fraga M., Lozano J 1.M., Picard A., Martinez-A C., Garcia-Sanz	us hybrid mRNA encodes TWE-PRIL, a habon protein."; 11-5720(2002). 11, AALSO443.1; 10, C:membrane; IEA. 4; F:tumor necrosis factor receptus; P: P:immune response; IEA. 1006052; TWF family. 1008983; TWF like.	; TNF; 1. 77; TNF; 1. 1251; TNF 1: 1. 1049; TNF 2; 2. 10 AA; 36588 MW; FC6F3BCA29C029AB	58.5%; Score 166; DB 4; Length arity 100.0%; Pred. No. 1.3e-155; Conservative 0; Mismatches 0; Inde (RSGRREGEFOTALLYPLALGIGIALLACUSICALLAVVSICALLAVVIC	RSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGS DODPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARR	AGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQ 	PRT; 410 AA. (TrEMBLrel. 23, Created) (TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 25, Last annotation update)

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ELIMINARY;

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MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome seque
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STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
Wei J. Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Bscherichia.
NCBI_TaxID=217992;
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Enterobacteriaceae, Shigella.
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3.5%; Score 10; DB 16; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                          3.5%; Score 10; DB 16; Length 111; 100.0%; Pred. No. 0.17; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
EMBL; AR016763; AAN81254.1;
Hypochetical protein; Complete proteome.
SEQUENCE 111 AA; 12196 MW; C0A977B6F77A4B87 CRC64;
                   PIR; A85866; A85866.

GO; GO:0016020; C:membrane; IEA.
InterPro; IPR000620; DUF6.
Pfam; PF00892; DUF6; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 111 AA; 12165 MW; 7CEFC93D786CD759 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved hypothetical protein.
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01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
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STRAIN=06:H1 / CFT073 / ATCC 700928;
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EMBL; AE005458; AAG57389.1; -.
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'ATCC BAA-587;

J54; PubMed=12910271;

J6baihia M., Preston A., Murphy L.D., Thomson N.,

J6lden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

J8 A.M., Temple L., James K., Harris B., Quail M.A.,

Kin R., Baker S., Basham D., Bason N., Cherevach T.,

T., Collins M., Cronin A., Davis P., Doggett J.,

J6ble A., Hamlin N., Hauser H., Holtoyd S., Jagels K.,

Jolle A., Hamlin N., Hauser H., Holtoyd S., Jagels K.,

Johle A., Sanders M., Saunders D., Seeger K.,

nonds M., Skelton J., Squares R., Squares S., Stevens K.,

Janead S., Barrell B.G., Maskell D.J.,

Janead S., Barrell B.G., Maskell D.J.,

Janead S., Barrell B.G., Maskell D.J.,

Japertussis,

Japertussis,
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nce of enterohaemorrhagic Bscherichia coli OL57:H7.";
9-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ceobacteria; Gammaproteobacteria; Enterobacteriales;
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935; PubMed=11206551;
lunkett G. III, Burland V., Mau B., Glasner J.D.,
yhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
ckett J., Klink S., Boutin A., Shao Y., Miller L.,
Davis N.W., Lim A., Dimalanta E.I., Potamousis K.,
nantharaman T.S., Lin J., Yen G., Schwartz D.C.,
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.eobacteria, Betaproteobacteria, Burkholderiales,
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rEMBLrel. 20, Last sequence update)
rEMBLrel. 24, Last annotation update)
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TEMBLrel. 25, Last sequence update)
TEMBLrel. 25, Last annotation update)
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); CAE37862.1; -.
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SEQUENCE FROM N.A.

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TABLES 2022145; PubMed=12024217;

A GASILVA A.C.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.

A GAILVA A.C.C.R., Ferro J.A., Reinach F.C., Camargo L.E.A.,

A live B. Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.

Alvee L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Cicarelli R.B., Coutinho L.L., Cursino-Santos J.R., Clapina L.P.

Ratia J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratia J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Ratia J.B., Ratia A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.

Ratiana J.B., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.W.

Locali B.C., Maidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Morelira L.A.F., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.

Trinade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Comparison of the genomes of two Xanthomonas pathogens with dif

Nature 417.459-463 (2002)

REMBI, AE011680; AAM3543.1; -.

ROJ, GO:001000489; F:electron transporter activity; IEA.

ROJ, GO:00100118 P:electron transporter IEA.
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M. Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., Webb E.A., Zinser B.R., Chieholm S.W., Former divergence in two Prochlorococcus ecotypes reflects oceaniche differentiation "b. Nature 424:1042-1047(2003).

Babl. MSTST100, CAE21944.1. -. Photosystem I; Complete proteome. SEQUENCE 749 AA; 83231 MW; BID496645FIC790C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JTD -2003 (TrEMBLrel. 24, Last annotation update)
C-type cytochrome biogenesis protein (Copper tolerance)
DSBD OR XACO534.
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InterPro; IPR006662; Thiored.
InterPro; IPR006663; Thioredox dom2.
Pfan; PF02683; D8bD; 1.
PROSITE; PS00194; THIOREDOXIN; 1.
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Best Local Similarity 100.00
Best Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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      N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
., Blattner F.R.;
iome sequence and comparative genomics of Shigella
ltype a strain 2457T.";
1.71:2775-2786(2003).
                                                                                                                                                                                                                                                                                                                            0;
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anobacteria, Prochlorophytes, Prochlorococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oteobacteria, Alphaproteobacteria, Rhizobiales, iaceae, Mesorhizobium.
                                                                                                                                                                                                                                                                Score 10; DB 16; Length 111;
Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5698; PubMed=12917642; rimer F.W., Lamerdin J., Malfatti S., Chain P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.2%; Score 9; DB 16; Length 142; 100.0%; Pred. No. 2.1; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA; 14884 MW; 0DCA7842CB5A5E6F CRC64;
                                                                                                                                                                                                            11 AA; 12224 MW; 7CFA06CC46A32672 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
I PsaB protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 18, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 18, Last annotation update)
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                                                                                                                                                                                                                                                                               100.0%; Pred. w...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2930; PubMed=1121496B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99; BAB49526.1; -.
                                                                                                                           1. 71:2//5
36; AAP17670.1; -.
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                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-338 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                            ALACLGL 49
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Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta
Spermatophyta; Magnollophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativan nipponbare(GA3) genomic DNA, chromosome 1, BAC "Oryza sativan nipponbare(GA3) genomic DNA, chromosome 1, BAC clone: B1085F09.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP0018015; BAA8734.1;
EMBL, AP002862; BAB17732.1;
EMBL, AP003103; BAB4106.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Nytya sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0003H10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
clone:OSJNBa0036802.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.8%; Score 8; DB 10; Length 151; 100.0%; Pred. No. 22; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (OSJNBA0036E02.6 protein) (B1085F09.2
2.8%; Score 8; DB 17; Length 143;
100.0%; Pred. No. 21;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AA; 16632 MW; EC68451ECA2BD71D CRC64;
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01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-UN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment)
Gamma-proteobacterium Hot 75m4.
Bacteria, anvironmental samples.
NCBL_TAXID=77133;
                                                                                                                                                                                                                                                                                                                                 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                8; Conservative
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                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                       61 LGLGLALA 68
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Best Local Similarity
      Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gramene; Q9SDI1;
                                                                                                                                                                                                                                                                                                                                                             Q9SDI1;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B1085F09.2.
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Q9SDI1
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edy S.P., Mahairas G.G., Berquist B., Pan M.,
Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
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, Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
tas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
owe T.M., Liang P., Riley M., Hood L., DasSarma S.,
nce of Halobacterium species NRC-1.",
cad. Sci. U.S.A. 97:12176-12181(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ome sequence of the marine planctomycete Pirellula sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  il3; PubMed=12835416;
., Kube M., Bauer M., Teeling H., Lombardot T.,
le D., Beck A., Borzym K., Heitmann K., Rabus R.,
Amann R., Reinhardt R.;
                                                                                                                                                                                                                                                                                                                                                                                                              octomycetes; Planctomycetacia; Planctomycetales; seae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 1208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
grchaeota, Halobacteria, Halobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA; 132047 MW; 0FFE225741021E8C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                          'rEMBLrel. 25, Last sequence update)
'rEMBLrel. 25, Last annotation update)
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}; CAD76265.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.2%; Score 9; DB 16
100.0%; Pred. No. 15;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 A.A.
                                                                                                                                                                                    PRT; 1208 AA
                                                                                                                                                                                                                                                                                                                                    multi-functional protein.
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frEMBLrel. 16, Last sequ
frEMBLrel. 24, Last annotement
                                                                                                                                                                                                                                              'rEMBLrel. 25, Created)
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GLAL 542
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3 AA;
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<sup>wall</sup> Here in the sease of a set in

(TrEMBLrel. 23, Created) (TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 24, Last annotation update)

protein.

190 AA.

RELIMINARY;

0;

0; Mismatches

2.8%; Score 8; I 00.0%; Pred. No.

100.0%;

Conservative

GRRG 119

GRRG 49

·.

DB 16; Length 190; 0; Indels

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STRAIN=cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C
"Oryza sativa chromosome 10 BAC OsJUNB0079H13 genomic sequence."
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M
Overton Il L.L., Tsirrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Ziemann V., Hsiao J., Blunt S
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.O., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBD0038H12 genomic sequence."
Submitted (SEP-2002) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyt
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Nipponbare;
The Rice Chromosome 10 Sequencing Consortium;
"In-depth view of structure, activity, and evolution of rice
                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2003 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
OSJNBA0079H13.8 OR OSJNBB0038H12.21.
193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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s agalactiae (serotype V). rmicutes; Lactobacillales; Streptococcaceae;

(TrEMBLrel. 23, Created) (TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 24, Last annotation update)

pothetical protein.

190 AA.

PRELIMINARY;

2.8%; Score 8; DB 1 100.0%; Pred. No. 27; iive 0; Mismatches

Conservative

larity

IRTLP 265

57

IRTLP

Complete proteome.

protein; Complete 90 AA; 22178 MW;

natal disease."; 51. 45:1499-1513(2002). 49; CAD46822.1; -.

5 / Serotype III; 2508; PubMed=12354221;

R008172; Adenylate\_cyc.

s1163;

CYTH; 1.

C:extrachromosomal DNA; IEA

protein; Plasmid.

30; AAO59972.1; -.

16495; MN.A.

"; 66-1569(2003).

ponbare;

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AAP52530.1; -.

rotein.

nservative

RGE 123

RGE 50

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F., Amanatides P.G., Scherer S.E., Holt R.A., Ends Q., Chen L.X., Sutcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutcon G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.I. Man K.H., Doyle C.C., Baxter B.G., Hell G., Nelson C.R., Miklos G.L. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin B. Ballew R.M., Baau A., Baxendale J., Borstein D., Bolshakov S., Berson R.Y., Bernos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burkis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dahlke C., Davenport L.B., Davies P., Dahlke C., Perraz C., Ferrisca S., Pleischman B. Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dedon K.J., Evangelista C.C., Ferraz C., Ferraz S., Fleischman B. P., Harris M., Harris M., Harvey D., Heinan T.J., Hernandez J.R., Houck J., Jalali M., Kalueh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lians Y., Levitesky A.A., Li J., Murphy L., Murphy L., Murphy L., Murphy L., Murphy L., Murphy L., Murphy L., Murphy L., Murphy L., Murphy L., Murphy L., Smith T., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith J. Shue S.M., Moyem R., Moodage T., Worley K.C., Wu D., Yang G., Zhao Q., Zheng X.H., Khong R.N., Morley K.C., Wu D., Yang G., Zhao Q., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao G., Zh
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Revans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y
Brans O.J., M. Center A., Champe M., Davengort L.B., Dietz S.M.,

A carlson J.W., Center A., Champe M., Davengort L.B., Dietz S.M.,

A podson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

A Ferritara S., Frise B., Galle R.P., Garg N.S., George R.A.,

A Ferritara S., Frise B., Houst B., Mattei B., Moshrefi A.,

A podlac M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

McIntosh T.C., Moy M., Murphy B., Nalson C., Nalson K.A., Nunco J.

A pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phousnenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.

A Williams S.M., Zaverii J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell: Misra S., Crosby M.A., Matthews B.B., Prochnik S.E., Smith C.D., Tradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N. Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.N.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.";
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                           STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
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                                                                         NCBI TaxID=7227;
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llayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
key E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
ltterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Sutton G.G., Felschman R.D., Eisen J.A., White O.,
Smith H.O., Venter J.C., Farser C.M.;
lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                             ng R.A., McCombie W.R., Messing J., Yuan Q.; -2003) to the EMBL/GenBank/DDBJ databases.; AAM54153.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 197;
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                                                                                                                                                                                                                                                                                                                 20812 MW; 719E44BFBC9A0790 CRC64;
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Last annotation update)
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'rEMBLrel. 12, Last sequence update)
'rEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. 28;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                  2.8%; Score 8; DB 1
100.0%; Pred. No. 27;
iive 0; Mismatches
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rotein TM0469

DSM 3109;

wgpaderemand서울한감워워워워워워워워워워워

ELIMINARY;

frEMBLrel. 13, C frEMBLrel. 22, I frEMBLrel. 24, I

##USEEEEE

ELIMINARY;

nnervative

EIS 142

EIS 9

-329 (1999)

72374.

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"Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
BNBL; AR005557; BAC51491.1; -..
GO; GO:0016020; Camembrane; IEA.
GO; GO:0005215; Firransporter activity; IEA.
GO; GO:0006810; Pitransporter activity; IEA.
GO; GO:0005215; BPD transp.
Fransporter PF00528; BPD transp.
Fransporter 232 AB; 23704 MW; CD805BDIF43F1B46 CRC64;
                                                                                                                                                                                                  Read T.D., Seehadri R., Nelson K.E., Eisen J.A., Heidelberg J. Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken Riedmuller S., Tettelin H., Gill S.R., White O., Salbberg S.D., Indder L.E., Halling S.M., Boyle S.M., Fraser C.M., The Brucella suis genome reveals fundamental similarities betwee animal and plant pathogens and symbionts."; EMEL, Acad. Sci. U.S.A., 99:13148-13153 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Bradyrhizobiaceae, Bradyrhizobium.
1018_TaxID=375;
                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBL_TaxID=29461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 AA; 24796 MW; AC2C060433169497 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Membrane protein, putative.
                                                                                                                                                                                        MEDLINE=22247741; PubMed=12271122;
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR007916; UPF0191.
Pfam; PF05252; UPF0191; 1.
Complete protecome.
SEQUENCE 220 AA; 24796 MW.
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Best Local Similarity 100.v
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Best Local Similarity 100.(
Matches 8; Conservative
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                                                         Brucella suis.
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Q89GW9
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                                                     S.E., Gibbs R.A., Rubin G.M., Venter C.J., to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                       2.8%; Score 8; DB 5; Length 211;
100.0%; Pred. No. 29;
tive 0; Mismatches 0; Indels
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                                                                                                                                                    P-2002) to the EMBL/GenBank/DDBJ databases.
7; AAF49452.2; -.
.0036638; CG13033.
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 R-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                       AA; 23779 MW; D2554983E91F5107 CRC64;
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Last annotation update)
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(TrEMBLrel. 23, Last sequence update)
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100.0%; Pred. No. 29;
ative 0; Mismatches
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TrEMBLrel. 21, Last sequ
TrEMBLrel. 24, Last anno
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PRELIMINARY;

79 16

MAST AWSL

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1 N.A.

3004011; Gyr.

GYR; 1. YLP; 5.

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onservative

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WSL 79 WYSE 16

GYR; 1. YLP; 5.

RELIMINARY;

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Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                         Query Match 2.8%; Score 8; DB 16; Length 278; Best Local Similarity 100.0%; Pred. No. 38; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.8%; Score 8; DB 16; Length 278; 100.0%; Pred. No. 38; 0; Indels ative 0; Mismatches 0; Indels
                                                                                                                                                                          PIR; D83080; D83080.
GO; GO:0016021; C:integral to membrane; IEA.
Transmembrane; Complete proteome.
SEQUENCE 278 AA; 30793 MW; C623F1AB0691CFEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 AA; 28113 MW; 9545813BCAC0BFA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 24, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                      opportunistic pathogen.";
Nature 406:959-964(2000).
BEBL, AF082575; ARC98764.1; --
EMBL, AE004866; AAG07309.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative metalloproteinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces avermitilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               70 LGLLLAVV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 LALGLGLA 66
                                                                                                                                                                                                                                                                                                                                                                  47 LGLLLAVV 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q82J43
Q82J43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAV2939.
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q82J43
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                                                                                                                                                                                                                                                                                                                                              "T. Kim C.J., Shinn P., Bowser L., Carningi P., 'ashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., iG., Kawai J., Lam B., Lin J., Miranda M., Narusaka M., iGra C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., wick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., 'zaki K., Davis R.W., Theologis A., Ecker J.R.; 'RF clones."; 'RF clones."; 'Amaloackes."; 'Amaloackes."; 'Amaloackes."; 'Amaloackes."; 'Amaloackes."; 'Relectron transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dargis M., Huletsky A.;
in Pseudomonas aertginosa encodes a negative regulator
lactamase expression.";
3-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                               idiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; rassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
5692 / PAO1;
337; PubMed=10984043;
?ham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eobacteria; Gammaproteobacteria; Pseudomonadales;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.8%; Score 8; DB 10; Length 276;
100.0%; Pred. No. 37;
ive 0; Mismatches 0; Indels
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31368 MW; 99DE3DA0CB2C0BDF CRC64;
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EMBLrel. 10, Last sequence update)
EEMBLrel. 24, Last annotation update)
                                                                                                                                                          rEMBLrel. 24, Created)
rEMBLrel. 24, Last sequence update)
rEMBLrel. 25, Last annotation update)
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                                                                                                                            276 AA.
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                                                                                                                            PRT;
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)89; ZF RING 2: 1.
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01841; Znf_ring.
zf-C3HC4; 1.
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3692 / PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nservative
                                                                                                                            ELIMINARY;
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LGL 209
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        rgr 65
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RELIMINARY;

20

TGLA

protein. (Mouse)

MEDILINES.LUES 600; PUDNEGELLAIVES, IN MEDILINES.LUES 600; PUDNEGELLAIVES, IN MEDILINES.LUES 600; PUDNEGELAIVES, KASHIDA M., Town M., Tawaw T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S. Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I. Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R. Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbus Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washid Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.I. Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P. Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K. Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitteker C., Wilmin Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., STRAIN=C57BL/6J; TISSUE=Head, and Spinal cord;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome transcriptome based on functional annotat
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK01727; BAB30899.1; -EMBL; AK010294; BAB26830.1; -EMBL; AK19979; AAK01207.1; --99VNPO, 0882E8; 01-MXY-2000 (TTEMBLTE1. 13, Created) 01-0CT-2002 (TTEMBLTE1. 22, Last sequence update) 01-0CT-2002 (TTEMBLTE1. 22, Last annotation update) CG1169 protein (RE07882p). CG1169. Drosophila melanogaster (Fruit fly). Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Auquier P.H., Chomez P.M., De Backer O.R., Bertrand M.J.M.; "Ten new murine members of the MAGE gene family."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. 2.8%; Score 8; DB 11; Length 279; 00.0%; Pred. No. 38; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. 279 AA; 31460 MW; FE2435919BD63160 CRC64; 306 AA. Query Match Best Local Similarity 100.0%; Pred. No. 34; Ansarches MEDLINE=21085660; PubMed=11217851; EMBL; AK076471; BAC36358.1; -. MGD; MGI:1913897; 5730494G16Rik. EMBL; BC034892; AAH34892.1; -. EMBL; AK049759; BAC33907.1; -. EMBL; AK076471; BAC36358.1; -. InterPro; IPR002190; MAGE. Nature 409:685-690(2001). PRELIMINARY; Pfam; PF01454; MAGE; 1. PROSITE; PS50838; MAGE; SEQUENCE 279 AA; 3146 TISSUE=Mammary gland; 80 GSRASLSA 87 41 GSRASLSA 48 SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. Strausberg R. O9VNP0 RESULT 28 O9VNPO SO DER CHARLES OF THE g ò ö /67, TISSUE=Medulla oblongata;
/660; PubMed=1121781;
/shead A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
/shibata A., Shibata K., Yoshino H., Adachi J., Fukuda S.,
/sawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
/saki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
/steuda H.A., Ashburner M., Batalov S., Gaavant T.,
/v. Gaasrerland T., Gissi C., King B., Kochiwa H.,
/v. Gaasrerland T., Nikaido I., Pesole G., Quackenbush J.,
/steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
/do T., Furuno M., Aono H., Baldarelli R., Barsh G.,
/do T., Furuno M., Aono H., Baldarelli R., Barsh G.,
/do T., Fletcher C., Fujita M., Gariboldi M.,
/do Jult C., Fletcher C., Fujita M., Gariboldi M.,
/ding B., Ringwald M., Rodriguez I., Sakamoto N.,
/droffman J., Modriguez I., Sakamoto N.,
/droff M., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
/do S., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Gaps etazoa, Chordata, Craniata, Vertebrata, Buteleostomi, theria, Rodentia, Sciurognathi, Muridae, Murinae, Mus stazoa; Chordata; Craniata; Vertebrata; Euteleostomi; heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus annotation of a full-length mouse cDNA collection."; ., (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
k protein (Mage-gl) (RIKEN cDNA 5730494Gl6 gene). 2.8%; Score 8; DB 11; Length 279; 100.0%; Pred. No. 38; ive 0; Mismatches 0; Indels M N.A. /6J; TISSUE=Embryo, and Embryonic stem cells; 18; MAGE; 1. AA; 31474 MW; 5E243590A99F15F0 CRC64; TrEMBLrel. 17, Created) TrEMBLrel. 17, Last sequence update) TrEMBLrel. 23, Last annotation update) 279 AA. PRT; 50; BAB31133.1; -. 3897; 5730494G16Rik.

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R002190; MAGE.

4; MAGE;

35-690 (2001

larity 100. Conservative

ASLSA 87 ASLSA 48 PRELIMINARY;

(Mouse)

Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

lyBase

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

STRAIN-Berkeley;

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106; PubMed=10731132;

106; PubMed=10731132;

107; Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,

10. Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,

10. Scherer S.E., Li P.W., Hookins R.A., Galle R.F.,

10. Rogers Y.-H.C., Blazel R.G., Champen M., Henderson S.N.,

10. Rogers Y.-H.C., Blazel R.G., Champen M., Pfeiffer B.D.,

10. Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,

10. Bayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,

10. Rogers Y.-Bernan B.P., Barndari D., Bolshakov S.,

10. Lenos P.V., Bernan B.P., Baroktein P., Brottier P.,

10. Usam D.A., Buller H., Cadieu E., Center A., Chandra I.,

10. Walley S., Dahlke C., Davemport L.B., Davies P.,

10. Leller A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

10. Pelcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

10. Pelcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

10. P. Jenian T.J., Hernandez J.R., Houck J.,

10. Stones M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

10. Vangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

10. Stone M. A., Howland T.J., Wei M.-H., Ibegvan C.,

10. Kraft C., Kravitz S., Kulp D., Lai Z.,

10. Stone M. A., Howland T.J., Wei M.-H., Ibegvan C.,

10. Kraft C., Kravitz S., Kulp D., Lai Z.,

10. Kraft C., Kravitz S., Kulp D., Lai Z.,

10. Kraft C., Kravitz S., Kulp D., Lai Z.,

10. Montosh T.C., Moreled M.P., Mochenson D.,

11. Simpson M.P., Morris J., Morsh M., Nelson D.L.,

10. Hishina N.V., Moberry C., Monris J., Puri V., Resee M.G.,

10. Minghy B., Murphy L., Murany D.M., Welson D.L.,

10. Hishina N.V., Moberry C., Wu D., Puri W., Smith T.,

10. Woodage T., Worley K.C., Wu D., Yang S., Yao Q., A.,

10. F., Zaveri J.S., Zhan M., Zhang S., Yao Q., Zheng L.,

10. Gertor C., Turner R., Venter E., Wang A.H.,

10. Woodage T., Worley K.C., Wu D., Yang S., Yao Q., Zheng L.,

10. Saveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

10. Saveri J.S., Zhan M., Zhang S., Zhu X., Smith H.O.,

10. Saveri J.S., Shan M., Venter J.C.,

10. Shang E.W., Sunit M. Shungaster.",

10. Scheeler M., Shungaster.",

10. Scheeler M.,
rosophilidae; Drosophila.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003600; AAF51889.2; -. EMBL; AY070982; AAL48604.1; -.

Patel S., Ph Celniker S.;

FlyBase; FBgn0037428; CG1169. SEQUENCE 306 AA; 34083 MW; 32B69371475A48F9 CRC64;

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Adams M.D., Kronmiller B., Wan K.H., Holt R.A., cayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., H., Baldwin D., Banzon J., Besson K.Y., Busam D.A., Center A., Champe M., Davenport L.B., Dietz S.M., rise E., Calle R.F., Garg N.S., George R.A., Houch U.E., Doyle C., Dresnek D., Farfan D., Trise B., Galle R.P., Hostin B., Mattei B., Moshrefi A., Hostin B.A., Hostin D., Howland T.J., 1ali M., Kruse D., Li P., Mattei B., Moshrefi A., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., agas V., Park S., Patel S., Pfeiffer B., Scheeler F., Strong R., Svirskas R., Tector C., Tyler D., Strong R., Swirskas R., Tector C., Tyler D., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Erosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jay M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Juang Y., Kaminker J.S., Prochnik S.E., Smith C.D., cgman C., Berman B., Carlson J.W., Celniker S.E., Jadle R., Emmert D., Frise E., de Grey A., Harris N., Marshall B., Millburn G., Richter J., Russo S., Smith E., Shu S., Smutniak F., Whitfield E., Gelbart M.M., Rubin G.M., Mungall C.J., Lewis S.E.; E. Drosophila melanogaster genome.", s-2000) to the EMBL/GenBank/DDBJ databases.
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Mundy N.I., Kelly J.;
"Evolution of a pigmentation gene, the melanocortin-1 receptor, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ō
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Am. J. Phys. Anthropol. 121:67-80 (2003).

BMBL, AY205086; AAP30960.1; -.

GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:001584; F:receptor activity; IEA.

GO, GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO, GO:000186; P:rhodopsin-like receptor activity; IEA.

GO, GO:000186; F:rhodopsin-like receptor protein signalin.

InterPro; IRR00206; GPRR Rhodpsn.

PROMITS; PRO0237; GFRRHODOSN.

PROSITE; PSS0237; GFRRHODOSN.

PROSITE; PSS0262; G_PROTEIN_RECEP_F1_1; 1.
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0
Query Match 2.8%; Score 8; DB 5; Length 306; Best Local Similarity 100.0%; Pred. No. 41; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                     S6 LVPLALGL 63
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01-OCT-2003
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Macara nigra (Celebes black macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22572539; PubMed=12687585;
Mundy N.I., Kelly J.;
"Evolution of a pigmentation gene, the melanocortin-1 receptor,
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                                                                                                                                                                                                                Length 317;
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                                                                                                                                              317 AA; 34782 MW; 96A807F178FCEC21 CRC64;
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                        Score 8; DB 6;
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                                                                                                                                                                                                        2.8%; Score o; __
100.0%; Pred. No. 42;
....ve 0; Mismatches
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BRNNS; PR00237; GPCRHODPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca silenus (Lion-tailed macaque).
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01-UUN 2003 (TEMBLICAL: 24, Last seqn
01-OCT-2003 (TEMBLICAL: 25, Last anno
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Best Local Similarity 100."
Matches 8; Conservative
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NCBI_TaxID=54600;
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01-JUN-2003
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72; F:receptor activity; IBA.
74; F:rhodopsin-like receptor activity; IBA.
76; P:rhodopsin-like receptor activity; IBA.
76; P:dopportein coupled receptor protein signalin. . .; IBA.
7000276; GPCR_Rhodopsn.
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stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                         stazoa, Chordata, Craniata, Vertebrata, Buteleostomi, .heria, Primates, Catarrhini, Hominidae, Pongo.
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Last annotation update)
                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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21; C:integral to membrane; IEA.
72; F:receptor activity; IEA.
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137; GPRRHODOPSN.
1237; G PROTEIN RECEP F1 1; 1.
1262; G_PROTEIN_RECEP_F1_2; 1.
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(TrEMBLrel. 24, Last seq
(TrEMBLrel. 25, Last anno
                                                                                                                                                                                     Created)
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TrEMBLrel. 24, I
TrEMBLrel. 25, I
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                                                                                                            RELIMINARY;
                                                                                                                                                                                                                                                                                                     receptor.
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MINA 144 CAIAA 167

arity

lae; Macaca.

M.A.

1 N.A.

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Bukaryota, Metazoa, Chordata, Crandata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Platyrrhini, Cebidae, Atelinae, Ate.
NCBI_TaxID=9510;
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Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Alouattinae,
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Mundy N.I., Kelly J.;
"Evolution of a pigmentation gene, the melanocortin-1 receptor,
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EMBL, AY205130; AAP31004.1; --

EMBL, AY205130; AAP31004.1; --

GO; GO:0016021; C:nteceptor activity; IEA.

GO; GO:0001584; F:rtodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rthodopsin-like receptor protein signalin.

Interbro; IPR00027; GPC. Rhodpsn.

PRINTS; PR00021; 7tm 1; 1.

PROMITS; PR00021; GPROTEIN RECEP F1 1; 1.

PROSITE; PS500262; G-PROTEIN RECEP F1 1; 1.
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EMBL; AY205131; AAP31005.1; -.

EMBL; AY205131; AAP31005.1; -.

EQ, GO:0016472; E:neceptral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:G-protein coupled receptor protein signalin.

InterPro: IPR00276; GPCR_Rhodpsn.

Pfam; PF00001; 7cm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.
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                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 42;
iive 0; Mismatches
                                                  317 AA.
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                                                                                                                                                                                                                            Ateles paniscus (Black spider monkey).
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1-JUN-2003 (TrEMBLrel. 24,
1-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 100.
Matches 8; Conservative
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                                                  PRELIMINARY;
                                                                                                                                                                             Melanocortin-1 receptor.
MCIR.
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01-JUN-2003
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SEQUENCE
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RESULT 35
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Fireceptor activity, IEA.
Fireceptor activity, IEA.
Fireceptor protein signalin. . ., IEA.
00276; GPCR_Rhodpsn.
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leria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
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100.0%; Pred. No. 42;
tive 0; Mismatches 0; Indels
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Last sequence update)
Last annotation update)
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ive 0; Mismatches
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262; G PROTEIN RECEP F1 2; 1.
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:62; G_PROTEIN_RECEP_F1_2; 1.
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                                                                          39; PubMed=12687585;
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Alouatta palliata (Mantled howler monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Alouattinae,
                                                                                  Mundy N.I., Kelly J.; 
 "Evolution of a pigmentation gene, the melanocortin-1 receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Am. J. Phys. Anthropol. 121:67-80(2003).

EMBL; AY205135; AAP31009.1; -.

EO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004472; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:00011584; F:rhodopsin-like receptor protein signalin.

InterPro; IPR000275; GPCR_Rhodopsin.
                                                                                                                                                               Am. J. Phys. Anthropol. 121:67-80 (2003).

EMBL; AY205134; AAP3100B.1; -.

EMBL; AY205134; AAP3100B.1; -.

EO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor protein signalin.

InterPro; IPR00027; GPC. Rhodops.

PRINTS; PR0037; GPC. Rhodops.

PRINTS; PR0037; GPC. RPOPEIN RECEP F1 1; 1.

PROSITE; PS500262; G_PROTEIN RECEP F1 1; 1.
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Mundy N.I., Kelly J.;
"Evolution of a pigmentation gene, the melanocortin-1 receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.8%; Score 8; DB 6; Length 317; 100.0%; Pred. No. 42; ative 0; Mismatches 0; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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PROSITE; PS00237; G PROTEIN RECEP F1_1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1_2; 1.
                              STRAIN=2;
MEDLINE=22572539; PubMed=12687585;
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Best Local Similarity
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SEQUENCE FROM N.A.
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21; C:integral to membrane; IEA.
22; F:receptor activity; IEA.
35; F:redodopsin-like receptor activity; IEA.
36; P:rodoopsin-like receptor protein signalin. . .; IEA.
3000276; GPCR_Rhodosn.
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etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Platyrrhini; Cebidae; Alouattinae;
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stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
:heria; Primates; Platyrrhini; Cebidae; Alouattinae;
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100.0%; Pred. No. 42;
iive 0; Mismatches 0; Indels
                                                                                                                                             DB 6; Length 317;
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                                                                                  7 AA; 34830 MW; 87F7EFAE347671E4 CRC64;
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(TrEMBLrel. 24, Last sequence update)
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)237; G PROTEIN RECEP_F1_1; 1.
)262; G_PROTEIN_RECEP_F1_2; 1.
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237; G_PROTEIN_RECEP_F1_1; 1.
1262; G_PROTEIN_RECEP_F1_2; 1.
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100.0%;
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Mammalia, Butheria, Primates, Strepsirhini, Lemuridae, Bulemur.
NCBI_TaxID=13515,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Strepsirhini, Lemuridae, Varecia.
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Mundy N.I., Kelly J.;
"Evolution of a pigmentation gene, the melanocortin-1 receptor,
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Am. J. Phys. Anthropol. 121:67-80(2003),
EMB.; ANC5140; Anthropol. 121:67-80(2003),
EMB.; ANC5140; C.integral to membrane; IEA.
GO; GO:0016021; C.integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000186; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; F:rhodopsin-like receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodopsn.
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PROSITE; PS000237; GPROTEIN_RECEP_F1_1; 1.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Melanocotin-1 receptor.
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Eulemur fulvus (brown lemur).
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                                                                                                                              Query Match
Best Local Similarity 100.0°
Matches 8; Conservative
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SEQUENCE FROM N.A.
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}; F:receptor activity, IEA.

}; F:receptor activity, IEA.

}; F:rhodopsin-like receptor activity; IEA.

}; P:G-protein coupled receptor protein signalin. . .; IEA.

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1; C:integral to membrane, IEA.
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5; P:G-protein coupled receptor protein signalin. ..; IEA.
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362; G PROTEIN RECEP F1 2; 1.
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X Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
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DNA Res. 5:55-76(1998).
EMBL, AP000003; BAA29917.1; -.
BR PRI, C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C71132; C711
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Lemur.
NCBI TaxID=9447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea, Buryarchaeota, Thermococci, Thermococcales, Thermococca
Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mundy N.I., Kelly J.; "Evolution of a pigmentation gene, the melanocortin-1 receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Am. 3. Phys. Anthropol. 121:67-80 (2003).

EMBL, AY205143; AAP31017.1;

GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor protein signalin.

InterPro; IPR00027; GPC_Rhodpsn.

PRINTS; PR00021; GPC_RHODPSN.

PRINTS; PR000237; GPC_RHODPSN.

PROSITE; PS500237; GPC_RHODPSN.

PROSITE; PS500262; G_PROTEIN_RECEP_FI 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 AA; 34667 MW; 3E7419FDEC2DE738 CRC64;
                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AN-1999 (TrEMBLrel. 09, Last sequence update)
01-UNA-12003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PH0824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=3;
MEDLINE=22572539; PubMed=12687585;
                                                                                                                                                                                                                   Lemur catta (Ring-tailed lemur).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                           Melanocortin-1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 RARRAIAA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 RARRAIAA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primates.";
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058554
ACCOCCOS ON THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE ST
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                                                                                                                                                                                                           11; C:integral, to membrane; IEA.

72; F:receptor activity; IEA.

74; F:receptor activity; IEA.

75; F:receptor activity; IEA.

76; F:receptor coupled receptor protein signalin. . .; IEA.

70; CFCR_Rhodpsn.
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                                                                       a pigmentation gene, the melanocortin-1 receptor, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iseus (Gray gentle lemur) (Bamboo lemur).
stazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
.heria; Primates; Strepsirhini; Lemuridae; Hapalemur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; C:integral to membrane; IEA.
72; F:receptor activity; IEA.
34; F:rhodopsin-like receptor activity; IEA.
35; P:G-protein coupled receptor protein signalin.
2000276; GPCR_Rhodopsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA; 34748 MW; DAF913C3B9ECC2AF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.8%; Score 8; DB 6;
100.0%; Pred. No. 42;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
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317 AA.

PRELIMINARY;

:539; PubMed=12687585;

IN.A.

Anthropol. 121:67-80(2003).

12; AAP31016.1; -.

237; GPCRRHODOPSN.

7tm 1; 1

2.8%; &

Conservative

larity

RAIAA 144 RAIAA 167

Anthropol. 121:67-80(2003).

11; AAP31015.

539; PubMed=12687585;

)237; G\_PROTEIN\_RECEP\_F1\_1; 1.)262; G\_PROTEIN\_RECEP\_F1\_2; 1.

37; GPCRRHODOPSN.

7tm

Conservative

CAIAA 144 WIAA 167 PRELIMINARY;

receptor.

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STRAIN=AV19 / DSM 6224 / JCM 9639;

STRAIN=AV19 / DSM 6224 / JCM 9639;

MEDLINE=12927647;

Slesarev A.I., Mezhevaya K.V., Makarcova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozyavkin S.A.,
The complete genome of hyperthermophile Methanopyrus kandleri AV:
and monophyly of archaeal methanogens.";
proc. Natl. Acad. Sci. UG.A., 99:4644-4649(2002).

EMBL; AR010455; AAMO2686.1;
GO, GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=H37RV;
MEDLINE=98295987; PubMed=9634230;
Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Bashiam D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares R.,
Sulston J.E., Taylor K., Whitchead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                         Euryarchaeota; Methanopyri; Methanopyrales; Methanopyrace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Permease subunit of a ABC-type transport system involved in lipoprotein release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.8%; Score 8; DB 17; Length 370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Hypothetical protein cysM3.
CYSM3 OR RV0848 OR MTV043.41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.85; occ. v. Best Local Similarity 100.08; Pred. No. 49; Matches 8; Conservative 0; Mismatches
                                                                                                                                                           370 AA.
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01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                         PRT;
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Pfam; PF02687; FteX; 1.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       Methanopyrus kandleri
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                                                        311 ALGLGLAL 318
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                    60 ALGLGLAL 67
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2320;
                                                                                                                                                                                                                                                                                                                                                              Methanopyrus
                                                                                                                                                                                                                                                                                                                                            Archaea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           azoa; Chordata; Craniata; Vertebrata; Buteleostomi; eria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; PubMed=8702217; on N., Grossman H.B.; on N., Lee S.W., Liebert M., Grossman H.B.; lysis of a gene, BBl, overexpressed in bladder and
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0
                                                        2.8%; Score 8; DB 17; Length 339; 00.0%; Pred. No. 45;
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                                                                                                 0; Indels
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rotein; Complete proteome.
AA; 37228 MW; E91697D5C8C3705F CRC64;
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                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
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V 100.0%; Pred. No. zo,
O; Mismatches
                                                                                                                                                                                                                                                                               342 AA.
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'rEMBLrel. 17, Last seg
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and Colon;
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                                                                                                   nservative
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AW 118
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LALA 103

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STRAIN-LL/S2;
WDDLINE=22557897; PubMed=12670979;
WDDLINE=22557897; PubMed=12670979;
WDDLINE=22557897; PubMed=12670979;
WDDLINE=22557897; PubMed=12670979;
WDDLINE=22557897; PubMed=1267097;
"Function and Regulation of the Formate Dehydrogenase Genes of the Methanogenic Archaeon Methanococcus maxipaludis.";
DBACE-101. LBS-12548-2554(12003).
BMBL; AX236516; AA008931-1; -
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005489; F:electron transport; IBA.
InterPro; IPR001450; 4F44S ferredoxin.
InterPro; IPR007525; FRNB FGNB.C.
InterPro; IPR007516; FRNB FGNB.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \ensuremath{\mathsf{Hopwood}} D.A.; "Complete genome sequence of the model actinomycete Streptomyces
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Bacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                                                                                         2.8%; Score 8; DB 1; Length 375;
100.0%; Pred. No. 49;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                      Pfam; PF00037; fer4; 1. Pfam; PF04422; FrhB FdhB C; 1. Pfam; PF04422; FrhB FdhB N; 1. PR051TE; PF040199; 4FE4S FEREDOXIN; 2. SEQUENCE 375 AA; 42431 MW; AB09678918AEC8AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 417:141-147(2002).
EMBL, ALB39124; CAB91118.1; -.
Complete proteome.
SEQUENCE 377 AA; 37614 MW; A35DA0437F044C46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 377 AA.
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MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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    SEQUENCE FROM N.A.
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Q9KYT3
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iglmeier K., Camus J.-C., Medina N., Mansoor H.,
hoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
kin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
genome sequence of Mycobacterium bovis.";
scad. Sci. U.S.A. 100:7877-7882 (2003).
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TrEMBLrel. 25, Last sequence update)
TrEMBLrel. 25, Last annotation update)
TremBlrels 25, Last annotation update)
TremBlrel 25, Last annotation update)
TremBlrel 25, Last annotation update)
TremBlrel 25, Last annotation update)
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neae; Mycobacteriaceae; Mycobacterium.
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100.0%; Pred. No. 49;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                            2.8%; Score 8; DB 16; Length 372;
                                                                                                                                                                                                                                                                                                 0; Indels
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/archaecta; Methanococci; Methanococcales;
seae; Methanococcus.
1152;
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2 AA; 40106 MW; 6FD459DFA6FE4284 CRC64;
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AA; 40118 MW; 927386BE1DF5FB6C CRC64;
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Last annotation update)
                                                                                               Rv0848; -. 9; F:lyase activity; IEA. 0; P:amino acid metabolism; IEA. 001926; B6_enzyme_beta.
                                                                                                                                                                                                                                                                                49;
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(TrEMBLrel. 24, Last seq
(TrEMBLrel. 25, Last ann
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me sequence.";
7-544(1998).
4; CAA17654.1; -.
H70813.
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LALA 103 LALA 68

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MEDLINE=21608550; PubMed=11743193;
MEDLINE=21608550; PubMed=11743193;
MEDLINE=21608550; PubMed=11743193;
MEDLINE=21608550; PubMed=11743193;
MEDLINE=21608550; PubMed=11743193;
Mood D.W., Setubal J.C., Kaul R., Mood G.E., Almeida N.F. Jr., Woo L.,
A. Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
A. Chapman P., Clendenning J., McChellad E., Ellet W., Grant C.,
A. Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
A. Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
A. Arang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.
A. Gordon-Kamm B., Liao Y., Biddle P., Jung M., Krespan W., Perry M.
A. Gordon-Kamm B., Liao Y., Tomb J.-F., Gordon M.P., Olson M.V.,
A. Moeter B.W.,
The genome of the natural genetic engineer Agrobacterium tumefaci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21608551; PubMed=11743194;
MEDLINE=21608551; PubMed=11743194;
MEDLINE=21608551; PubMed=11743194;
MEDLINE=21608551; PubMed=11743194;
Qurollo B., Hinkle G., Gattung S., Miller N., Halling C., Mullin Gurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Mollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz F. Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Gielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciene C58.";
Science 294:2323-2328(2001).
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MEDLINE=22825697; PubMed=12917641;
Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain
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                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                          Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium.
NCBI TaxID=176299;
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PROSITE; PS00307; LECTIN LEGIME BETA; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 397 AA; 41708 MW; 700748E32A46AEB6 CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atu3948.
ATU3948 OR AGR L. 1808.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Possible bicarbonate transporter, ICT family
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100.0%; Pred. No. 52;
ive 0; Mismatches
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EMBL, AE008289; AAR89478.1; --
PIR; AH3041; AH3041.
PIR; D98244; D98244.
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InterPro, IPR001608; UPF0001.
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8; Conservative
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Best Local S
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Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
hen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
lin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
rusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87; FubMed=10617197; ... Romito M.-I., Town C.D., ... Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., ason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., tchum K.A., Lee J.J., Romning C.M., Koo H., Moffat K.S., hen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., rrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., ..., Preuss D., Nlerman W.C., White O., Eisen J.A., analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                      H., Cheuk R., Kim C.J., Lim J., Meyers M.C., Banh J., ninci P., Chang E., Dale J.M., Goldsmith A.D., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., B., Lee J.M., Lin J., Miranda M., Narusaka M., B., Lae J.M., Lin J., Miranda H.L., Sakurai T., Satou M., wick A., Tang C.C., Toriumi M., Wu H.C., Yamada K., u G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                            aliana (Mouse-ear cress).
idiplantae, Streptophyta; Embryophyta, Tracheophyta;
Magnoliophyta; eudicotyledons; core eudicots; rosids;
rassicales, Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ull Length cDNA Clones.";
-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40584 MW; AF6C6B3BAC9BF69A CRC64;
                   rEMBLrel. 13, Created)
rEMBLrel. 13, Last Sequence update)
TEMBLrel. 25, Last annotation update)
1.20 (At2945000 protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rity 100.0%; Preu. wc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD32835.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clones.";
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                                                                                                                   L2G45000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EED 100
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GLLL 371

lasmid .03756.

N.A.

GLLL 74

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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                    MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; M., James K.D., Churcher C., Mungall K.L.
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.D.
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plagu
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN=KIMS / Biovar Mediaevalis;

MEDLINE=2137863; PubMed=12142430;

Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Listerna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,

Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner

Perry R.D.;

"Genome sequence of Yersinia pestis KIM.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A00347; AC0047.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0015520; F:tetracycline:hydrogen antiporter activity; IEA.

GO; GO:0005221; F:transporter activity; IEA.

GO; GO:0015904; F:tetracycline transport; IEA.

GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Complete proteome.
SEQUENCE 465 AA; 50176 MW; 0CC273F10BB3F5ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.8%; Score 8; DB 16;
100.0%; Pred. No. 60;
tive 0; Mismatches (
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InterPro; IPR008282; Sub transporter.
InterPro; IPR001411; TCR_TetB.
Pfan; PF00083; sugar tr; 1.
PRINTS; PR01036; TCRTETB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Bacteriol. 184:4601-4611(2002).
EMBL; AJ414154; CAC92102.1; -.
EMBL; AE013741; AAM84955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transport protein, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100...
68 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                Nature 413:523-527(2001).
  YEGB OR YPO2850 OR Y1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 LLLAVVSL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 LLLAVVSL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                          SEQUENCE FROM N.A.
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                       fersinia pestis.
                                                                                 NCBI_TaxID=632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Genin S., Artiguenave F., Gouzy J., Mangenot S., lault A., Brottier P., Camus J.C., Cattolico L., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Claudel-Renard C., Cunnac S., Demange N., Cle M., Moisan A., Robert C., Saurin W., Schiex T., hebault P., Mhalen M., Wincker P., Levy M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ince of the plant pathogen Ralstonia solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 20, Created)
TrEMBLrel. 20, Last sequence update)
TrEMBLrel. 25, Last amotation update)
TremBlrel. 25, Last amotation update)
Tremplerel (Putative permease, major facilitator)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; F:ATP binding; IEA.
0; F:nucleoside diphosphate kinase activity; IEA.
1; P:CTP biosynthesis; IEA.
13; P:CTP biosynthesis; IEA.
18; P:UTP biosynthesis; IEA.
Regala W., Allen E.E., McCarren J., Paulsen I., Partenaky, F., Nebb E.A., Waterbury J.; f a motile marine Synechococcus."; 37-1042(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.8%; Score 8; DB 16; Length 435;
100.0%; Pred. No. 56;
iive 0; Mismatches 0; Indels
                                                                                                                                                              DB 16; Length 431; . 56;
                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47048 MW; CCD859D9C54DDB5A CRC64;
                                                                                                                     AA; 46300 MW; 66295F913903DBAE CRC64;
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TrEMBLrel. 20, Last sequence update)
TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anacearum (Pseudomonas solanacearum).
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                                                                                                                                                              2.8%; Score 8; DB 1
100.0%; Pred. No. 56;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     879; PubMed=11823852;
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lete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             smembrane protein.
                                                                               9; CAE06799.1; -.
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                                                                                                                                                                                                       onservative
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                                                                                                                                                                                                                                                                                                                                                                                           RELIMINARY;
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0; Indels

VLAL 224 VLAL 365

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Length 465;

aft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., in H., Jiang L., Pamphile W., Crosby M., Shen M., Lam P., McDonald L., Utterback T., Zalewski C., Araxind L., Daly M.J., Mniton K.W., Fleischmann R.D., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,

ce of the radioresistant bacterium Deinococcus

Gaps

0,

DB 16; Length 471;

47974 MW; 96B2BEBF6E445D27 CRC64;

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mazaki M., Watanabe K., Kumagai A., Itakura S., 
ujimori Y., Komiyama M., Sugiyama T., Irie R., 
O H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., 
Saito K., Nishikawa T., Kimura K., Yamashita H., 
iamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., 
anchori K., Takahashi-Fujii A., Oshima A., Sugiyama A., 
uzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      azoa; Chordata; Craniata; Vertebrata; Euteleostomi; eria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NA sequencing project.";
:-2001) to the EMBL/GenBank/DDBJ databases.
}; BAB71043.1; --
104299; MBOAT_fam.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                  rEMBLrel. 19, Created)
rEMBLrel. 19, Last sequence update)
rEMBLrel. 22, Last annotation update)
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100.0%; Pred. No. 61;
iive 0; Mismatches
2.8%; Score 8; DB 1
100.0%; Pred. No. 61;
tive 0; Mismatches
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frEMBLrel. 21, L
frEMBLrel. 22, L
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0; Indels

61;

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Arakawa T., Shinagawa A., Fukunishi Y., Koshino M., Itoh M., Ishii Y. Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S. Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I. Saito T., Okazaki Y., Gojobri T., Bono H., Kasukawa T., Saito R. Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleichmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio B. Bakai K., Okido T., Furuno W., Ano H., Balarelli R., Bareh G., Blake J., Boffelli D., Bojunga N., Carninci P., Ge Bonaldo M.F., Bulke J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N. H. Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Rordon P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Stock K., Wang K., Hasegawa Y., Kawiy H., Kohtsuki S., Markarian M., Hangana Y., Kawiya M., Laka M., Markarian M., Hume D.A., Kawiya M., Lee N. H. Sasaki H., Sato K., Voshida K., Hasegawa Y., Kawai H., Kohtsuki S., Markarian M., Hangawa Y., Kawai H., Kohtsuki S., Markarian M., Hayashizaki Y., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.
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5730589L02RIK.
Bukarwilus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                             DB 11; Length 473;
                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                        Strausberg R.; Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC023417; AAH23417.1; MGD; MGI:1924832; 5730589L02Rik. InterPro; IPR004299; MBOAT_fam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004299; MBOAT fam.
Pfam; PF03062; MBOAT; 1.
SEQUENCE 473 AA; 53504 MW; CE6FBE93C3D01C4F CRC64;
                                                                                                                                                                                                             Pfan; PF03062; MBOAT; 1. -
SEQUENCE 473 AA; 53382 MW; DAALFEODA78013EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 AA.
                                                                                                                                                                                                                                                                             Query Match
2.8%; Score 8; DB 11
Best Local Similarity 100.0%; Pred. No. 61;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK019981; BAB31950.1; -.
MGD; MGI:1924832; 5730589L02Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                 436 LALACLGL 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 LALACLGL 443
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Best Local Similarity
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                                                                                      SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    65 LALACLGL
                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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RELIMINARY;

COR MBB1.

(Mouse)

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SEQUENCE FROM N.A.
Haing Y.C., Chow T., Chen C., Wu H., Chu M., Chao Y., Liu S.,
"Oryza sativa PAC P0699E04 genomics sequence, complete sequence."
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP001111; BAA90509.1; -..
Gramene, Q9LUM0; --..
SEQUENCE 522 AA; 54697 MW, 21C6BAD2441B56BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nonomuraea sp. ATCC 39727.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                  01-OCT-2000 (TrEMBLrel. 15, Created)
1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Similar to an Arabidopsis thialiana chromosome BAC genomic
                                                                                                                                                                                                                                                                                                                                                              Query Match 2.8%; Score 8; DB 10; Length 522; Best Local Similarity 100.0%; Pred. No. 67; Matches 8; Conservative 0; Mismatches 0; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRPMH8,
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Oligopeptide transporter.
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 PRT;
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DBV20.
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Best Local Similarity 100.
Matches 8; Conservative
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         43 RRRGRRGE 50
                                                                                                                       Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=93944;
                                                                                                                                                                                        NCBI_TaxID=4530;
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                Q9LIW0;
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OMIT60
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                                                                                                                                                                                                                                                           cayama I., Fujino M.A.;
id characterization of novel human and mouse genes, which
in the digestive tract.";
B-2001) to the EMBL/GenBank/DDBJ databases.
0, BACS1808.1, -
832; 5730589102R.k.
(004299; MBOAT_fam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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.ridiplantae, Streptophyta, Embryophyta, Tracheophyta;
!; Magnoliophyta, Liliopsida, Poales; Poaceae;
!; Oryzeae; Oryza.
                                                                                                                                                       stazoa, Chordata, Craniata, Vertebrata, Buteleostomi, heria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.8%; Score 8; DB 10; Length 496; 100.0%; Pred. No. 64; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     2.8%; Score 8; DB 11; Length 473; 100.0%; Pred. No. 61; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ZnF_C3H1; 3.
AA; 51701 MW; 3AFBA80FC0AFA115 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   AA; 53435 MW; CFB4FE0DB2951C4F CRC64;
                                                TrEMBLrel. 23, Created)
TrEMBLrel. 23, Last sequence update)
TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TrEMBLrel. 23, Last sequence update)
TrEMBLrel. 25, Last annotation update)
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'6; F:nucleic acid binding; IEA.
                  473 AA
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RELIMINARY;

ACLGL 443 ACLGL 72

protein.

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VDGV 208

VDGV 221

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MBOAT;

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Tumpey T.M., Suarez D.L., Perkins L.E.L., Senne D.A., Lee J.G.,
RA Tumpey T.M., Suarez D.L., Perkins L.E.L., Senne D.A., Lee J.G.,
A Lee Y.J., Mo I.P., Sung H.W., Swayne D.E.;
RT "Characterization of a Highly Pathogenic H5N1 Avian Influenza A V.
RT "Characterization of a Highly Pathogenic H5N1 Avian Influenza A V.
RT "Characterization of a Highly Pathogenic H5N1 Avian Influenza A V.
RT J. Virol., 76:6344-6355(2002).
C -!- FUNCTION: HEMAGGLUTIMIN IS RESPONSIBLE FOR ATTACHING THE VIRUS
C -!- SUBUNIT: HOMOTRIMER. EACH OF THE MONDMERS IS FORMED BY TWO CHIP
C -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
C -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
C -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
C -!- SIMILARITY: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
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                                                                                                                                                                                                                                                                                      DB 12; Length 564; . 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza A virus (A/Goose/Hong Kong/3014.5/2000(H5N1)). Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                      NON TER 564 564 SEQUENCE 564 AA, 63562 MW, B317179A7F3E6F98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00509; Hemagglutinin, 1.
PRINTS; PR00329; HEMAGGLUTN12.
Prodom, PD000225; Hemagglutn; 1.
Envelope protein; Glycoprotein; Hemagglutinin.
SEQUENCE 568 AA; 64244 MW; E0D741A75CBE76FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR001364; Hemagglutn.
Pam; PF00509; Hemagglutnin; I.
PRINTS; PR00329; HEMAGGLUTN12.
PRODON; PD00225; Hemagglutni; 1.
PRVelope protein; Glycoprotein; Hemagglutini.
NON_TER
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                                                                                                                                                                                                                                                                                      Query Match
2.8%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=A/Goose/Hong Kong/3014.5/2000;
MEDLINE=22016166; Pubmed=12021367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hemagglutinin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       72 LLLAVVSL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LLLAVVSL 13
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Matches 8; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ø
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Q8JN92
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QBQPL0
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                                                                                                                                                                                       "CC 13902 / XV 101;
"45; PubMed=12034217;
"7; Ferro JA., Reinach F.C., Farah C.S., Furlan L.R.,
Monteiro-Vitorello C.B., Van Sluys M.A., Almeda N.F.,
do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
Erreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
F. Franco M.C., Graggio C.C., Gruber A.,
Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
Achado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
"Takta M.A., Tamura R.E., Terxeira B.C., Tezza R.I.D.,
antos M., Truffi D., Tsai S.M., White F.F.,
Kitajima J.P.;
Lice genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEWAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO "TORS AND FOR INITIATING INFECTION (BY SIMILARITY).

(GMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS (A2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).

1. BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.

3. AAD13573.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02; PubMed=9882316; Zhou N.; Kawaoka Y., Webster R.; Alycopretins of H5 influenza viruses isolated from ins, and wild aquatic birds have distinguishable
                             conopodis (pv. citri).
eobacteria; Gammaproteobacteria; Xanthomonadales;
ae; Xanthomonas.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA; 58369 MW; 7844C0C0FE1E8670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'YEMBLrel. 10, Created)
'YEMBLrel. 10, Last sequence update)
'YEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , AAM36320.1; -. C.membrane; IEA.
; F: transporter activity; IEA.
P:oligopeptide transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.8%; Score 8; DB 16 rity 100.0%; Pred. No. 68; mservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potsdam/2216-4/84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-463 (2002) .
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Q9N8US,

Q9N8US,

Q1-0CT-2000 (TrEMBLrel. 15, Created)

O1-0CT-2000 (TrEMBLrel. 24, Last sequence update)

O1-0TN-2003 (TrEMBLrel. 24, Last annotation update)

Hypothetical protein.

Hypothetical protein.

Trypanosoma brucei.

Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-TREU927;
Hall N., Berriman M., Lennard N.J., Harris B.R., Gerrard C.S.,
Atkin R.J., Barron A.J., Bart-Delabesse E.N., Bownan S.,
Bray-Allen S.P., Bringaud F., Clark L.N., Corton C.H., Cronin A.,
Davies R., Doggett J., Fraser A., Gruter E., Hall S., Harper D.A.
Hertz-Fowler C., Kay M.P., Leech V., Mayes R., Price C., Quail M.
Rabbinowitsch E., Rutherford K., Sasse J., Sharp S., Shownkeen R.
Gull K., Barrell B.G., Melville S.E.,
"The sequence and analysis of the highly polymorphic chromosome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypanosoma brucei.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanos
                                                                                                                                                                                                                                                                                                                                         Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the African trypanosome, Trypanosoma brucei.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL929607; CAB95571.1; -
                                                                                                                                                                                                                                                                                   620 AA; 67314 MW; E9904BFF039B6AEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 656 AA; 72138 MW; CBAC892D25937FAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNI-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
host specificities.";

Nature 417:459-463(2002).

EMBL, ABO12240, AAM40703.1; -..

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006857; P:oligopeptide transport; IEA.

InterPro; IRR00109; PTR2.

Pfan; PF00854; PTR2.

COMPLET PS01022; PTR2.

COMPLET PS01022; PTR2.

COMPLET PS01023; PTR2.

COMPLET PS01023; PTR2.

COMPLET PS01023; PTR2.

COMPLET PS01023; PTR2.
                                                                                                                                                                                                                                                                                                                                         2.8%; Score 8; DB 16;
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82;
                                                                                                                                                                                                                                                                                                                                                                          78;
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2.8%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 82;
Matches 8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 LALACLGL 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 EELVAEED 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 LALACLGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9DBN60
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                                                                                                                                                                                                                                                                                                                                                                                                                         HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS TO PETORS AND FOR INITIATING INFECTION (BY SIMILARITY).
HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO CHAINS HAZ) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
Y: BELONGS TO THE INFLUENZA HEMAGGLUTININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                 uza Viruses Isolated from Geese in Southeastern China:
Genetic Reassortment and Interspecies Transmission to
                                                                                                                                                                               ie/Hong Kong/3014.8/2000(HSNI);
832; PubMed=11878904;
is M., Kong K.F., Dyrting K.C., Ellis T.M., Sit T.,
thortridge K.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ampestris (pv. campestris).
teobacteria; Gammaproteobacteria; Xanthomonadales;
eae; Xanthomonas.
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100.0%; Pred. No. 72;
iive 0; Mismatches 0; Indels
                          irus (A/Goose/Hong Kong/3014.8/2000(H5NI)).
A negative-strand viruses; Orthomyxoviridae;
iruses; Influenzavirus A.
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TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1225; Hemagglutn; 1.
ein; Glycoprotein; Hemagglutinin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; C:viral envelope; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Hemagglutinin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; HEMAGGLUTN12.
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iman M., Lennard N.J., Harris B.R., Gerrard C.S.,
arron A.J., Bart-Delabesse E.N., Bowman S.,
S., Bringaud F., Clark L.N., Corton C.H., Cronin A.,
3gett J., Fraser A., Gruter E., Hall S., Harper D.A.,
Z., Kay M.P., Leech V., Mayes R., Price C., Quail M.A.,
E., Rutherford K., Sasse J., Sharp S., Shownkeen R.,
all B.G., Melville S.E.,
and analysis of the highly polymorphic chromosome I of
cypanosome, Trypanosoma brucei.",
2-2002) to the EMBL/GenBank/DDBJ databases.
i; CAB95435.1;
Ol1656; UPF0024.
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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.azoa; Chordata; Craniata; Vertebrata; Buteleostomi;
.eria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'illa F., Graziano M.; phism of goat beta-lactoglobulin proximal promoter
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rEMBLrel. 10, Last sequence update)
rEMBLrel. 25, Last annotation update)
rotein (Fragment).
homatis.
mydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                 2.8%; Score 8; DB 5; Length 1523; irity 100.0%; Pred. No. 1.8e+02; nservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                       33 AA; 168322 MW; 077BDC751CDD1E5A CRC64;
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100.0%; Pred. No. 52;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA; 3372 MW; 0C56BD579B3DC190 CRC64;
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rEMBLrel. 17, Last sequence update)
rEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                       rotein.
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AC 14
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               STRAIN=L2 434B;
Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
"Gene identification of Chlamydia trachomatis by random DNA
sequencing.";
                                                                                                                                                                                                                                 0; Indels
                                                                          Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF087333; AAD04107.1; -.
Hypothetical protein.
                                                                                                                                                                                                 Length 35;
                                                                                                                             NOW TER 1 1
NOW TER 35 35
SEQUENCE 35 AA; 3519 MW; 46686B72BAF28F7D CRC64;
                                                                                                                                                                                              Query Match 2.5%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 57; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                           Search completed: April 7, 2004, 17:58:55
                                                                                                                                                                                                                                                              174 NSSSPLR 180
                                                                                                                                                                                                                                                                                           8 NSSSPLR 14
SEQUENCE FROM N.A.
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Aam20858 Pej Abb42637 Pej Aam36451 Pej Abb25983 Pr: Aam76342 Hui	Aam63528 Hui	Abgs8050 Hul Abg45635 Hul Aam21621 Pej	Abb43981 Pej Aam37923 Pej	Abb26890 Pro	Aam64984 Hui	Abg46737 Hur	Abgu3723 No. Abg03663 No.	Aau61282 Pro	Abms7801 Pro Abg20259 No	Aao08094 Hui	Abb67712 Dr. Abb28041 St.	Aam23684 Hui	Abp41674 Hur	Abglez/9 No. Abg01186 No.	Adb79952 Rai	Abg13391 No.	ADGUSULZ NO. ADG18115 NO.	Abu36537 Pro	Abgls613 Nor Aam23752 Hii	Adc08203 Ric	Adc64562 Syn	Abb57908 Dro	Adas4710 Hui Aba20260 No	Add46285 Hur	Ade62980 Hui	Aausz148 No Aban3722 No	Ade79006 Hui	Abg20261 No.	Ade08475 No	Abul6705 Pro	AGASSBEL AC: Dark6780 Ce	Abp82261 G 1	Abb09088 Hur	Abg62026 Hur	AdaSO609 HC	Abq62030 Hun	Aay34189 Hur	Aab18622 Ant	Aaw89072 Po.	Aae01449 Hur	Aae01489 hur Abbs1243 Hur	Abq63884 Hun	Abg63885 Hun	Abo45500 Not	Abo26980 Pro	Abg02779 Nov	I (	գո	Abme0061 Pro	App00382 Hur
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1 H B

Human; tumour necrosis factor; Apo-3 ligand; lymphotoxin; apopto NF-kappaB-dependent transcription; JNK/SAPK-dependent response; 61 VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHP: 1 MSLLDFEISARRLPLPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTAL 61 LGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQD NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGODGAOAGVDGTVSGWEEARINS 121 NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINS 181 YNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAA The present sequence represents a human tumour necrosis factor ('Imphotoxin homologue designated Apo-3 ligand, Apo-3 ligand has cytostatic activity, Apo-3 ligand can be used to induce apoptosi mammalian cancer cells, to induce NF-kappaB-dependent transcript 36 MAARRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEP 1 MAARRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEP 96 VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHP. 61 LGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQD YNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAA Human tumour necrosis factor Apo-3 ligand protein sequence. New human Apo3- ligand (a tumor necrosis factor) homologue. Length 249; 241 QLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 284 QLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 284 to induce JNK/SAPK-dependent responses in mammalian cells Indels 87.7%; Score 249; DB 2; Lv 100.0%; Pred. No. 2.6e-220; ive 0; Mismatches 0; Pitti R; AAY09369 standard; protein; 249 AA Claim 1; Fig 1; 74pp; English. 98WO-US021407. 97US-0062037P. 97US-0069862P. Ashkenazi AJ, Marsters SA, 15-JUL-1999 (first entry) Matches 249; Conservative (GETH ) GENENTECH INC. WPI; 1999-287982/24. N-PSDB; AAX56000. Query Match Best Local Similarity Sequence 249 AA; Homo sapiens. 09-OCT-1998; WO9919490-A1 10-OCT-1997; 17-DEC-1997; 22-APR-1999. 121 241 AAY09369; 181 ð В ð g ð 쉽 ö g ò 쉽 ₽ qq ö rders in mammals (especially humans), e.g. tumours, and inflammatory diseases or inherited genetic disorders, by into cells, and expressing, therapeutically effective amounts e.g. a virus comprising a gene encoding TRELL. It may also the preparation of prepare probes for screening hetic DNAs for TRELL-encoding sequences and for antisense immune treating cancer, at, suppress or alter immune responses (especially involving arcinoma cells) involving a signal pathway between TRELL and It's coding sequence can be used in gene therapy for TRELL-LDFEISARRIPLPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALLVPLA 60 Adc97100 E. faeciu Abb65500 Drosophil LL or active fragments can be included with a carrier in a compositions to treat canner, autoimmune diseases or uses to tissue grafts, or to stimulate or suppress the immuns useful to screen for TRELL receptors, by labelling with a babel and screening compositions for binding. Agents with TRELL-receptor binding can also be screened for, can alstered, optionally with interferon-gamma, to induce cell c necrosis factor related ligand; tnf; treatment; cancer; sease; immune system; stimulation; suppression; Gaps is that of human tumour necrosis factor related ligand 0 100.0%; Score 284; DB 2; Length 284; 100.0%; Pred. No. 2e-252; ive 0; Mismatches 0; Indels C tumour necrosis factor related ligand (TRELL). sis factor related ligand - useful for, e.g. tilisease and immune responses to tissue grafts. ALIGNMENTS GENEVA FACULTY MEDICINE, ABB65500 50-51; 69pp; English. dard; protein; 284 AA. he Y, Browning JL; 96US-0023541P. 96US-0028515P. 97US-0040820P. Larity 100.0%; Conservative 0 97WO-US013945. 99 5619/13. വവ Ą.

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Marsters SA;

Gurney AL,

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The present sequence is that of human antitumour protein PRO207, deduced from a foetal kidney cDNA clone (see AAA49717). PRO207 shamino acids sequence identity to tumour necrosis factor family mem emperially human lymphotoxin-beta (23.4%) and human CD40 ligand (Mol.wt. is 27,216. A claimed method for inhibiting the growth of cell comprises exposing the tumor cell to PRO199, PRO207, PRO320, PRO221, PRO224, PRO328, PRO310, PRO526, PRO362, PRO365, PRO365, PRO369 or (see AAY95337-49), their agoniers or chimeric polypeptides incorp them. The tumour is especially a cancer selected from breast, ovarenl, colorectal, uterine, prostate, lung, bladder and central n system cancer, melanoma and leukaemia. Methods for the recombinan expression of the antitumour proteins are also provided
                                                                                                                                                                                                                                  Novel composition to inhibit neoplastic cell growth or for treati. in mammal comprises polypeptides PRO119, PRO207, PRO320, PRO219, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO360 or PRO866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARAIAAHYEVHPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TWEAK protein; immunological disorder; immune response; inflammat TWEAK blocking agent; autoimmune disease; organ transplant reject Graft-versus-Host disease; GVHD; lymphoid cell malignancy; shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 MAARRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAARRSQRRRGRRGERGTALLVPLALGGGLALACGGLLLAVVSLGSRASLSAQEPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 LLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LLVDGVLALRCLEEPSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a soluble recombinant human TWEAK protein.
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87.7%; Score 249; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 2.6e-220;
Matches 249; Conservative 0; Mismatches 0; Indels
                                                                                                                   Godowski PJ,
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                                                                                                                                                                                                                                                                                                                   Claim 19; Fig 4; 172pp; English.
                                                                                                         Goddard A, Goguw
99US-0145698P.
99WO-US021090.
99WO-US021547.
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                                                                                                  Ashkenazi AJ, Goduda...
--- MA. Pitti RM,
                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                             WPI; 2000-442668/38.
                                                                                                                                                                                                 N-PSDB; AAA49717.
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26-JUL-1999;
15-SEP-1999;
15-SEP-1999;
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                                                         VDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antitumour; tumour; therapy; cytostatic; breast cancer;
                  VVDGTVSGWEEARINSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDRGKAVYLKLD
                                                                                                VLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL
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125. .131
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|abel= Signal_peptide
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99US-0134287P.
99US-0144758P.
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24. .35 /note= "L

27. .33

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10. .14 /note= ".

.249

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.127

.124

/note= 118. .1

101

note=

134 .143

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/note= ' 139. .14

first entry)

FOVH 249 FQVH 284

99WO-US028565. 98US-0113296P. 99WO-US005028.

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The present invention relates to the isolation of novel human PR polypeptides and the polymucleotide sequences encoding them. The polypeptides, agonists, antagonists or anti-PRO antibodies are u treating benign or mailgnant tumours (e.g. renal, kidney, bladde breast, etc), leukaemias and lymphoid malignancies, other disord as neuronal, glial, astrocytal, hypothalamic, glandular, macroph stromal and blastocoalic disorders, inflammatory, immune and ang disorders. The polymucleotide sequences are also useful in gene AAUB66162 represent the human PRO polypeptides of the in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thirty five nucleic acids encoding PRO polypeptides, useful for benign or malignant tumors, leukemias and lymphoid malignancies, inflammatory, anglogenic and immunologic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 MAARRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.7%; Score 249; DB 5; Length 249; 100.0%; Pred. No. 2.6e-220;
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Smith V,
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RM, Roy MA,
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Dan J, Pitti RM,
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                                                                                                                                                                              99WO-US005028.
99US-0123972P.
99US-0133453P.
99US-0140650P.
99US-0140653P.
99US-0144758P.
99US-0144758P.
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99WO-US021090.
99WO-US028313.
99WO-US028301.
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2000WO-US000219
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Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
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 neuroprotective.
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                                                                        WO200153486-A1.
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                                    Homo sapiens.
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Watanabe CK,
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22-JUN-1999;
22-JUN-1999;
20-JUL-1999;
26-JUL-1999;
17-AUG-1999;
31-AUG-1999;
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15-SEP-1999;
30-NOV-1999;
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11-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents a TWEAK protein. The specification method for preventing or treating an immune response in an animal. The method comprises of a TWEAK blocking agent. The method may be used for nd treating immune disorders associated with inappropriate nd/or activity of TWEAK. These disorders include autoimmune use and chronic inflammation, organ transplant rejection,—Host disease (SMID), lymphoid cell malignancies, septic and of shock, loss of immune responsiveness (as seen in human ency virus. (HIV) infections) and failure of the immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oenign tumour; malignant tumour; lymphoid malignancy;
euronal disorder; stromal disorder; blastocoelic disorder;
disorder; immune disorder; angiogenic disorder; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRSQRRRGRRGEPGTALLVPLALGIGIALACLGLILAVVSLGSRASLSAQEPAQEEL
                                                                                                                                                                                                                                                                  nd treating immune responses using modulators, especially of TWEAK, TWEAK receptors and TWEAK ligands, useful for . inflammation and graft versus host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.7%; Score 249; DB 3; Length 249; 100.0%; Pred. No. 2.6e-220; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ndard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                             Fig 1; 45pp; English.
                                                                                    2000WO-US001044.
                                                                                                                      99US-0116168P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide.
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The invention relates to an isolated nucleic acid molecule encoditumour necrosis factor family ligand. A composition comprising thisolated antibody or its fragment is used for treating an individual of decreased level of endokine alpha activity. The endokine polypeptide present in a heterotrimeric complex is used for treat individual having a disorder associated with excessive bone resor osteoporosis, Paget's disease or arterial calcification. Tre individual having a disorder associated with insufficient bone recomprises administering an endokine alpha antagonist, which is the antibody that binds specifically to endokine alpha polypeptide. Tantibody that binds specifically to endokine alpha polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                         human, tumour necrosis factor, TNF ligand, endokine alpha, excessive bone resorption disorder; osteoporosis, Paget's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / that binds specifically to endokine alpha polypeptide. T sequence represents the amino acid sequence of a tumour n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Endokine alpha gene useful for preparing a composition for tr
disease associated with excessive or insufficient bone resorption
          216 LLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLK
                                   36 MAARRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAARRSQRRRGERGEPGTALLVPLALGLGLALACIGLLLAVVSLGSRASLSAQEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoporosis, Paget's disease or arterial calcification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 24; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nardelli B;
                                                                                                                                                                                                                             ADC35206 standard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                     Human TNF ligand family member #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-AUG-2002; 2002US-00218547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-2001; 2001US-0312542P.
                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ni J, Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                     arterial calcification
                                                                                      276 TYFGLFOVH 284
                                                                                                                            241 TYFGLFOVH 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor family ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NI J.
ROSEN C A.
NARDELLI B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-696072/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADC35205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003100074-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 249 AA;
                                                                                                                                                                                                                                                                                                             L8-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-2003.
                                                                                                                                                                                                                                                                       ADC35206;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YUGG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NIJJ/)
(ROSE/)
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                                                                                                                                                                                                              ADC35206
                                            엄
                                                                                                                            g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equence is the protein sequence for human TWEAK protein. The ates to compositions comprising heterotrimeric complexes of is factor (TMF) ligand family members, and their use in the evention and treatment of disease. In one embodiment, the complex comprises full-length or extracellular portions of l-length or extracellular portions of preferably vGGI or VVGI-SV. The heterotrimeric complexes in are useful for treating an autoimmune disease, cancer or and particularly for inhibiting cancer cell proliferation, or inducing apoptosis of I cells selection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
GVLALRCLEBFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DODPSELNPQTEESODPAPFLNRLVRPRRSAPKGRKTRARRALAAHYEVHPRPGQD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3VDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3VDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       timeric complex having a first polypeptide member of the s factor (TNF) ligand family, and a second different member family, useful for treating cancer, osteoporosis or an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSORRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEEL
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0
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                                                                                                                                                                                                                                                                                                                                               necrosis factor; ligand; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.7%; Score 249; DB 6; Le
100.0%; Pred. No. 2.6e-220;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              age 368-369; 388pp; English.
                                                                                                                                                                                     dard; protein; 249 AA.
                                                                                                                                                                                                                                                                                                                                                                      or; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002WO-US023782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-0307838P.
                                                                                                                                                                                                                                                               (first entry)
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                                          LFOVH 284
                                                                                  LFOVH 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen CA;
                                                                                                                                                                                                                                                                                                                                                   tumour
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EDQDPSELNPQTEESQDFAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGGD 120 AGVDGTVSGWEEBARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD 180 OGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL 240 EDODPSELNPOTEESODPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGGD 155 AGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD 215 DGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL 275 SLFQVH 284 SLFOVH 249

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ndard; protein; 249 AA.

(first entry)

andothelium proliferative agent protein.

lium proliferative agent; TREPA; wound healing; cancer; ing; vascularisation; apoptosis; autoimmune; birth control.

98WO-US002859.

97US-00798692. 98US-00021706.

IT LAB.

7255/38.

cleic acid encoding TREPA - useful for diagnosis and autoimmune disease, tumours and inflammation.

ge 123-4; 142pp; English.

ted endothelium proliferative agent (TREPA), or its
r agonists, are used to treat a deficit of TREPA, e.g. to
l healing or tissue grafting, by promoting vacularisation,
ce apoptosis for treating cancer and eliminating autoreactive
an adjunct to cancer chemotherapy or antiviral treatment.
es can also be used to target cytocoxic agents or for
lation of the corresponding receptor, the nucleic acid for
used to transform thumour cells to render them more
or TREPA and to screen for TREPA minics. Riboxymes, antisense
dies or peptides, are used to treat TREPA-associated
g. tumours and metastases (by inhibiting vascularisation),
or a wide range of autoimmune conditions, conditions
normal stimulation of epithelial cells (e.g.
sis), for birth control (inhibiting ovulation and placental
r other angiogenic conditions (e.g. ulcers)

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84.9%; Score 241; DB 2; Length 249; 100.0%; Pred. No. 5.9e-213;
                      larity
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Matches 241; Conservative 0; Mismatches 0; Indels 0; 4 RRGRRGEPGTALLVPLANGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAE	104 SELNPÇTEESQDPAPFLNRLVRPRRSAPKGRKTRARRA1AAHYEVHPRPGQDGAQ 	164 TVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLV 	224 IRCLEBERATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPPLTYF 	284 H 284	249 H 249	RESULT 9 AAE00891 ID AAE00891 standard; protein; 249 AA.	AAE00891;	04-JUL-2001 (first entry)	Human TREPA (TNF related endothelium proliferative agent).	Human; tumour necrosis factor; TNF; angiogenesis; wound healing; TNF related endothelium proliferative agent; tumour; metastasis; grafting; vulnerary.	Homo sapiens.	Key Location/Qualifiers Domain 98249 /label= Extracellular_domain	US6207642-B1.	27-MAR-2001.	26-JUN-1998; 98US-00105343.	12-PEB-1997; 97US-00798692. 10-PEB-1998; 98US-00021706.	(ABBO ) ABBOTT LAB.	Wiley SR;	WPI; 2001-280760/29. N-PSDB; AAD04350.	Inducing angiogenesis in mammal at desired sites for promoting whealing, by administering soluble fragment of extracellular doma tumor necrosis factor related endothelium proliferative agent pr	Claim 1; Col 75-76; 53pp; English.	The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family mole designated as TREPA (TNF related endothelium proliferative agent Soluble biologically active TREPA are used to treat TREPA-associ diseases, tumours or metastases. TREPA is used for inducing angin human for promoting wound healing and for vascularising graft for successful grafting and to promote tissue grafts. The presen acid sequence is clone ID #690050 human TREPA
Ma Qy Db	ζζ QΩ	Qy du	λ Q	ð	qq	REST AAEC ID	X Z I	X E	<b>X</b> E	X & & & \$	SO	XEELS	X N	X & 3	<b>₹</b>	1 K K K	<b>4 &amp; 3</b>	됩	* # # # #	<b>\</b> \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	3 S	\$88888888

GEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAREDQDP 103 283 QTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDG 163 EEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLA 223 BEARINSSSPLRYNROIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLA 188 EFSATAASSLGPOLRICQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQV 248 QTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDG GEPGTALLIVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVABEDQDP BFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQV Gaps .; 0 84.9%; Score 241; DB 4; Length 249; 100.0%; Pred. No. 5.9e-213; ive 0; Mismatches 0; Indels nservative

protein; 273 AA. ard;

first entry)

lular domain-containing fusion protein.

lular domain; tumour necrosis factor; TNF; angiogenesis; ularisation; diabetic retinopathy; neovascular glaucoma; retinopathy of prematurity; retrolental fibroplasia; tis; macular degeneration; arthritis; rheumatism; neovascularisation; psoriasis; metastatic condition; ur; sarcoma; carcinoma; benign tumour; haemophilic joint; condition; myocardial angiogenesis; wound granulation; ascular adhesion; telangiectasia; ischaemia; human; plaque neovascularisation; coronary atherosclerosis; erosclerosis; pDC409-LZ-TWEAK; TWEAK receptor; TWEAKR;

000WO-US034755.

99US-0172878P 000US-0203347P.

75/44.

iogenesis in a mammal for treating diseases mediated by e.g. solid tumors and vascular deficiencies of cardiac or sue, by administering antagonist or agonist of TWEAK

Example 1; Page 41; 46pp; English.

The sequence represents a a fusion protein encoded by the express vector pDC409-LZ-TWEAK. The fusion protein comprises a growth hor leader, a leucine zipper multimerisation domain, and the extracel domain of human TWEAK. The fusion protein was used in the isolati human TWEAK receptor (TWEAKR)-expressing clones from a COS cell h cDNA library. The TWEAKR protein is a member of the tumour necrosi (TNF) family and induces angiogenesis. TWEAKR may therefore be us screen for and develop TWEAKR agonists and antagonists for the moof angiogenesis, to be used in the treatment and diagnosis of hum of angiogenesis, to be used in the treatment and diagnosis of hum characterised by ocular neovascularisation such as diabetic retin neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrofental fibroplasia, rubecats, uveitis, macular degeneration corneal graft neovascularisation, and inflammatory diseases such arthritis, rheumatism and psoriasis. Other treatable diseases incommitted that the continue continue continue and metastatic conditions such as sarcomas and carcinom. benign tumours and preneoplastic conditions, myocardial angiogenes haemophilic joints, scleroderma, vascular adhesions, atheroscleroplaque neovascularisation, telangiectasia, wound granulation, corratherosclerosis, peripheral atherosclerosis and ischaemia

68

Sequence 273 AA;

; Length 273; 0; Indels 72.9%; Score 207; DB 4; Le 100.0%; Pred. No. 1.2e-181; ive 0; Mismatches 0; Best Local Similarity 100. Matches 207; Conservative Query Match Best Local S

SLGSRASLSAQEPAQEELVABEDQDPSELNPQTEESQDDAPFLNRLVRPRRSAPKGI 67 SLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKG 78 à q

127 ARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRA ARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAK 138 à d

187 LYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALI LYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALI 198 8 d

247 SLRIRTLPWAHLKAAPFLTYFGLFQVH 273 SLRIRTLPWAHLKAAPFLTYFGLFQVH 284 258 ਨੋ 셤

AAE00895 standard; protein; 146 AA AAE00895;

04-JUL-2001 (first entry)

Human TREPA (TNF related endothelium proliferative agent) fragment

Human; tumour necrosis factor; TNF; angiogenesis; wound healing; TNF related endothelium proliferative agent; tumour; metastasis; grafting; vulnerary.

Homo sapiens.

US6207642-B1

27-MAR-2001.

98US-00105343. 26-JUN-1998;

97US-00798692. 98US-00021706. 12-FEB-1997; 10-FEB-1998;

(ABBO ) ABBOTT LAB

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0760/29
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iogenesis in mammal at desired sites for promoting wound administering soluble fragment of extracellular domain of is factor related endothelium proliferative agent protein.

## ig 1, 53pp; English.

ogically active TREPA are used to treat TREPA-associated mours or metastases. TREPA is used for inducing angiogenesis promoting wound healing and for vascularising grafted tissue il grafting and to promote tissue grafts. The present amino is human TREPA fragment invention relates to extracellular signal molecules, members of tumour necrosis factor (TNF) family molecules 3 TREPA (TNF related endothelium proliferative agent).

0; Gaps Length 146; 0; Indels Score 146; DB 4; Le Pred. No. 7.8e-126; 51.4%; bcc. 100.0%; pred. No. '...
100.0%; Pred. No. '...
0; Mismatches Conservative larity

198 9 AAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYL AAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYL

120 258 HEDEGKAVYLKLDLLVDGVLAIRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSS HFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSS

# VILPWAHLKAAPFLTYFGLFQVH 284

TILLITITITITITITI

## idard; protein; 189 AA

#### (first entry)

indothelium proliferative agent protein 2.

proliferative agent; TREPA; wound healing; cancer; vascularisation; apoptosis; autoimmune; birth control. Lium

### 98WO-US002859.

97US-00798692.

#### LAB. £

#### 7255/38

leic acid encoding TREPA - useful for diagnosis and autoimmune disease, tumours and inflammation.

Je 125-6; 142pp; English

The TNF-related endothelium proliferative agent (TREPA), or its activators or agonists, are used to treat a deficit of TREPA, epromote wound healing or tissue grafting, by promoting vascularialso to induce apoptosis for treating cancer and eliminating autorate to induce apoptosis for treating cancer and eliminating autorated to include a madjunct to cancer chemotherapy or antiviral treat treps peptides can also be used to target cyctocoxic agents or for affinity isolation of the corresponding receptor, the nucleic activity isolation of the corresponding receptor, the nucleic activity isolation of the corresponding receptor, the nucleic activities and to screen for TREPA minics. Ribozymes, a responsive to TREPA and to screen for TREPA minics. Ribozymes, a computation or a wide range of autoimmune conditions, condition infolving abnormal stimulation of epithelial cells (e.g. involving abnormal stimulation of epithelial cells (e.g. ulcers) contation or other angiogenic conditions (e.g. ulcers)

## Sequence 189 AA;

. 0 50.4%; Score 143; DB 2; Length 189; 100.0%; Pred. No. 5.7e-123; ive 0; Mismatches 0; Indels Matches 143; Conservative Similarity Query Match Local

## LAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLY 47 IAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLY 142

ठ g

; 0

202 VHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPOLRLCQVSGLLALRPG à g

#### 167 RTLPWAHLKAAPFLTYFGLFQVH 189 RILPWAHLKAAPFLTYFGLFQVH 284 262

à g

#### RESULT 13

AAE00892 standard; protein; 189 **AAE**00892

#### AAE00892;

04-JUL-2001 (first entry) 

# Human UL4flag TREPA soluble construct.

Human, tumour necrosis factor, TNF, angiogenesis, wound healing, TREPA, TNF related endothelium proliferative agent, metastasis, vulnerary, HUVEC, human umbilical vein endothelial cell; UL4flag

#### Homo sapiens.

US6207642-B1.

#### 27-MAR-2001

98US-00105343. 26-JUN-1998;

#### 97US-00798692. 12-FEB-1997; 10-FEB-1998;

(ABBO ) ABBOTT LAB

#### Wiley SR;

WPI; 2001-280760/29.

Inducing angiogenesis in mammal at desired sites for promoting we healing, by administering soluble fragment of extracellular doma: tumor necrosis factor related endothelium proliferative agent  $p\kappa$ 

Example 2; Col 75-78; 53pp; English.

nvention relates to extracellular signal molecules, members of tumour necrosis factor (TWP) family molecules TREPA (TWT related endothelium proliferative agent). gically active TREPA are used to treat TREPA-associated ours or metastases. TREPA is used for inducing angiogenesis promoting wound healing and for vascularising grafted tissue 1 grafting and to promote tissue grafts. The present amino is human Uniting TREPA soluble construct. This sequence ologically active molecule is capable of inducing in HUVEC (human umbilical vein endothelial cells) cells

8888888888**3**\$

0 0; Gaps Length 189; 0; Indels 50.4%; Score 143; DB 4; Le 100.0%; Pred. No. 5.7e-123; ive 0; Mismatches 0; onservative

YEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQ 201 

> S 75 Ä

EGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRI 166 EGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRI 261

VAHLKAAPFLTYFGLFOVH 284 WAHLKAAPFLTYFGLFOVH 189

dard; protein; 208 AA.

rotein.

is factor receptor; signal transducer molecule; TNF; APO4; abnormality; gestational abnormality; prostate cancer; PO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease; PM9; TNRL-1; antibody preparation; breast carcinoma;

98WO-US018393.

97US-00924634.

MASHINGTON

.91/17.

rosis Factor family receptor polypeptides and ligands -agnosis and treatment of prostate cancer and developmental abnormalities.

13A; 156pp; English.

or by describes isolated Tumor Necrosis Factor (TNF) family speptides: APO4, APO6, APO8 and APO9 or their active 1 isolated TYP related ligands 1 and 3 (TNRL1 and TNRL3) fragments. APO4 is useful for diagnosing prostate cancer

treated using levels of APO4 in an individual. Prostate cancer can treated using APO4 selective binding agents linked to a therapeut moietry. APO4 polypeptides are also useful for identifying selective binding agents, useful in diagnosis/treatment of disease by binding agents to the polypeptide/active fragment which is extracellular, expressed on the cell surface. The binding is preferably performed vivo. APO4 polypeptides/ active fragments are also useful for scrifor agonists and antagonists by binding and observing the changes activity. Effective pharmacological agents useful in diagnosis on treatment of disease are also identified using APO4 polypeptides/ fragments and APO4 signal transducer molecules that specifically with a cytoplasmic domain of APO4 and detecting a change in level activity. The method is performed in vivo or in vitro. APO polype activity. The method is performed in vivo or in vitro. APO polype are all useful for diagnosis/treatment of developmental or gestational useful for diagnosis/treatment of developmental or gestational and programmities. · · 77 VSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPK 1 VSLGSRASLSAQEPAQEELVABEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPF 137 RARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTK RARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYYRQIGEFIVTF 197 YLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLA 37.7%; Score 107; DB 2; Length 208; 99.5%; Pred. No. 7.8e-90; ive 0; Mismatches 1; Indels SSLRIRTLPWAHLKAAPFLTYFGLFQVH 284 MCF-7, and induced apoptosis Matches 207; Conservative Best Local Similarity Sequence 208 AA; 19 257 Query Match ð a ð 셤 ð

RESULT 15 AAW93591

AAW93591 standard; protein; 211 AA.

AAW93591;

18-JUN-1999 (first entry)

Mouse TNRL3 protein.

Tumour necrosis factor receptor; signal transducer molecule; TNF; developmental abnormality; gestational abnormality; prostate ca APO6; APO9; APO9; TNRL-3; diagnosis; treatment; therapy; cytoplasmic domain; immunogen; antibody preparation; breast carci apoptosis; mouse. 

Mus sp.

WO9911791-A2.

11-MAR-1999.

98WO-US018393. 04-SEP-1998;

05-SEP-1997;

UNIW ) UNIV WASHINGTON

Chaudhary PM;

WPI; 1999-205191/17.

N-PSDB; AAX23425

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crosis Factor family receptor polypeptides and ligands - lagnosis and treatment of prostate cancer and developmental
                                                                                        abnormalities.
```

3 13B; 156pp; English

on describes isolated Tumor Necrosis Factor (TNF) family ppeptides: APO4, APO6, APO8 and APO9 or their active and isolated TNF related ligands I and 3 (TNRLL and TNRL3) or fragments. APO4 is useful for diagnosing prostate cancer by levels of APO4 in an individual. Prostate cancer can also be APO4 selective binding agents linked to a therapeutic polypeptides are also useful for identifying selective ts, useful in diagnosis/treatment of disease by binding of e polypeptide/active fragment which is extracellular, or the cell surface. The binding is preferably performed in olypeptides/ active fragments are also useful for screening and antagonists by binding and observing the changer in APO4 fiscase are also identified using APO4 polypeptides/active disease are also identified using APO4 polypeptides/active disease are also identified using APO4 polypeptides also in a method is performed in vivo or in vitro. APO polypeptides ul as immunogens for preparing antibodies. APO4 is also lagnosis/treatment of developmental or gestational nduced apoptosis

```
Gaps
                 .,
Length 211;
                0; Indels
DB 2; Le
9.6e-34;
               0; Mismatches
Score 46;
Pred. No.
16.2%;
                Conservative
```

. 0

## LRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 284 LRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 211

ndard; protein; 225 AA.

(first entry)

tumour necrosis factor related ligand (TRELL),

necrosis factor related ligand; tnf; treatment; cancer; isease; immune system; stimulation; suppression;

Location/Qualifiers

/note= "hydrophobic, transmembrane domain"

97WO-US013945.

96US-0023541P. 96US-0028515P. 97US-0040820P.

3N INC. GENEVA FACULTY MEDICINE.

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The sequence is that of mouse tumour necrosis factor related lic (TRELL). TRELL or active fragments can be included with a carrie pharmaceutical compositions to treat cancer, autoimmune diseases immune responses to tissue grafts, or to stimulate or suppress t system. It is useful to screen for TRELL receptors, by labelling detectable label and screening compositions for binding. Agents interfering with TRELL receptor binding can also be screened for then be administered, optionally with interferon-gamma, to induct then be administered, optionally with interferon-gamma, to induct then be administered, optionally with interferon-gamma, to induct then be administered, optionally with interferon-gamma, to induct the administered calls involving a signal pathway between the seceptor. It's coding sequence can be used in gene therapy for elated disorders in mammals (especially humans), e.g. tumours, autoimmune and inflammatory diseases or inherited genetic disord introducing into cells, and expressing, therapeutically effective of a vector, e.g. a virus comprising a gene encoding TRELL. It me be of use in the preparation of prepare probes for screening thereof.
                                                                                                                    Tumour necrosis factor related ligand - useful for, e.g. treating auto-immune disease and immune responses to tissue grafts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.3%; Score 32; DB 2; Length 225; 100.0%; Pred. No. 7.6e-21; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 RRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEE 170
                                                                                                                                                                                               Claim 12; Page 48-50; 69pp; English.
Chicheportiche Y, Browning JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32; Conservative
                                            WPI; 1998-145619/13.
N-PSDB; AAV18599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
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RESULT 17

.. 0

AAB07527

AAB07527 standard; protein; 225 AA. AAB07527;

20-OCT-2000 (first entry)

Amino acid sequence of a soluble recombinant murine TWEAK protei 

TWEAK protein; immunological disorder; immune response; inflamma TWEAK blocking agent; autoimmune disease; organ transplant rejec Graft-versus-Host disease; GVHD; lymphoid cell malignancy; shock

Mus sp.

WO200042073-A1.

20-JUL-2000.

14-JAN-2000; 2000WO-US001044.

99US-0116168P 15-JAN-1999;

(BIOJ ) BIOGEN INC.

Rennert P;

WPI; 2000-476036/41.

Preventing and treating immune responses using modulators, espec: antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, useful : treating e.g. inflammation and graft versus host disease.

ig 1; 45pp; English.

ethod for preventing or treating an immunological disorder ting an immune response in an animal. The method comprises a TWEAK blocking agent. The method may be used for d treating immune disorders associated with inappropriate d/or activity of TWEAK. These disorders include autoimmune te and chronic inflammation, organ transplant rejection, Host disease (GVHD), lymphoid cell malignancies, septic and f shock, loss of immune responsiveness (as seen in human ney virus (HIV) infections) and failure of the immune equence represents a TWEAK protein. The specification umour growth

\$#\$\$BBBBBBBBBBBB

Gaps .; 0 Score 32; DB 3; Length 225; Pred. No. 7.6e-21; 0; Indels 100.0%; Preu. ... 11.3%; onservative

AAHYEVHPRPGQDGAQAGVDGTVSGWEE 170 AAHYEVHPRPGQDGAQAGVDGTVSGWEE 111

dard; protein; 249 AA.

(first entry)

Ķ.

3AK; TNF relatedness and weak ability to induce cell death; scrosis Factor; TWEAK; fibrosis; cardiac disease; ; lung disease; kidney disease; skin disease; le disease, adipose Lissue disease, nal tract disease, pancreatic disease, organ disease, neural disease, cartilage disease, connective tissue disease, cellular death, hepatotropic; i, gastrointestinal; osteopathic.

72

:003WO-US011350

3002US-0371611P

I INC.

Hahm K; ۲, Zheng cubowski A,

56/78.

ARK-related condition, e.g. liver, gastrointestinal, kidney, i.c., cartilage or neural tissue condition in a subject instering to the subject a TWEAK agonist or antagonist. O ID NO 1; 120pp; English.

equence is murine transmembrane FL-TWEAK (TNF relatedness ty to induce cell death, where TNF is Tumour Necrosis (is a member of the TNF Family. TWEAK agonists or re useful for transing a TWEAK related condition, e.g. liac disease; liver disease; lung disease; kidney disease;

skin disease; skeletal muscle disease; adipose tissue disease; agastrointestinal tract disease; pancreatic disease; reproductive disease; neural disease; cartilage disease; bone disease; crise disease; callular death; and a pathological condition of a expressing a TWEAK receptor. Sequence 249 AA; 88888888

ö Length 249; Indels DB 7; Le 11.3%; Score 32; DB 100.0%; Pred. No. 8.4cive 0; Mismatches Best Local Similarity 100.0 Matches 32; Conservative Query Match

·

104 RRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEE 135 139 RRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEE 170 g à

RESULT 19 AAG01265

0

AAG01265 standard; protein; 58 AA

AAG01265;

(first entry) 06-0CT-2000

Human secreted protein, SEQ ID NO: 5346.

Human; 5' EST; expressed sequence tag; secreted protein; cDNA iso gene therapy; chromosome mapping. 5' EST;

Homo sapiens.

EP1033401-A2.

06-SEP-2000

21-FEB-2000; 2000EP-00200610.

99US-0122487P

26-FEB-1999;

(GEST ) GENSET

Duclert A, Giordano J; Dumas Milne Edwards J,

WPI; 2000-500381/45. N-PSDB; AAC01271 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo diagnostic, forensic, gene therapy and chromosome mapping procedu

Claim 13; SEQ ID NO 5346; 71pp + Sequence Listing; English.

The present sequence is a polypeptide encoded by one of a large n 5' ESTs derived from mRNAs encoding secreted proteins. The 5' EST prepared from total human RNAs or polyA+ RNAs derived from 30 dif tissues. EST sequences usually correspond mainly to the 3' untran region (UTR) of the mRNA because they are often obtained from old primed cDNA libraries. Such ESTs are not well suited for isolating sequences derived from the 5' ends of mRNAs and even in those cas longer cDNA sequences have been obtained, the full 5' UTR is rare included. 5' ESTs are derived from mRNAs with intact 5' ends and therefore be used to obtain full length cDNAs and genomic DNAs. 5' are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory seand to design expression and secretion vectors 

Sequence 58 AA;

., 0; Indels Length 58; DB 3; 3.2%; Score 9; DB 3 100.0%; Pred. No. 2.9 tive 0; Mismatches 9; Conservative Query Match Best Local Similarity Matches 9; Conserva

ĕ

54 DFEIS 9 DFEIS dard; protein; 58 AA.

ed protein, SEQ ID NO: 5347

expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping.

2000EP-00200610

99US-0122487P.

Duclert A, Giordano J; dwards J,

381/45

orensic, gene therapy and chromosome mapping procedures. expressed sequence tag (5' EST) for As that correspond to 5'ESTs and for genomic DNAs that that is a 5' and cid

ID NO 5347; 71pp + Sequence Listing; English.

requence is a polypeptide encoded by one of a large number of red from mRNAs encoding secreted proteins. The 5' ESTs were a total human RNAs or polyA+ RNAs derived from 30 different sequences usually correspond mainly to the 3' untranslated of the mRNA because they are often obtained from oligo-drained in the ESTs are not well suited for isolating cDNA: braries. Such ESTs are not well suited for isolating cDNA: the from the 5' ends of mRNAs and even in those cases where sequences have been obtained, the full 5' UTR is rarely ESTs are derived from mRNAs with intact 5' ends and can used to obtain full length cDNAs and genomic DNAs. 5' ESTs in diagnostic, forensic, gene therapy and chromosome dures. They are used to obtain upstream regulatory sequences expression and secretion vectors

Gaps 0 0; Indels Length 58; 3.2%; Score 9; DB 3; 100.0%; Pred. No. 2.9; tive 0; Mismatches onservative arity

ö.

DFEIS 9

DFEIS 54

dard; protein; 365 AA.

(first entry)

Human DITHP receptor.

Human; dithp; diagnostic and therapeutic polynucleotide; diagnos: cancer, eell proliferative disorder; autoimmune disorder; inflammatory disorder; infection; hormonal disorder; metabolic dieurological disorder; gastrointestinal disorder; transport disorder. connective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genotyping; transgenic animal; l disease model; toxicological testing; transcript imaging; recept

Homo sapiens

WO200297031-A2

05-DEC-2002

27-MAR-2002; 2002WO-US010056.

28-MAR-2001;

2001US-0280067P 2001US-0280068P 2001US-0291849P 2001US-0291849P 2001US-0298429P 2001US-0298428P 29-MAR-2001; 2 29-MAR-2001; 2 17-MAY-2001; 2 17-MAY-2001; 2 117-MAY-2001; 2 117-MAY-2001; 2 20-UN-2001; 2

2001US-0300001P

(INCY-) INCYTE GENOMICS INC.

Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gersti:
H, David MH, Lewis SA, Chen AJ, Panzer SR, Harris:
Marwaha R, Lo A, Lan RY, Urashka ME; Dufour GE, Hillman JL, Daughtery SC, Dam TC, Peralta CH, David MH, Flores V, Marwaha R, Daffo A,

WPI; 2003-129518/12.

N-PSDB; ACC46177.

Novel human diagnostic and therapeutic polypeptide useful for id test compound which specifically binds to a polypeptide encoded diagnostic and therapeutic polymucleotide, and to induce antibod.

Claim 27; SEQ ID NO 770; 591pp; English.

The invention relates to novel human diagnostic and therapeutic polymucleotides designated dithp (ACC46080-ACC46749) and to their polymucleotides designated dithp (ACC46080-ACC46749) and to their proteins (DITHP, ABR41136-ABR41812). The invention also relates polymucleotide sequences at least 90% identical to the dithp CDN, sequences of the invention; recombinant vectors, host cells and transpagenic organisms comprising a dithp nucleic acid sequence; the recombinant production of DITHP proteins; antibodies specific for proteins; microarrays comprising dithp nucleic acid sequences; medetecting dithp nucleic acid sequences; medetecting dithp nucleotide and protein sequences; medetecting dithp nucleotide and protein sequences and DITHP proteins may be use probe. Dithp nucleic acid sequences and DITHP proteins may be use the compounds which sportfically bind a DITHP proteins may be use diagnosis of a wide variety of conditions including cancer and of proliferative disorders; autoimmune or inflammatory disorders; be viral, fungal or parasitic infections; hormonal disorders; metabor disorders; and connective tissue disorders. They may also be used disorders; and connective tissue disorders. They may also be use screen for modulators of protein activity or gene expression. DIT or cell type and to induce antibodies. They may also be used or cell type and to induce antibodies. The dithp nucleic acids and additionally be used in analysis of the proteome of or cell type and to induce antibodies. The dithp nucleic acids and additionally be used in analysis of the dictore. mentioned above, as a source of antisense sequences, as a source probes and primers, in genotyping and identification of individual the generation of transgenic animal models of human disease or kn humanised animals, in toxicological testing, and in transcript in The present sequence represents a DITHP protein which has recept activity. Note: The sequence data for this patent did not form positivity.

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pecification, but was obtained in electronic format directly ftp.wipo.int/pub/published_pct_sequences
```

Sequence 748 AA;

X S

AA;

Gaps . Length 365; 0; Indels DB 6; . 17; 0; Mismatches Score 9; D Pred. No. 100.0%; 3.2%; onservative GRRGE 50

0;

GRRGE 30

dard; protein; 748 AA.

(first entry)

o acid sequence for GVs-9.

l maturation; infectious disease; immune disorder; cancer;
yettem; wycobacterial infection; allergy; tubercullosis;
yidosis; lung cancer; asthma; skin disorder; psoriasis;
czema; alopecia areata; skin cancer; basal carcinoma; vaccae protein; antigen; T cell activation; cytokine; carcinoma; melanoma.

vaccae.

98WO-NZ000189

97US-00996624. 97US-00997080. 97US-00997362. 98US-00095855. 98US-00156181 98US-00205426

IS RES & DEV CORP LTD.

Prestidge RL; Skinner MA, n J, Visser ES,

163/36.

nne response to an antigen.

209-210; 243pp; English.

provides heat-Killed Mycobacterium vaccae, or recombinant teins. The M. vaccae proteins may be employed to activate T iral killer cells, to stimulate the production of cytokines, e expression of co-stimulatory molecules on dendritic cells, and to enhance dendritic cell maturation and function. The be expressed by standard recombinant methodology.

I compositions comprising the proteins or nucleic acid oding the proteins can be used for the treatment, and detection of disorders including infectious diseases, ers and cancer. In particular, the compounds and methods are timent of diseases of the respiratory system, such as infections, astham, allergies, tuberculosis, leprosy, and lung cancers, and disorders of the skin such as opic dermatitis, eczema, allergic context dermatitis. ta, and skin cancers such as basal carcinoma, squamous cell melanoma

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Skin disorder, psoriasis, atopic dermatitis, allergic contact der alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cyt antipsoriatic; dermatological; antiinflammatory; antiallergic; Th2 immune response; immunomodulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting skin inflammation associated with skin disorder e.g. sporiasis, by administering composition comprising delipidated ar deglycolipidated Mycobacterium vaccae cells or Mycobacterium vacculture filtrate.
                                ·.
           Length 748;
                                0; Indels
         DB 2;
        3.2%; Score 9; DB 2
100.0%; Pred. No. 34;
tive 0; Mismatches
                                                                                                                                                                                        M vaccae GVs-9 protein SEQ ID NO: 154
                                                                                                                         ABB73512 standard; protein; 749 AA.
                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                            Tan PLJ, Prestidge R;
                                                                                                                                                                                                                                                                                                                              99US-00324542.
                                                                                                                                                                                                                                                                                                                                                  97US-00997080.
                                                                                                                                                                  08-APR-2002 (first entry)
                              Conservative
                                                                      282 ALGLGLALA 290
                                                   68
                                                                                                                                                                                                                                                                Mycobacterium vaccae.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-138361/18.
N-PSDB; ABL36274.
                                                   60 ALGLGLALA
                                                                                                                                                                                                                                                                                    US6328978-B1.
                                                                                                                                                                                                                                                                                                                             02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                 23-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                            Watson JD,
                                                                                                                                              ABB73512;
                                                                                                    RESULT 23
                                                                     a
                                                                                                                                              à
```

Sequence 749 AA;

The present invention relates to a method of inhibiting skin inflassociated with a skin disorder selected from psoriasis, atopic dermatities and allergic contact dermatities, which involves adminia composition containing delipidated and deglycolipidated Mycobac vaccae cells or M. vaccae culture filtrate. The skin disorder to treated may also include alopecia areata, and skin cancers such a cell carcinoma, squamous cell carcinoma and melanoma. The composiacts by inhibiting the Th2 immune response. The present sequence protein described in the exemplification of the invention

Example 6; Col 161-164; 116pp; English.

ö 3.2%; Score 9; DB 5; Length 749; 100.0%; Pred. No. 34; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 9; Conservative

U

60 ALGLGLALA 68

à

RESULT 24

ndard; protein; 54 AA.

erium acnes immunogenic protein #12759.

s; synovitis; acne; pustulosis; hypertosis; osteomyelitis; ohthalmitis; bone; joint; central nervous system; ELISA, esion; acne vulgaris; enzyme linked immunosorbent assay; al; osteopathic; neuroprotectant ophthalmitis; bone;

erium acnes.

2001WO-US012865.

2000US-0199047P. 2000US-0208841P.

2000US-0216747P

Mitcham JL, Wang SS, Bhatia A; Jen S, Carter D; J, Zhang Y, Persing DH,

6774/71.

erium acnes polypeptides and nucleic acids useful for against and diagnosing infections, especially useful for vulgaris.

EQ ID NO 13058; 1069pp; English.

hypertobia and osceomyelite), uveitis and endophthalmitis.

also involved in infections of bone, joints and the central
em, however it is particularly involved in the inflammatory
clated with acne vulgaris. A method for detecting the
absence of P. acnes in a patient comprises contacting a
a binding agent that binds to the protectins of the invention
ing the amount of bound protein in the sample. The
may be used as antigens in the production of antibodies
P. acnes proteins. These antibodies can be used to
expression and activity of P. acnes polypeptides and
eat P. acnes infections. The antibodies may also be used as
gents for determining P. acnes presence, for example, by
i immunosorbent assay (ELISA). Note: The sequence data for
all ont form part of the printed specification, but was
electronic format directly from WIPO at U39105-AAU68017 represent Propionibacterium acnes immunogenic. The proteins and their associated DNA sequences are used in t, prevention and diagnosis of medical conditions caused by The process and these associated of providing cale disorders include SAPHO syndrome (synovitis, acre, 'pub/published\_pct\_sequences

Gaps .. 0 2.8%; Score 8; DB 4; Length 54; 00.0%; Pred. No. 23; ve 0; Mismatches 0; Indels 100.08; Conservative larity

28 PLPRS

PLPRS 18

```
Propionibacterium acnes predicted ORF-encoded polypeptide #13058
                                                                                                                                                 Maisonneuve JI
Jones R, Cart
                                                  Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                 Bhatia A,
Benson DR,
                                                        Immunostimulant; immune response; vaccine.
                                                                                                                                                 Mitcham JL, Skeiky YAW, Persing DH,
Zhang Y, Wang S, Jen S, Lodes MJ,
ABM48382 standard; protein; 54 AA.
                                                                                                                                                       Wang S, Jen S, Lode
Vallieve-Douglass J;
                                                                                                            11-OCT-2002; 2002WO-US032727.
                                                                                                                       15-OCT-2001; 2001US-00978825.
                         (first entry)
                                                                      Propionibacterium acnes.
                                                                                                                                                                          WPI; 2003-381789/36.
                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                 WO2003033515-A1.
                         20-0CT-2003
                                                                                               24-APR-2003.
            ABM48382;
                                                                                                                                                       Zhang Y,
Barth B,
```

New Propionibacterium acnes polypeptides and polynucleotides enc polypeptide, useful for diagnosing, preventing or treating acne or for stimulating an immune response specific for a P. acnes pr

N-PSDB; ACF64481

Example 1; SEQ ID NO 13058; 1481pp; English

The invention relates to an isolated polymucleotide (ACF64435-Ac encoding a Propionibacterium acnes protein. The invention also rencoding a Propionibacterium acnes protein. The invention also repolymucleotides (ABM3524-ABM64536) immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprision proteins comprising a polypeptide of the invention; fusion proteins comprising a polypeptide of the invention; fusion proteins comprising a polypeptide and an isolated T cell population comprising T cells to polypeptide and an isolated T cell population comprising T cells via this method; a vaccine composition (comprising P. acnes polypeptides, autibodies, fusion proteins, T cell populations of antigen-presenting cells that express the polypeptide); a method for inhibiting the development of P. acnes antient; and a method for inhibiting the development of P. acnes patient; and a method for inhibiting the development of P. acnes proteins, T cell populations or antigen-presenting cells that expressions of professions of proteins. T cell populations or antigen-presenting cells that collypeptides are useful for diagnosing, preventing or treating a protein. The polymucleotides can also be used as probes or prime nucleic acid hybridisation. The vaccine composition is useful for stimulating an immune response against P. acnes, or for treat and the kit is useful for performing a diagnostic assay. The presentence represents a polymeptide predicted to be encoded by an equence represents a polymely protein of a nimmune response against P. acnes, or for treat and the kit is useful for performing a diagnostic assay. The presentence represents a polymely protein of a nimmune response against P. acnes, or form the printed specification, but was obtained in electronic format the printed specification, but was obtained in electronic format the printed specification, but was obtained in electronic format.

Sequence 54 AA;

6

. Indels 2.8%; Score 8; DB 6; Length 54; 00.0%; Pred. No. 23; ve 0; Mismatches 0; Indels Query Match 2.0%; Dr. Best Local Similarity 100.0%; Pr. Conservative 0;

11 RRLPLPRS 18

à

28

LPRS

(first entry)

Peptide #10143 encoded by human foetal liver single exon probe. (first entry) Conservative Hanzel DK, 19 61 LGLGLALA 68 WPI; 2001-483447/52 Query Match Best Local Similarity Matches 8; Conserv 12 LGLGLALA Sequence 55 AA; WO200157277-A2 Homo sapiens 04-FEB-2000; 26-MAY-2000; 09-AUG-2001 17-0CT-2001 AAM36451; Penn SG, RESULT 28 AAM36451 à nvention relates to human single exon nucleic acid probes 110066-AA128459). The present sequence is a peptide encoded robe. The SENPS are derived from human Heida cells. The SENPS or produce a single exon microarray, which can be used for an gene expression in a sample derived from human cervical lls. By measuring gene expression, the probes are therefore ling and/or staging of diseases of the cervix, notably ar. Note: The sequence data for this patent did not form rinted specification, but was obtained in electronic format WIPO at ftp.wipo.int/pub/published\_pct\_sequences ö derived single exon nucleic acid probes useful for analyzing on in human cervical epithelial cells. encoded by probe for measuring cervical gene expression. microarray, gene expression, cervical epithelial cell; Gaps ; 2.8%; Score 8; DB 4; Length 55; 100.0%; Pred. No. 23; 0; Mismatches 0; Indels tive 0; Indels ID NO 25684; 487pp; English. Rank DR; dard; protein; 55 AA. Chen W, ULAR DYNAMICS INC 2000US-00632366. 2001WO-US000670 2000US-0180312P 2000US-0207456P. 2000US-00608408. 2000US-0234687P. 2000US-0236359P. 2000GB-00024263.

zel DK,

The invention relates to a single exon nucleic acid probe for meaning mene expression in a sample derived from human foetal liver single exon nucleic acid probes may be used for predicting, measu displaying gene expression in samples derived from human fetal lip present sequence is a peptide encoded by a single exon nucleic at of the invention. Note: The sequence data for this patent did not part of the printed specification, but was obtained in electronic directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences · Human; foetal liver; gene expression; single exon nucleic acid p: Peptide #10488 encoded by probe for measuring placental gene expr Human genome-derived single exon nucleic acid probes useful for gene expression in human fetal liver. 0 Claim 27; SEQ ID NO 35272; 639pp + Sequence Listing; English. 0; Indels 2.8%; Score 8; DB 4; Length 55; 100.0%; Pred. No. 23; ive 0; Mismatches 0; Indels Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder. Chen W, Rank DR; AAM36451 standard; protein; 55 AA. (MOLE-) MOLECULAR DYNAMICS INC 30-JUN-2000; 2000US-0060B40B. 03-MG-2000; 2000US-00632366 21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-0235559P. 04-OCT-2000; 2000GB-00024263. 2000US-0180312P. 2000US-0207456P. 30-JAN-2001; 2001WO-US000669 30-JAN-2001; 2001WO-US000663. 04-FEB-2000; 2000US-0180312P. WO200157272-A2. Homo sapiens. 09-AUG-2001 

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dard; peptide; 55

onservative

19 68

(first entry)

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The present invention relates to single exon nucleic acid probe measuring human gene expression in a sample derived from human ABA21535-ABA41305). The present sequence is a protein encoded by probe. The probes may be used for predicting, measuring and disigned expression in samples derived from the human heart via micing measuring gene expression, the probes are useful for predicting human heart and vascular system e.g. cardiovascular disease hypertension, cardiac arrhythmias and congenital heart disease. Sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly fine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probes which are derived from genomic sequences expressed in the bone marrow. They can be used to measure gene expression in bone samples, which may enable the improved diagnosis and treatment o such as lymphoma, leukaemia and myeloma. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bone marrow expressed probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                               2.8%; Score 8; DB 4
100.0%; Pred. No. 23;
tive 0; Mismatches
                                     Claim 15; SEQ ID NO 27753; 530pp; English.
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30-UUN-2000; 2000US-0060B408
03-AUG-2000; 2000US-033366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
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                                                                                                                                                                                                                                                                                                               Sequence 55 AA;
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                                                                                                                                                                                                                                  -derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                       invention relates to single exon nucleic acid probes (SENP:
-AA157546). The present sequence is a peptide encoded by one
The probes are useful for producing a microarray for
measuring and displaying gene expression in samples derived
lacenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded by probe for measuring heart cell gene expression.
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                                                                                                                                                                                                                                                                                       ID NO 36720; 654pp; English.
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Pred. No.
                                                                                                                                                              Chen W, Rank DR;
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100.0%; Pred
0; N
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2000US-0207456P.
2000US-00608408.
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2000US-0236359P.
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Conservative

larity

GLALA 68 GLALA 19

disorders

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0; Indels Length 55;

DB 4;

nzel DK,

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nzel DK,

ABG58050

by one of the probes of the invention

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6:25:19 2004

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Gaps

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0; Indels Length 55;

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an be used to measure gene expression in brain cell samples, ble the diagnosis and improved treatment of nervous system as Alzheimer's disease, multiple sclerosis, schizophrenia, cancers. The present sequence is a protein encoded by one of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed exon; gene expression analysis; probe; microarray; isease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                     xpressed single exon probe encoded protein SEQ ID NO: 35633.
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100.0%; Pred. No. 23;
.ive 0; Mismatches 0; Indels
DB 4;
2.8%; Score 8; DB 4;
100.0%; Pred. No. 23;
iive 0; Mismatches
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2000US-00608408.
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2000US-0236359P.
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||ALA 19
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The invention relates to a single exon nucleic acid probe (SENP) measuring human gene expression in a sample derived from human acliver, comprising one of 13109 defined nucleotide sequences giver specification (or complements/ fragments). The probe hybridises a stringency to a nucleic acid molecule expressed in the human adul (I) may be used for predicting, measuring and displaying gene ext in samples derived from human adult liver. The genes identified means the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the samples of the sam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia associated with coronary heart disease. ABG47348-ABG5930 repress liver single exon encoded peptides of the invention. Note: The st information for this patent does not appear in the printed specified but was obtained in electronic format directly from WIPO at ftp:wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                          Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for gene expression in human adult liver.
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                                                                                                                                                                         Human liver peptide, SEQ ID No 36698.
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ABG58050 standard; peptide; 55 AA.
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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03-AUG-2000;
21-SEP-2000;
27-SBP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
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Gaps

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encoded by genome-derived single exon probe SEQ ID 35300.

dlak syndrome, sarcoidosis; pulmonary haemosiderosis; stiocytosis; lymphangioleiomyomtosis; Karagener syndrome; veolar proteinosis; fibrocystic pulmonary dysplasia; ary dyskinesis; pulmonary hypertension; e exon probe; asthma; lung cancer; COPD; ILD; ructive pulmonary disease; interstitial lung disease; opathic pulmonary fibrosis; neurofibromatosis; erosis; Gaucher's disease; Niemann-Pick disease; rane disease

2001WO-US000665

2000GB-00024263. 2000US-0180312P 2000US-0207456P. 2000US-00608408. 2000US-00632366 2000US-0234687P 2000US-0236359P

JULAR DYNAMICS INC.

Chen W, Rank DR; zel DK,

iressable set of single exon nucleic acid probes, used to expression in human lung samples.

ID NO 35300; 634pp; English.

probes for measuring gene expression in a sample derived ing comprising single exon nucleic acid probes having one of a acid sequences mentioned in the specification, or their or the 12387 open reading frames derived from the 12614 included are a microarray comprising the novel set of probes set of probes which hybridise at high stringency to a nucleic at in the human lung; measuring gene expression in a sample human lung, comprising (a) contacting the array with a detectably labeled nucleic acids derived from human lung measuring the label detectably bound to each probe of the fying exons in a eukaryotic genome, comprising (a) in the predicting at least one exon from genomic sequences of it and the first of th ic acids from eukaryote lung mRNA, to a single exon probe, ment identical to the predicted exon, the probe is included mentioned microarray; assigning exons to a single exon probe, i) identical to the predicted exon, the probe is included mentioned microarray; assigning exons to a single gene, i) identifying exons from genomic sequence by the method measuring the expression of each of the exons in several raying a probe with the exon, where a common pattern of the exons in the tissues and/or cell types indicates that uld be assigned to a single gene; a peptide comprising one iences, mentioned in the specification, or encoded by the reading frames (ORF). The probes are used for gene expression if for identifying exons in a gene, particularly using human mRNA, and for the study of lung diseases such as asthma, lung lung diseases such as asthma, lung lisease (COPD), interstitial lung iic obstructive pulmonary disease (COPD), interstitial lung familial idiopathic pulmonary fibrosis, neurofibromatosis, reosis, Gaucher's disease, Niemann-Pick disease, Hermanskyme, sarcoidosis, pulmonary haemosiderosis, pulmonary i, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, drome, fibrocystic pulmonary dysplasia, primary ciliary ulmonary hypertension and hyaline membrane disease. The 1 relates to a spatially-addressable set of single exon

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0; Indels

2.8%; Score 8; DB 4;

100.0%; Pred. No. 27; ive 0; Mismatches

Conservative

Best Local Similarity Matches 8; Conserv

Query Match

Sequence 65 AA;

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Human genome-derived single exon nucleic acid probes useful for a gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human single exon nucleic acid; (SENP: see AA110068-AA128459). The present sequence is a peptide by one such probe. The SENPs are derived from human Hela cells. The be used to produce a single exon microarray, which can be use measuring human gene expression in a sample derived from human cepithelial cells. By measuring gene expression, the probes are the useful in grading and/or staging of diseases of the cervix, notate cervical cancer. Note: The sequence data for this patent did not part of the printed specification, but was obtained in electronic directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
present sequence is a peptide/protein encoded by a single exon the invention. Note: The sequence data for this patent did not for the printed specification, but was obtained in electronic for directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                      Peptide #8055 encoded by probe for measuring cervical gene expre
                                                                                                                                                                                                                                                                                                                                                                                                      Probe; human; microarray; gene expression; cervical epithelial c
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                                                                                                                                            0; Indels
                                                                                                                Length 55;
                                                                                                                            23;
                                                                                                           2.8%; Score 8; DB 5
100.0%; Pred. No. 23;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 26447; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W, Rank DR;
                                                                                                                                                                                                                                                                            AAM21621 standard; protein; 65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0207456P.
2000US-00608408.
2000US-00632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0234687P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0236359P
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                        Local Similarity 100.
                                                                                                                                                                         61 LGLGLALA 68
                                                                                                                                                                                                   12 iGLGLALA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                      cervical cancer.
                                                                                Sequence 55 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                           12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                                            AAM21621;
                                                                                                            Query Match
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Matches
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   88888
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29 9

LALA LALA (first entry)

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The present invention relates to single exon nucleic acid probes see AA131315-AA157546). The present sequence is a peptide encoded such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples d from human placenta. The probes are useful for antenatal diagnosi human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for a gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein #8889 encoded by probe for measuring heart cell gene expr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
               Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder.
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Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 38192; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB26890 standard; protein; 65 AA.
                                                                                                                                                                                           04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0204466P.
30-UJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-023468P.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                               30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FBB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
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                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 LGLGLALA 29
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LGLGLALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 65 AA;
                                                                                             WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157274-A2
                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-2002
                                                                                                                              09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                 Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB26890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB26890
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           relates to a single exon nucleic acid probe for measuring pression in a sample derived from human foetal liver. The cleic acid probes may be used for predicting, measuring and expression in samples derived from human fetal liver. The ce is a peptide encoded by a single exon nucleic acid probe on. Note: The sequence data for this patent did not form inted specification, but was obtained in electronic format WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lerived single exon nucleic acid probes useful for analyzing on in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                         liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                        encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 65;
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5. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8%; Score 8; DB 4
100.0%; Pred. No. 27;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank
                                                                                                       dard; peptide; 65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lard; protein; 65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JLAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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2000US-00608408.
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zel DK,

147/52.

(first entry)

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nservative

68 ALA 29

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                                                                                                                                                                                                                                                                                                                                                                                                                                       nan gene expression in a sample derived from human heart (see 11305). The present sequence is a protein encoded by one such cobes may be used for predicting, measuring and displaying on in samples derived from the human heart via microarrays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression, the probes are useful for predicting, jrading, staging, monitoring and prognosing diseases of the and vascular system e.g. cardiovascular disease, cardiac arrhythmias and congenital hear disease. Note: The 1 for this parent did not form part of the printed in electronic format directly from WIPO int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                         nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rrow expressed probe encoded protein SEQ ID NO: 38012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             ID NO 28660; 530pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 8; I
Pred. No.
                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dard; protein; 65 AA.
                                                                                                                                             CULAR DYNAMICS INC.
                 2000US-00632366.
2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8%; £
100.0%;
2000US-00608408
                                                                                           2000GB-00024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LALA 68
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probes which are derived from genomic sequences expressed in the bone marrow. They can be used to measure gene expression in bone samples, which may enable the improved diagnosis and treatment o such as lymphoma, leukaemia and myeloma. The present sequence is protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probes which are derived from genomic sequences expressed in the brain. They can be used to measure gene expression in brain cell which may enable the diagnosis and improved treatment of nervous diseases such as Alzheimer's disease, multiple sclerosis, schizog epilepsy and cancers. The present sequence is a protein encoded the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; mir Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in brains.
                                                Human genome-derived single exon nucleic acid probes useful for
                                                                                                                            present invention provides a number of single exon nucleic
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                                                                                            Example 4; SEQ ID NO 38012; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; SEQ ID NO 37089; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                            DB 4; Length 65; . 27;
                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                         Query Match
2.8%; Score 8; DB 4
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W, Rank DR,
                                                                gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM64984 standard; protein; 65 AA.
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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2000US-0207456P.
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                                                                                                                                                                                                                                                                                                                                                                       22 LGLGLALA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                       61 LGLGLALA 68
                WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483446/52
                                                                                                                                                                                                                                            Sequence 65 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM64984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM64984
à
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Gaps
                    ·,
                    0; Indels
    Length 65;
DB 4 27;
  2.8%; Score 8; DB 4.00.0%; Pred. No. 27; Ive 0; Mismatches
         100.0%; Pr
                   nservative
                                                 29
                                  ALA 68
            ırity
                                                 ALA
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;

0

ard; peptide; 65 AA.

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SEQ ID No 38009.
first entry)
                     ptide,
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cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; olaemia; coronary heart disease.

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001WO-US000664.
                        000US-0180312P.
                                      300US-0207456P
                                               000US-00608408
                                                            000US-00632366.
                                                                                      000US-0236359P
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LAR DYNAMICS INC.

000GB-00024263

Rank DR; Chen W, el DK,

erived single exon nucleic acid probes useful for analyzing in human adult liver.

ID NO 38009; 658pp; English.

relates to a single exon nucleic acid probe (SENP) (1) for n gene expression in a sample derived from human adult ing one of 1310 defined nucleotide sequences given in the (or complements/ fragments). The probe hybridises at high a nucleic acid molecule expressed in the human adult liver. I for predicting, measuring and displaying gene expression ived from human adult liver. The genes identified may be netic liver diseases such as cirrhosis, hyperlipidaemia and hypercholesterolaemia which is normary heart disease. ABG47348-ABG59930 represent human con encoded peptides of the invention. Note: The sequence ribis patent does not appear in the printed specification ed in electronic format directly from WIPO at

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·;
                                     Gaps
                                     .,
                                   0; Indels
2.8%; Score 8; DB 4; Length 65;
rity 100.0%; Pred. No. 27;
nservative 0; Mismatches 0; Indels
```

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Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndra pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                       Human peptide encoded by genome-derived single exon probe SEQ ID
                                                                                                                      Human; single exon probe; asthma; lung cancer; COPD; ILD;
                                                       ABG46737 standard; peptide; 65 AA.
                                                                                         (first entry)
                                                                                                                                                                                         hyaline membrane disease.
61 LGLGLALA 68
          ||||||||
LGLGLALA 29
                                                                                        19-AUG-2002
              22
                                       RESULT 41
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26-MAY-2000; 2000US-0207456P. 30-JUN-2000; 2000US-00608408. 03-AUG-2000; 2000US-00632366. 21-SEP-2000; 2000US-023468PP. 27-SEP-2000; 2000US-023559P. 04-OCT-2000; 2000GB-00024263. (MOLE-) MOLECULAR DYNAMICS INC 2000US-0180312P

30-JAN-2001; 2001WO-US000665

WO200186003-A2. Homo sapiens.

15-NOV-2001

Chen W, Rank DR; Hanzel DK, Penn SG,

WPI; 2002-114183/15.

Spatially-addressable set of single exon nucleic acid probes, usec measure gene expression in human lung samples. Spatially-addressable set

Claim 27; SEQ ID NO 36402; 634pp; English.

The invention relates to a spatially-addressable set of single exc nucleic acid probes for measuring gene expression in a sample deriform human lung comprising single exon nucleic acid probes having 12614 nucleic acid sequences mentioned in the specification, or the complements or the 1287 open reading frames derived from the 1261 complements or the 1287 open reading frames derived from the 1261 complements or the 1287 open reading frames derived from the 1261 complements or the 1287 open reading frames derived from the 1261 contact from human lung; measuring gene expression in a caid expressed in the human lung; measuring gene expression in a caid extred from human lung; comprising (a) contaction to detectably labeled nucleic acids derived from human man, in the label detectably bound to each probe of array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequence the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon in the above mentioned microarray; assigning exons to a single exon comprising (a) in the above and (b) measuring the expression of each of the exons in several common pattern of microarrays having a probe with the exon, where a common pattern o

**♣** 

the exons in the tissues and/or cell types indicates that build be assigned to a single gene, a peptide comprising one bences, mentioned in the specification, or encoded by the reading frames (ORP). The probes are used for gene expression if for identifying exons in a gene, particularly using human mRNA and for the study of lung diseases such as asthma. Ung it cobstructive pulmonary disease (COPD), interstitial lung it, familial idiopathic pulmonary fibrosis, neurofibromatosis, rosis, Gaucher's disease, Nlemann-Pick disease, Hermanskyme, sarcoidosis, pulmonary haemosiderosis, pulmonary si lymphangioleiomyomicosis, pulmonary alveolar proteinosis, ulmonary hypertension and hyaline membrane disease. The more is a peptide/protein encoded by a single exon probe of n. Note: The sequence date for this patent did not form part si specification, but was obtained in electronic format new NEPO at fib. wipo.int/pub/published\_pot\_sequences

. 0; Indels 2.8%; Score 8; DB 5; Length 65; 100.0%; Pred. No. 27; or Indels ive 0; Mismatches 0; Indels onservative 68

0

Gaps

LALA 29

dard; protein; 69 AA.

(first entry)

liagnostic protein #3714.

some mapping, gene mapping; gene therapy, forensic, int; medical imaging; diagnostic; genetic disorder.

2001WO-US008631.

2000US-00540217, 2000US-00649167.

INC.

Tang YT; Liu C,

362/73.

polynucleotide and encoded polypeptides, useful in forensics, gene mapping, identification of mutations or genetic disorders or other traits and to assess

ID NO 34082; 103pp; English.

relates to isolated polymucleotide (I) and polypeptide (II) is useful as hybridisation probes, polymerase chain primers, oligomers, and for chromosome and gene mapping, inant production of (II). The polymucleotides are also used s as expressed sequence tags for identifying expressed useful in gene therapy techniques to restore normal

activity of (II) or to treat disease states involving (II). (III)

cuseful for generating antibodies against it, detecting or quantity peptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical of sites expressing (II). (I) and (II) are useful in medical involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutation cresponsible for genetic disorders or other traits to assess biod and to produce other types of data and products dependent on DNA amino acid sequences. ABG00010-ABG30377 represent novel human diamino acid sequences of the invention. Note: The sequence data f patent did not appear in the printed specification, but was obtance the wipo.int/pub/published\_pct\_sequences Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. 0 Query Match 2.8%; Score 8; DB 4; Length 69; Best Local Similarity 100.0%; Pred. No. 29; Matches 8; Conservative 0; Mismatches 0; Indels Novel human diagnostic protein #3654. ABG03663 standard; protein; 71 AA. Tang YT; 30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167 13-FEB-2002 (first entry) 61 LGLGLALA 68 16 LGLGLALA 23 Drmanac RT, Liu C, (HYSE-) HYSEQ INC. Sequence 69 AA; WO200175067-A2. Homo sapiens. 11-OCT-2001. Query Match RESULT 43 ABG03663 8888888888888888888888 ð 

biodiversity.

The invention relates to isolated polymucleotide (I) and polypept sequences. (I) is useful as hybridisation probes, polymerase chaireaction (PCR) primers, oligomers, and for chromosome and gene ma and in recombinant production of (II). The polymucleotides are all in diagnostics as expressed sequence tags for identifying express accessivity of (II) or to treat disease states involving (II) useful for generating antibodies against it, detecting or quantit

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

WPI; 2001-639362/73.

N-PSDB; AAS67850

It issue, as molecular weight markers and as a food il and its binding partners are useful in medical imaging ssing (II). (I) and (II) are useful for treating disorders trant protein expression or biological activity. The nd polynuclectide sequences have applications in forensics, gene mapping, identification of mutations or genetic disorders or other traits to assess biodiversity other types of data and products dependent on DNA and quences. ABG80010-ABG30377 represent novel human diagnostic tubences of the invention. Note: The sequence data for this cappear in the printed specification, but was obtained in rmat directly from WIPO at

ö Gaps . 0 0; Indels 2.8%; Score 8; DB 4; Length 71; 29; 100.0%; Preu. ... onservative

TALA 68

23

lard; protein; 84 AA.

(first entry)

lium acnes immunogenic protein #22178.

sy synovitis; acne; pustulosis; hypertosis; osteomyelitis; ohthalmitis; bone; joint; central nervous system; ELISA; esion; acne vulgaris; enzyme linked immunosorbent assay; osteopathic; neuroprotectant.

ium acnes.

001WO-US012865,

000US-0199047P. 000US-0208841P.

CORP.

Bhatia A; SS, Wang SS rter D; Carter Mitcham JL, Jen S, Zhang Y, ersing DH,

74/71.

ium acnes polypeptides and nucleic acids useful for ainst and diagnosing infections, especially useful for vulgaris.

ID NO 22477; 1069pp; English.

9105-AAU68017 represent Propionibacterium acnes immunogenic The proteins and their associated DNA sequences are used in prevention and diagnosis of medical conditions caused by disorders include SAPHO syndrome (synovitis, acne, pertosis and osteomyelitis), uveitis and endophthalmitis. so involved in infections of bone, joints and the central, however it is particularly involved in the inflammatory

lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting sample with a binding agent that binds to the proteins of the invand determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antiboc specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used to diagnostic agents for determining P. acnes presence, for example, this patent did not form part of the printed specification, but we obtained in electronic format directly from WIPO at O .. 0; Indels Length 84; 2.8%; Score 8; DB 4; 100.0%; Pred. No. 34; iive 0; Mismatches ftp.wipo.int/pub/published\_pct\_sequences 8; Conservative 259 LRIRTLPW 266 34 LRIRTLPW 41 Query Match Best Local Similarity Sequence 84 AA; Best Loca Matches 88888888888888888 ठे g

RESULT 45

ABM57803

ABM57801 standard; protein; 84 AA. ABM57801;

(first entry) 20-OCT-2003

Propionibacterium acnes predicted ORF-encoded polypeptide #22477.

Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.

Propionibacterium acnes.

WO2003033515-A1.

24-APR-2003.

11-OCT-2002; 2002WO-US032727.

15-OCT-2001; 2001US-00978825.

(CORI-) CORIXA CORP.

Maisonneuve JL; Jones R, Carter Persing DH, Bhatia A, Lodes MJ, Benson DR, Zhang Y, Wang S, Jen S, Lode Barth B, Vallieve-Douglass J; Skeiky YAW, Mitcham JL, 

WPI; 2003-381789/36.

N-PSDB; ACF64544.

New Propionibacterium acnes polypeptides and polynucleotides encoc polypeptide, useful for diagnosing, preventing or treating acne vuor for stimulating an immune response specific for a P acnes prot

Example 1; SEQ ID NO 22477; 1481pp; English.

The invention relates to an isolated polynucleotide (ACF64435-ACF6 encoding a Propionibacterium acnes protein. The invention also relaply peptides encoded by the polynucleotides (ABM35624-ABM64536) an immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprise polynucleotide of the invention; antibodies against polypeptides convention; fusion proteins comprising a polypeptide of the invention method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells by via this method; a vaccine composition (comprising P. acnes polype

les, antibodies, fusion proteins, T cell populations, or anting cells that express the polypeptide); a method and kit a or determining the presence or absence of P. acres in a a method for inhibiting the development of P. acres in a P. acres polypeptides, polymucleotides, antibodies, fusion cell populations or antigen-presenting cells that express the are useful for diagnosing, preventing or treating acre for stimulating an immune response specific for a P. acres polymucleotides can also be used as probes or primers for hybridisation. The vaccine composition is useful for the of an immune response against P. acres, or for treating acre is useful for preforming a diagnostic assay. The present resents a polypeptide predicted to be encoded by an ORF (open so contained within the P. acres polymucleotides of the other sequence data for this patent did not form part of specification, but was obtained in electronic format directly ftp.wipo.int/pub/published\_pct\_sequences

Gaps .; 0; Indels DB 6; Length 84; 2.8%; Score 8; DB 6 100.0%; Pred. No. 34; ative 0; Mismatches Conservative RILPW 266

·,

idard; protein; 110 AA.

(first entry)

liagnostic protein #20250.

osome mapping; gene mapping; gene therapy; forensic; ent; medical imaging; diagnostic; genetic disorder.

2001WO-US008631.

2000US-00540217,

2000US-00649167.

INC.

362/73

Tang YT;

Liu C,

polynucleotide and encoded polypeptides, useful in forensics, gene mapping, identification of mutations or genetic disorders or other traits and to assess 446

) ID NO 50618; 103pp; English.

relates to isolated polynucleotide (I) and polypeptide (II) is useful as hybridisation probes, polymerase chain primers, oligomers, and for chromosome and gene mapping, inhant production of (II). The polynucleotides are also used as as expressed sequence tags for identifying expressed used in gene therapy techniques to restore normal

The invention relates to human polynucleotides (AAI79941-AAI93841 the encoded proteins (AA00010-AA013910) that exhibit activity electokine, cell proliferation or cell differentiation or which may production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vacc peptide therapy. The polypeptides have various cytokine-like acti e.g. stem cell growth factor activity, haematopoiesis regularing activity, tissue growth factor activity, immunomodulatory activit

Isolated nucleic acids and polypeptides, useful for preventing d: and treating e.g. leukemia, inflammation and immune disorders.

Tang YT, Liu C, Drmanac RT;

(HYSE-) HYSEQ INC.

WPI; 2001-514838/56.

N-PSDB, AAI88025.

Claim 20; SEQ ID NO 21986; 1399pp + Sequence Listing; English.

patent did not appear in the printed specification, but was obta electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences Human, cytokine, cell proliferation, cell differentiation, gene vaccine; peptide therapy, stem cell growth factor; haematopoiesi tissue growth factor; immunomodulatory, cancer; leukaemia; nervous system disorders, archritis, inflammation. activity of (II) or to treat disease states involving (II). (II) 0 2.8%; Score 8; DB 4; Length 110; 100.0%; Pred. No. 45; tive 0; Mismatches 0; Indels AA008094 standard; protein; 117 AA. Human polypeptide SEQ ID NO 21986. 26-FEB-2001; 2001WO-US004927. 28-FEB-2000; 2000US-00515126. 18-MAY-2000; 2000US-00577409. Query Match
Best Local Similarity 100... 06-NOV-2001 (first entry) 61 LGLGLALA 68 44 LGLGLALA 51 WO200164835-A2. Homo sapiens. 07-SEP-2001. AA008094; RESULT 47 AA008094 25555555555555555<del>x</del>8 ð 셤

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cancer, leukaemia, nervous system disorders, arthritis and Note: The sequence data for this patent did not form part specification, but was obtained in electronic format
in activity and may be useful in the diagnosis and/or
                                                                                                                                                        WIPO at ftp.wipo.int/pub/published_pct_sequences
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RARRARA

Gaps 0 Length 117; 0; Indels DB 4; Mismatches 2.8%; Score 8; I .00.0%; Pred. No. 100.0%; Pre nservative 68 arity ALA

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61 \_\_ \_\_ \_\_\_ \_\_\_\_ lard; protein; 184 AA.

(first entry)

anogaster polypeptide SEQ ID NO 29928.

velopmental biology; cell signalling; insecticide;

lanogaster.

:001WO-US009231.

2000US-0191637P.

₹P NY.

Myers EW; Li PWD, lams M,

160/75.

ucleic acid detection reagent for detecting 1000 or more sophila and for elucidating cell signaling and cell-cell

## ID NO 29928; 21pp + Sequence Listing; English.

18 relates to an isolated nucleic acid detection reagent ecting 1000 or more genes from Drosophila. The invention important blology and in elucidating cell signalling and tractions in higher eukaryotes for the development of therapeutics and pharmaceutical drugs. The invention mic DNA sequences (ABL16176-ABL30511), expressed DNA M10840-ABL16175) and the encoded proteins (ABB57737-18 sequence data for this patent did not form part of the ication, but was obtained in electronic format directly itp.wipo.int/pub/published\_pct\_sequences

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0
                       Gaps
                       ·.
  DB 4; Length 184;
                      0; Indels
             73;
2.8%; Score 8; DB 4
100.0%; Pred. No. 73;
ive 0; Mismatches
                     nservative
                                        VSL 79
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Streptococcus; GAS; GBS; group B streptococcus; Streptococcus aga group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                       Masignani V, Margarit Y RosI, Grandi G,
                                                                                    Streptococcus polypeptide SEQ ID NO 5258.
                                      ABP28041 standard; protein; 190 AA.
                                                                                                                                                                                                27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                 29-OCT-2001; 2001WO-GB004789.
                                                                     (first entry)
                                                                                                                                                                                                                                        (GENO-) INST GENOMIC RES.
                                                                                                                                    Streptococcus agalactiae.
                                                                                                                                                                                                                                                                               WPI; 2002-352536/38.
                                                                                                                                                                                                                                (CHIR-) CHIRON SPA.
LLLAVVSL
                                                                                                                                                                                                                                                                                        N-PSDB; ABN68672.
                                                                                                                                                  WO200234771-A2.
                                                                    02-JUL-2002
                                                                                                                                                                  02-MAY-2002.
                                                                                                                                                                                                                                                               Tettelin H;
                                                                                                                                                                                                                                                       Telford J,
                                                     ABP28041;
16
                               4BP2804
```

New Streptococcus protein for the treatment or prevention of infe disease caused by Streptococcus bacteria, such as meningitis, and detecting a compound that binds to the protein.

ΰ

Claim 1; Page 3689; 4525pp; English.

streptococcus pyogenes), comprising one of 5403 sequences (S1), the process pyogenes), comprising one of 5403 sequences (S1), the specification. The proteins have antibacterial and antibinflam activity. (I), nucleic acides encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicament the teatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogen (I) are used (I) are used to detect Streptococcus in a biological sample. (I) are used to detect Streptococcus in (I). A composition comprising (I) or a nucleic acid encoding (I), used as a vaccine or disquostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may used in gene therapy. Antibodies to (I) are used for affinity characterspaphy, immunoassays, and distinguishing/identifying The invention relates to a protein (ABP25413-ABP30895) from group Streptococcus proteins

Sequence 190 AA;

ĕ ; Length 190; 0; Indels 2.8%; Score 8; DB 5; 100.0%; Pred. No. 75; ive 0; Mismatches Best Local Similarity 100. Matches 8; Conservative Query Match

258 SLRIRTLP 265 50 SLRIRTLP

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57

idard; protein; 198 AA.

(first entry)

oded protein SEQ ID NO: 1209.

pig; cow; fruit fly; yeast; hamster; macaque; horse; y; dog; sea urchin; expressed sequence tag; EST; forensic test; gene mapping; genetic disorder; biodiversity; nutrition

2001WO-US002687.

2000US-00617746. 2000US-00491404. 2000US-00631451.

2000US-00663870

Chen R, Asundi V; ou P, Qian XB, Wang Z, Zhang J, Werhman T; Zhou P, lac RA, ນີ

164/51

peptide for treatment of diseases, diagnostics, raising id research use.

e 873; 1275pp; English.

nivention provides the protein and coding sequences of novel a variety of organisms, including human, dog, car, horse, neter, monkey, macaque, yeast, bacteria, fruit fly, sea mato. These were derived from expressed sequence tags (ESTs) mism of interest. They can be used in diagnostics, ince mapping, identification of mutations, to assess and for nutritional purposes. The present sequence is a invention

. 0 DB 4; Length 198; . 78; 0; Indels 2.8%; Score 8; DB 4 100.0%; Pred. No. 78; iive 0; Mismatches onservative

ö

Gaps

PLAL 61

6

dard; protein; 222 AA.

(first entry)

1 antigen HPAMG11, SEQ ID NO:2806.

un antigen; ovary; ovarian; breast; cancer; tumour; ir; breast cancer; tumour; reproductive system disorder;

infertility; pregnancy disorder, anovulation; polycystic ovary s PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; respiratory system disorder; disorder; another disorder; urinary system disorder; drug screeni ane trapp; chromosome mapping; forenaic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotect antiinflammatory; gynaecological; reproductive.

Homo sapiens.

WO200200677-Al.

03-JAN-2002

07-JUN-2001; 2001WO-US018569.

07-JUN-2000; 2000US-0209467P.

(HUMA-) HUMAN GENOME SCI INC.

Birse CE, Rosen CA;

2002-147878/19.

N-PSDB; ABQ54751

Isolated nucleic acid molecules encoding novel ovarian polypeptic useful in the prevention, treatment and diagnosis of cancer (e.g cancer), immune disorders, cardiovascular disorders and neurolog: diseases

Claim 11; SEQ ID NO 2806; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP4. ABP4328) and to CDNAs encoding them (ABD54131-ABQ56305), and all encompasses polypeptides 90% identical and polynucleotides 95% is to the sequences of the invention. The invention additionally recrecombinant vectors and host cells comprising human ovarian antigens. To polynucleotides, antibodies against human ovarian antigens, and of ovarian antigen polynucleotides and polypeptides in diagnosing treating, prognosing or preventing varian soncer and breast can disorders. Such conditions include ovarian cancer and breast can metastatic tumours of ovarian or breast origin, reproductive syst disorders (e.g., infertility, disorders origin, reproductive syst disorders, infections (e.g., champwida, HIV, toxoplasmosis, and shock syndrome, ovarian cancer and dynamoral, encompanies, infections (e.g., champwida, HIV, toxoplasmosis, and shock syndrome), inflammatory conditions (e.g., mastitis, ophor: vaginitis), immune disorders (e.g., anaemia), cardiovascular disorder respiratory disorders neurological disorders, gastrointestinal cand urinary system disorders, ovarian antigen polypeptides and polymucleotides may also be used in screening for compounds which further he used for gene a carrivity. The polymucleotific than the nead to a carrivity. The polymucleotic further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodi useful in disease diagnosis, drug targeting and phenotyping. The sequence represents a human ovarian antigen of the invention. N sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly f at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 222 AA;

. Length 222; 0; Indels 2.8%; Score 8; DB 5; 100.0%; Pred. No. 87; tive 0; Mismatches Conservative Query Match Best Local Similarity Local 8; Conserve

g

à

dard; protein; 286 AA.

(first entry)

iagnostic protein #16270.

some mapping; gene mapping; gene therapy; forensic; nt; medical imaging; diagnostic; genetic disorder.

2001WO-US008631.

2000US-00540217. 2000US-00649167,

Tang YT; iu C,

362/73

##GBAAKAWA&&&XW#WACOP#OREOXQEOXAKOKKKWWHHHHHHHHHHHHHHHHHHHHHH

oolynucleotide and encoded polypeptides, useful in forensics, gene mapping, identification of mutations or genetic disorders or other traits and to assess

ID NO 46638; 103pp; English.

ub/published pct sequences

Gaps . 0 DB 4; Length 286; 0; Indels 2.8%; Score 8; DB 4 (rity 100.0%; Pred. No. 1.1 )nBervative 0; Mismatches

GSS 76

GSS 258

ABG01186 standard; protein; 307 AA. ABG01186

ABG01186; 

13-FEB-2002 (first entry)

Novel human diagnostic protein #1177.

Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic; genetic disorder. Human;

Homo sapiens.

WO200175067-A2.

11-0CT-2001.

30-MAR-2001; 2001WO-US008631.

31-MAR-2000; 2030US-00540217. 23-AUG-2000; 2030US-00649167.

(HYSE-) HYSEQ INC.

Tang YT; Drmanac RT, Liu C,

WPI; 2001-639362/73. N-PSDB; AAS65373 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 31545; 103pp; English.

The invention relates to isolated polymucleotide (I) and polypept sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene ma and in recombinant production of (II). The polymucleotides are all in diagnostics as expressed sequence tags for identifying express; genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) useful for generating antibodies against it, detecting or quantit polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical in a supplement. (II) and (II) are useful for treating di involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in polypeptide and polymucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodical and to produce other types of data and products dependent on DNA amino acid sequences. ABG00010-ABG30377 represent novel human dias amino acid sequences. ABG00010-ABG30377 represent novel human dias amino acid sequences. amino acid sequences of the invention. Note: The sequence data patent did not appear in the printed specification, but was obtain electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 307 AA;

ö ; 0 2.8%; Score 8; DB 4; Length 307; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels Ouery Match Query Match Best Local Similarity 100.00 Best Local Similarity 100.00

77 VSLGSRAS 84 ਨੇ

0

3 VSLGSRAS 10

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RESULT 54 ADB79952 ID ADB7

ADB79952 standard; protein; 342 AA.

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BB 1 progression enhanced protein, SEQ ID 192.
                                                                     ain; streptozocin-induced diabetes; rat.
                                                                                                                                                                                                                                                                                                                                            Pinnock RD;
                                                                                                                                                                                                                                                                                                                                            Lee K,
                                                                                                                                                                                                                2002EP-00255249.
                                                                                                                                                                                                                                                    2001GB-00018354
                                                                                                                                                                                                                                                                      2002GB-00002910
(first entry)

    Dixon AK,

                                                                                                                                                                                                                                                                                                        3R LAMBERT CO.
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5407/38.

ed gene sequences and encoded polypeptides that are in the spinal cord in response to streptozocin-induced screening compounds for the treatment of pain, or for

invention relates to nucleotide sequences which are useful in 3 of compounds for the treatment of pain, or for the pain. The nucleotide sequences are up-regulated in the in response to streetozocin-induced diabetes. The present used to illustrate the invention. 326-327; 334pp; English.

2.8%; Score 8; DB 7; Length 342; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels arity 100. GLAL 67

GLAL 317

8

dard; protein; 370 AA.

mapping; gene mapping; gene therapy; forensic; nedical imaging; diagnostic; genetic disorder. liagnostic protein #13382. (first entry) Some

2001WO-US008631. ć,

2000US-00540217.

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The invention relates to isolated polynucleotide (I) and polypep sequences. (I) is useful as hybridisation probes, polymerase cha reaction (PCR) primers, oligomers, and for chromosome and gene m and in recombinant production of (II). The polynucleotides are a in diagnostics as expressed sequence tags for identifying expressing enes. (I) is useful in gene therapy techniques to restore norma activity of (II) or to treat disease states involving (II) ? (II) useful for generating antibodies against it, detecting or quantity of speptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical. (I) such that it is binding partners are useful for treating of involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutation and or many of any areas biody and a contert traits to a seese biody and a contert traits to a seese biody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and to produce other types of data and products dependent on DNA amino acid sequences. ABG00110-ABG30377 represent novel human di amino acid sequences of the invention. Note: The sequence data f patent did not appear in the printed specification, but was obta electronic format directly from WIPO at ftp. Wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 43750; 103pp; English.
                                                                                            Tang YT;
23-AUG-2000; 2000US-00649167
                                                                                                                                        WPI; 2001-639362/73.
                                                                                            Drmanac RT, Liu C,
                                          (HYSE-) HYSEQ INC.
                                                                                                                                                               N-PSDB; AAS77578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 370 AA;
                                                                                                                                                                                                                                                                               biodiversity.
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2.8%; Score 8; DB 4; Length 370; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels 8; Conservative Sest Local Similarity Query Match Matches

63 LGLALACL 70

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Gaps

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ABG05012 standard; protein; 370 AA. (first entry) 28 LGLALACL 35 13-FEB-2002 ABG05012; RESULT 56 ABG05012 d

Human; chromoscme mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. Novel human diagnostic protein #5003.

30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. 11-OCT-2001 

WO200175067-A2.

Homo sapiens.

medical

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Tang YT;
           iu C,
ING.
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362/73.

polynucleotide and encoded polypeptides, useful in forensics, gene mapping, identification of mutations or genetic disorders or other traits and to assess

ID NO 35371; 103pp; English.

primers, to ligomers, and for chromosome and gene mapping, in useful as hybridisation probes, polymerase chain primers, oligomers, and for chromosome and gene mapping, inant production of (II). The polymucleotides are also used useful in gene therapy techniques to restore normal illow to treat disease states involving (II). (II) is levating antibodies against it, detecting or quantitating a trisue, as molecular weight markers and as a food Itisue, as molecular weight markers and as a food Itisue, as molecular weight markers and as a food Itisue, as molecular weight markers and as a food Itisue, as molecular weight markers and as a food Itisue, as molecular weight markers and as a food Itisue, as molecular weight markers and set a foot in session (II). (II) and (II) are useful in medical imaging issing (II). (I) and (II) are useful for treating disorders rant protein expression or biological activity. The dolynucleotide sequences have applications in corensics, gene mapping, identification of mutations of genetic disorders or other traits to assess biodiversity other types of data and products dependent on DNA and pences. ABG00010-ABG30377 represent novel human diagnostic (uences of the invention. Note: The sequence data for this appear in the printed specification, but was obtained in mat directly from WIPO at relates to isolated polymucleotide (I) and polypeptide (II)

Gaps .. 2.8%; Score 8; DB 4; Length 370; rity 100.0%; Pred. No. 1.46+02; nservative 0; Mismatches 0; Indels

ACL 70

ard; protein; 370 AA.

first entry)

agnostic protein #18106.

e mapping; gene mapping; gene therapy; forensic; medical imaging; diagnostic; genetic disorder.

001WO-US008631

000US-00540217. 000US-00649167.

Tang YT; Drmanac RT, Liu C,

WPI; 2001-639362/73. N-PSDB; AAS82302 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 48474; 103pp; English.

The invention relates to isolated polymuclectide (I) and polypept sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene ma and in recombinant production of (II). The polymuclectides are all in diagnostics as expressed sequence tags for identifying express genes. (I) is useful in gene therapy techniques to restore normal extivity of (II) or to treat disease states involving (II). (II) useful for generating antibodies against it, detecting or quantity useful for generating antibodies against it, detecting or quantity useful for generating antibodies against it, detecting or quantity useful for generating antibodies against it, detecting or quantity of supplement. (II) and its binding partners are useful in medical of supplement. (II) and its binding partners are useful in medical in nyphypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodicand to produce other types of date and products dependent on DNA amino acid sequences. Abs(00010,-Abs(3037) represent novel human diagnetent did not appear in the printed specification, but was obtain electronic format directly from WIPO at the electronic format directly from WIPO at the electronic format directly from WIPO at the electronic format directly sequences

Sequence 370 AA;

; 0 2.8%; Score 8; DB 4; Length 370; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 8; Conservative Query Match

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RESULT 58

ABU36537

(first entry) 19-JUN-2003

Protein encoded by Prokaryotic essential gene #22064.

WO200277183-A2.

03-OCT-2002.

21-MAR-2002; 2002WO-US009107

06-SEP-2001; 2001US-00948993 25-0CT-2001; 2001US-0342923P 08-FEB-2002; 2002US-00072851 06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

<u>%%#%#@@%&&&&%%%%</u>

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ABU36537 standard; protein; 372 AA. ABU36537;

Antisense; prokaryotic essential gene; cell proliferation; drug de

Mycobacterium tuberculosis.

21-MAR-2001; 2001US-00815242.

Zyskind JW; Xu HH; Haselbeck R, Ohlsen KL, Yamamoto R, Forsyth RA, Malone C, Carr GJ, ıdio C, vick JD,

926/02

nucleic acids, useful for identifying proteins or screening is nucleic acids required for cellular proliferation to idate molecules for rational drug discovery programs.

ID NO 64461; 1766pp; English.

sense sequences given in the specification where expression c acid inhibits proliferation of a cell. Also included are comprising a promoter operably linked to the nucleic acid lypeptide whose expression is inhibited by the antisense (2) a host cell containing the vector; (3) an isolated of it is inhibited by the antisense (5) a host cell containing the vector; (3) an isolated of its inhibited by the antibody capable of specifically binding de,(5) producing the polypeptide; (6) inhibiting cellular or the activity of a gene in an operon required for it or the activity of a gene in an operon required for it or that has an activity against a biological pathway proliferation, or that inhibits cellular proliferation; (8) igene required for cellular proliferation of the proliferation-required gene or its gene product lies which the test compound that inhibits proliferation of an itivity; (11) a culture comprising strains in which the gene exexpressed or underexpressed; (12) determining the extent of the strains is present in a culture or collection of 13) identifying the target of a compound that inhibits the carea proliferation of the strains is present in a culture or collection of 13) identifying the target of a compound that inhibits the careant of an organism. The antisense nucleic acids are useful for proliferation of the careant or for manisher modeling and proliferational confideration of the careant or collections or screening for homologous nucleic acids required proliferation of the careant or confideration of the careant or collection of the careant Y programs, or for screening homologous nucleic acids proliferation in cells other than S. aureus, S. typhimurium, or P. aeruginosa. The present sequence is encoded by one of okaryotic essential genes. Note: The sequence data for this form part of the printed specification, but was obtained pub/published\_pct\_sequences. 1 relates to an isolated nucleic acid comprising any one of

Gaps . 2.8%; Score 8; DB 6; Length 372; 100.0%; Pred. No. 1.4e+02; ive 0; Mismatches 0; Indels arity 100.

68 LALA

LALA 103

dard; protein; 424 AA.

(first entry)

lagnostic protein #15604.

some mapping; gene mapping; gene therapy; forensic; nt; medical imaging; diagnostic; genetic disorder.

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The invention relates to isolated polynucleotide (I) and polypept sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCN) primers, oligomers, and for chromosome and gene me and in recombinant production of (II). The polynucleotides are a in diagnostics as expressed sequence tags for identifying expressing the state of the polymerase of a critical and seaful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) useful for generating antibodies against it, detecting or quantity of sequence in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical: of sites expressing (II). (I) and (II) are useful for treating dinvolving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits to assess biod: and to produce other types of data and products dependent on DNA amino acid sequences. Agalon10-ABG30377 represent novel human disamino acid sequences of the invention. Note: The sequence data for patent did not appear in the printed appearing appearing the mutPO at the electronic format directly from MPO at the electronic format directly from WPO at the electronic format directly from WPO at the fire and products dependent on DNA electronic format directly from WPO at the fire appeared and products dependent on the electronic format directly from WPO at the fire and products dependent on the electronic format directly from WPO at the fire and products dependent on the electronic format directly from WPO at the fire and products dependent on the electronic format directly from WPO at the fire and products dependent on the electronic format directly from WPO at the fire and products dependent on the electronic format directly from WPO at the fire and products dependent on the electronic format dependent on the fire New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation: responsible for genetic disorders or other traits and to assess biodiversity. Claim 20; SEQ ID NO 45972; 103pp; English. 30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. Tang YT; Drmanac RT, Liu C, WPI; 2001-639362/73. (HYSE-) HYSEQ INC N-PSDB; AAS79800. Sequence 424 AA; 

Length 424; 0; Indels Query Match
2.8%; Score 8; DB 4; Ler
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 0; Mismatches 0;

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6 g

0

RESULT 60 AAM23752

AAM23752 standard; protein; 430 AA.

AAM23752; 

12-OCT-2001 (first entry)

Human EST encoded protein SEQ ID NO: 1277.

Human, sheep, pig, cow, fruit fly, yeast, hamster, macaque, horse tomato, monkey, dog, sea urchin, expressed sequence tag, EST, diagnostics, forensic test, gene mapping, genetic disorder, biodi gene therapy; nutrition.

Homo sapiens

WO200154477-A2

02-AUG-2001.

164/51. C, Zh ac RA,

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This invention, in the area of plant biotechnology, relates to not polymerical comprising a nucleotide sequence encoding a prote is involved in or associated with the synthesis, metabolism or degradation of carbohydrates in the plant grain and the expressic which is up-regulated during grain filling. The plant is selected corn, towato, banana, canola, cotton, peanue, sorghum, tobacco, sugarbeet, wheat, and rice. The invention may be useful for the improvement of protein, oil, starch, fibre and moisture content cereal grains. In addition, carbohydrate levels may be modified to desirable level using the present invention. The present sequence of a rice protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the fib. wipo.int/pub/publishedpot_sequences.
                                                                       New plant genes encoding polypeptides having an activity involved associated with the synthesis, metabolism or degradation of carbotin the plant grain useful in generating plants having improved nutritional properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Obtaining plants having enhanced growth and/or fruit yield and/or flowering rate, specifically C3 plants grown under limiting condit useful in plant molecular biology and commercial plant breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method of obtaining plants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant growth; commercial yield; plant breeding; fruit yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7; Length 431;
0. 1.6e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mittler R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.8%; Score 8; DB 7
100.0%; Pred. No. 1.6
tive 0; Mismatches
                                                                                                                                                                   Claim 34; SEQ ID NO 508; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaplan A, Lieman-Hurwitz J, Schatz D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechococcus sp. Synwh0268 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC64562 standard; protein; 431 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002; 2002WO-IL000250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-APR-2003; 2003US-00410432,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechococcus sp.; WH 8102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 ORRRGRRG 379
                   WPI; 2003-229341/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 QRRRGRRG 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                     N-PSDB; ADC08202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003192076-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC64562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC64562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                      a variety of organisms, including human, dog, cat, horse, ster, monkey, macaque, yeast, bacteria, fruit fly, sea nato. These were derived from expressed sequence tags (ESTs) ism of interest. They can be used in diagnostics, he mapping, identification of mutations, to assess and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ology; carbohydrate synthesis; carbohydrate metabolism; legradation; carbohydrate; plant grain; grain filling; corn; canola; cotton; peanut; sorghum; tobacco; sugarbeet; rotein; oil; starch; fibre; molsture content; cereal grain;
                                                                                                                                                                                                                                                                                                                                                                                        avention provides the protein and coding sequences of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                       peptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                     Chen R, Asundi V;
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Ricke D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 430; . 1.6e+02;
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Kreps J, Provart N,
                                                                                                                                                                               Zhou P, Qian XB, Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.8%; Score B; DB 4
100.0%; Pred. No. 1.6
cive 0; Mismatches

    920; 1275pp; English.

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         2001WO-US002687.
                                           2000US-00491404.
2000US-00617746.
                                                                                 2000US-00631451.
2000US-00663870.
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                                                                                                                                                                                                                                                                                                                 research use.
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Katagiri F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
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PLAL 61 9

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Rachmilevitch

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wth and/or commercial yield under growth limiting conditions. omprises obtaining a population of plants transformed to lypeptide having at least 60% sequence identity to any of 8 d sequences, growing the plants and selecting plants he polypeptide. The methods and compositions of the present e useful in commercial plant breeding, particularly for lants having enhanced growth and/or fruit yield and/or te. The present sequence represents Synechococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                          otein.
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Ä,

. 0 Gaps · 0 2.8%; Score 8; DB 7; Length 431; 100.0%; Pred. No. 1.66+02; ive 0; Mismatches 0; Indels Conservative larity

74

dirir 371

ndard; protein; 454 AA.

elanogaster polypeptide SEQ ID NO 516.

developmental biology; cell signalling; insecticide;

elanogaster.

2001WO-US009231.

2000US-0191637P 2000US-00614150

RP NY

Myers EW; Li PWD, **з**датв М,

860/75.

nucleic acid detection reagent for detecting 1000 or more cosophila and for elucidating cell signaling and cell-cell

EQ ID NO 516; 21pp + Sequence Listing; English.

irelates to an isolated nucleic acid detection reagent stecting 1000 or more genes from Drosophila. The invention is reloopmental biology and in elucidating cell signalling and eractions in higher eukaryotes for the development of therapeutics and pharmaceutical drugs. The invention nomic DNA sequences (ABL16176-ABL30511), expressed DNA 1001840-ABL16175) and the encoded proteins (ABB57737-ie sequence data for this patent did not form part of the fication, but was obtained in electronic format directly ftp.wipo.int/pub/published\_pct\_sequences

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DB 4; Length 454;
2.8%; Score 8; D
100.0%; Pred. No.
            arity
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Cytostatic, Anti-inflammatory, Osteopathic, Neuroprotective, Noc
Gene Therapy, human, secretory protein, membrane proteins, cance
inflammatory disease, osteoporosis, neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel human secretory or membra proteins (ADA54072-ADA55710) and their coding sequences (ADA5243. ADA54071). The coding sequences are useful in the gene therapy o diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides encoding full-length polypeptides, e.g. secr and/or membrane proteins, useful for developing medicines for diwhich the gene is involved, or as target molecules for gene ther.
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.8%; Score 8; DB 6; Length 472;
100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0; Indels
     ..
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; SEQ ID NO 2278; 205pp; English.
                                                                                                                     ADA54710 standard; protein; 472 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG20260 standard; protein; 586 AA.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-2001; 2001JP-00328381.
24-JAN-2002; 2002US-0350435P.
                                                                                                                                                                                                                                                                                                                                                               21-MAR-2002; 2002EP-00006586.
                                                                                                                                                                                                   Human protein, SEQ ID 2278.
                                                                                                                                                                          (first entry)
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J, Isono Y,
Yoshikawa T,
                                                     170 LVPLALGL 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-395539/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 ALGLGLAL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 8; Corserv
                          56 LVPLALGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADA53071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 472 AA;
                                                                                                                                                                                                                                                                                                         EP1293569-A2.
                                                                                                                                                                          20-NOV-2003
                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                     19-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamamoto J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isogai T,
                                                                                                                                                 ADA54710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG20260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seki N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Matches
                                                                                            RESULT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 65
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                                                                                                          ADA5471
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us-09-245-198a-4.oligo.rag

iagnostic protein #20251.

some mapping; gene mapping; gene therapy; forensic, nt; medical imaging; diagnostic; genetic disorder.

2001WO-US008631.

2000US-00540217. 2000US-00649167.

Tang YT; tiu C,

362/73.

polynucleotide and encoded polypeptides, useful in forensics, gene mapping, identification of mutations or genetic disorders or other traits and to assess

ID NO 50619; 103pp; English.

ls useful as hybridisation probes, polymerase chain primates, oligomers, and for chromosome and gene mapping, inant production of (II). The polymucleotides are also used sax expressed sequence tags for identifying expressed useful in gene therapy techniques to restore normal II) or to treat disease states involving (II). (II) is nerating antibodies against it, detecting or quantitating a tissue, as molecular weight markers and as a food II) and its binding partners are useful in medical imaging sssing (II). (I) and (II) are useful for treating disorders rant protein expression or biological activity. The olymucleotide sequences have applications in forensics, gene mapping, identification of mutations of genetic disorders or other traits to assess biodiversity of the invention. Note: The sequence data for this impublished pot\_sequences. relates to isolated polynucleotide (I) and polypeptide (II)

Gaps .. 2.8%; Score 8; DB 4; Length 586; 100.0%; Pred. No. 2.2e+02; 0; Indels 100.0%; Preα. ... '... 0; Mismatches nservative arity

21

68

lard; protein; 586 AA.

(first entry)

P36269, SEQ ID NO 11960.

Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

Homo sapiens.

WO2003016475-A2.

27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-033347P.

(GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG

Costigan M; Befort K, D'urso D, Woolf C,

WPI; 2003-268312/26. GENBANK; P36269. New composition comprising two or more isolated polypeptides, use preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolor human polynucleotides or a polynucleotide which represents a far derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain kit to perform the method, an array, a method for identifying an that increases or decreases the expression of the polynucleotide subjected to pain, a method for identifying a compound which regulate expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first argument of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound or small composit method for identifying a compound or small composit method for identifying a compound or small molecule that regulate compound to a polymucleotide or more of the polypeptides or their antibodies. The polymucleotide or the compound a pharmaceutical composition comprising the one or more pain and a pharmaceutical composition comprising the one or more modulates its activity is useful for preparing a medicament for pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gether any complex of the specification) which is differentially expressed during pain. The sequence data for this patent did not form part of the prince from in the prince of the pri ftp.wipo.int/pub/published\_pct\_sequences. 

Sequence 586 AA;

ò

·: 0 Length 586; 0; Indels Ouery Match
2.8%; Score 8; DB 7; Len
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 8; Conservative 0; Mismatches 0;

Ü

ઠે g RESULT 67 ADE62980

ADE62980 standard; protein; 586 AA.

SX H

ADE62980;

(first entry)

n P36269, SEQ ID NO 8914.

neuronal tissue; gene therapy; ital nerve injury; chronic constriction injury; CCI; injury; SNI; Chung. intal

-A2.

2002WO-US025765.

2001US-0346382P. 2001US-0312147P. 2001US-0333347P.

HOSPITAL CORP.

Costigan M; Befort K, urso D,

8312/26.

ion comprising two or more isolated polypeptides, useful for medicament for treating pain in an animal.

=; 1017pp; English.

n discloses a composition comprising two or more isolated rat functionides or a polynucleotide which represents a fragment, rallelic variation of the nucleic acid sequence. Also a vector comprising the nucleic acid sequence. Also ellawer the method for identifying a nucleotide sequence ferentially regulated in an animal subjected to pain and arm the method, an array, a method for identifying a nucleotide sequence sentially expressed in neuronal tissue of a first animal search and for identifying a compound which regulates on of a polynucleotide sequence which is differentially an animal subjected to pain, a method for identifying a compound which regulates the arm animal subjected to pain, a method for identifying a compound of a polynucleotide sequence which is differentially an animal of one or more of the left, a method for producing a pharmaceutical composition, a lentifying a compound useful in treating armaceutical composition comprising the one or more or their antibodies. The polynucleotide or the compound that is activity is useful for preparing, chronic constriction and spared nerve injury (SNI)) in an animal (e.g. gene should be a presented is a human protein (shown in Table 2 of ithion) which is differentially expressed during pain. Note: data for this patent did not form part of the printed 'bub/bublished oct sequence formed and experience of the printed bub/bublished oct sequence formed and sparent did not form part of the printed 'bub/bublished oct sequence formed and parameters of the printed bub/bublished oct sequence formed and sparent did not form part of the printed 'bub/bublished oct sequence formed and sparent did not form part of the printed 'bub/bublished oct sequence formed and segmented in electronic form directly from Note: pub/published\_pct\_sequences.

Gaps ., 2.8%; Score 8; DB 7; Length 586; 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0; Indels Conservative LALA 68

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Human, vaccination; gene therapy, nutritional supplement, stem cell proliferation; haematopoiesis, nerve tissue regenerati immune suppression; immune stimulation; anti-inflammatory; leuk
                                                                                                                                                                                                                                                         Nucleic acids encoding a range of human polypeptides, useful in vaccination, testing and therapy.
               AAU32148 standard; protein; 592 AA.
                                                               Novel human secreted protein #2639.
                                                                                                                                                                 .6-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                                         Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
                                               (first entry)
                                                                                                                                                                                                                                         WPI; 2001-611725/70.
                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                WO200179449-A2.
                                                                                                                 Homo sapiens.
                                               18-DEC-2001
                                                                                                                                                25-OCT-2001.
                                AAU32148;
RESULT 68
        AAU32148
```

The invention relates to novel human secreted polypeptides. The Claim 20; Page 562-563; 765pp; English.

polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease assoc with altered levels of polypeptide. The polypeptides are also us identifying agents (agonists and antagonists) that bind to them. Expressing the proteins are useful for identifying a therapeutic of or use in treatment of a pathology related to aberrant expressing physiological interactions of the polypeptide vectors comprising nucleic acids encoding the polypeptides and cells genetically ento express them are also useful for producing the proteins. The are nutritional supplements. They may be used to increase stem control or regulate haematopoiesis, and in bone, cartiage and or nerve tissue growth or regeneration; immune suppression a stimulation, as anti-inflammatory agents; and in treatment of le AAU29510-AAU3304 represent the amino acid sequences of novel hursely agentes of secreted proteins of the invention

Sequence 592 AA;

. 0 2.8%; Score 8; DB 4; Length 592; 100.0%; Pred. No. 2.2e+02; ive 0; Mismatches 0; Indels Conservative Local Similarity Query Match Best Loca Matches

RESULT 69 ABG03722 #####

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ABG03722 standard; protein; 603 AA.

ABG03722;

(first entry) 13-FEB-2002

|||| |:LALA 21

agnostic protein #3713.

some mapping; gene mapping; gene therapy; forensic; tt; medical imaging; diagnostic; genetic disorder.

:001WO-US008631.

00000S-00540217.

INC.

Tang YT; iu C,

62/73.

olynucleotide and encoded polypeptides, useful in orensics, gene mapping, identification of mutations or genetic disorders or other traits and to assess

ID NO 34081; 103pp; English.

relates to isolated polynucleotide (I) and polypeptide (II) is useful as hybridisation probes, polymerase chain primers, oligomers, and for chromosome and gene mapping, nant production of (II). The polynucleotides are also used as expressed sequence tags for identifying expressed useful in gene therapy techniques to restore normal I) or to treat disease states involving (II). (II) is erating antibodies against it, detecting or quantitating a tissue, as molecular weight markers and as a food I) and its binding partners are useful in medical imaging ssing (II). (I) and (II) are useful for treating disorders rant protein expression or biological activity. The d polynucleotide sequences have applications in orensics, gene mapping, identification of mutations r genetic disorders or other traits to assess biodiversity uences. ABG00010-ABG30377 represent novel human diagnostic sences of the invention. Note: The sequence data for this appear in the printed specification, but was obtained in ub/published\_pct\_sequences other types of data and products dependent on DNA and

0; Gaps 2.8%; Score 8; DB 4; Length 603; 00.0%; Pred. No. 2.38+02; ve 0; Mismatches 0; Indels 2.5., 100.0%; Pic nservative

0;

ALA 68

447

ard; protein; 617 AA.

first entry)

nodification and maintenance molecule (PMMM)-44.

protein modification and maintenance molecule; PMPMY,

protein modification; protein maintenance; protein function;

protein modification; protein maintenance; protein function;

protein conformation; protein stabilisation; protein degradation;

phosphatase; protease inhibitor; isomerase; transferase;

molecular chaperone; anti-HIV; antiallergic; antiniflammatory;

molecular chaperone; anti-HIV; antiallergic; antiniflammatory;

antiansemic; antiparkinsonian; nootropic; antionvulsant;

antiateriosclerocic; antiathation; immunosuppressive; antithyro

cytostatic; hepatotropic; dermatological; antidiabetic; nephrotro

cytostatic; hepatotropic; dermatological; antidiabetic; nephrotro

motigout; thyromimelic; neuroprotective; osteopathic; ophthalmo

mutiparasitic; antihelminitc; antibacterial; virucide; protozoacide

muticheumatic; haemostatic; antibacterial; virucide; protozoacide

muticheumatic; haemostatic; antibacterial; virucide; protozoacide

muticheumatic; haemostatic; antibacterial; primary thromobocytopae

cancer; developmental disorder; anaemia; mental retardation;

neurological disorder; Alzheimer's disease; parkinson's disease;

epilepsy; autoimmune disorder; inflammatory disorder; AIDS; aller

asthma; autoimmune disorder; inflammatory disorder; AIDS; aller

asthma; autoimmune disorder; inflammatory disorder; AIDS; aller

asthma; osteoporosis; pancreatitis; Sjogren's syndrome;

microbial infection; human.

Homo sapiens.

WO2003063688-A2.

07-AUG-2003.

23-JAN-2003; 2003WO-US002500.

25-JAN-2002; 2002US-0351928P.

25-FEB-2002; 2002US-0359903P. 21-MAR-2002; 2002US-0366837P.

Chawla NK, Sprague WW, Lee SY,
Khare R, Emerling BW, Kable
e S, Swarnakar A, Baughn MR;
kins P, Jiang X, Jackson AA;
Ho A, Zheng W, Ison CH, Marc
Y, Honchell CD, Becha SD; (INCY-) INCYTE GENUMIAL CHAWLE .....

Hafalia AJA, Li JX, Gorvad AE, Chawle R, Emerim.

I Chang H, Elliott VS, Ramkumar J, Khare R, Emerim.

I Tang YT, Yue H, Gietzen KJ, Lee S, Swarnaka A, Baud YT, Yue H, Gietzen KJ, Hawkins PR, Jiang K, Jac..., Ten AD, Trill JD, Blake JJ, Ho A, Zheng W, Ison Trill JD, Blake JJ, Ho A, Zheng W, Ison Chan BA, Xu Y, Honchell CD, Bec 

WPI; 2003-636761/60. N-PSDB; ADE79064.

New human protein modification and maintenance molecules and polynucleotides, useful for diagnosing, treating or preventing aut or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis or cancer.

Claim 1; SEQ ID NO 44; 405pp; English.

This invention relates to novel isolated human proteins, which are protein modification and maintenance molecules (PWMM). The cellula processes regulating modification and maintenance of protein molec coordinate their function, conformation, stabilisation and degrada Each of these processes is mediated by key enzymes or proteins suc kinases, phosphatases, proteases, protease inhibitors, isomerases, transferases and molecular chapterones. Compounds which modulate the proteins of the invention may have anti-HIV, antiallargic, antionial antidiabeti antioniflammatory, antianaemic, antiatrhisonian, nootropic, antiparatic, antiatrhisonian, notropic, antiparasic, antipartorpic, dermatological, antidiabeti nephrotropic, antiparasic, antihelminic, antipacriatic, uropat ophthalmological, antiphrasic, happacotropic, dermatological, anticitation and maintenance molecules (PMMMS), the DNA septoteins of the invention may be useful for gene therapy. The huma protein modification and maintenance molecules (PMMMS), the DNA septotession of PMMM, particularly cell proliferative disorders associated with aberr expression of PMMM, particularly cell proliferative disorders (for

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riosclerosis, hepatitis, polycythaemia vera, psoriasis, mobocytopaenia or cancer), developmental disorders (for mia or mental retardation), neurological disorders (for elmer's disease, Parkinson's disease or epilepsy), nflammatory disorders (for example AIDS, allergies, asthma, hyroiditis, Crohn's disease, diabetes mellitus, storm's syndrome, multiple sclerosis, steoporosis, pancreatitis, Sjogren's syndrome) or microbial the present sequence is the amino acid sequence of a human
                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
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Gaps ; 0 2.8%; Score 8; DB 7; Length 617; 100.0%; Pred. No. 2.3e+02; ative 0; Mismatches 0; Indels Conservative larity

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9 SLALA 21 ndard; protein; 633 AA.

(first entry)

liagnostic protein #20252.

osome mapping; gene mapping; gene therapy; forensic; ant; medical imaging; diagnostic; genetic disorder.

2001WO-US008631.

2000US-00540217. 2000US-00649167.

Tang YT; Liu C,

polynucleotide and encoded polypeptides, useful in forensics, gene mapping, identification of mutations or genetic disorders or other traits and to assess 362/73

## ID NO 50620; 103pp; English.

relates to isolated polynucleotide (I) and polypeptide (II) is useful as hybridisation probes, polymerase chain primers, oligomers, and for chromosome and gene mapping, inant production of (II). The polymucleotides are also used as expressed sequence tags for identifying expressed useful in gene therapy techniques to restore normal II) or to treat disease states involving (II). (II) is netating antibodies against it, detecting or quantitating a nitisate, as molecular weight markers and as a food II) and its binding partners are useful in medical imaging essing (II). (I) and (II) are useful for treating disorders rrant protein expression or biological activity. The nd polynucleotide sequences have applications in

The invention relates to isolated polymucleotide (I) and polypept sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene me and in recombinant production of (II). The polymucleotides are all in diagnostics as expressed sequence tags for identifying express of the second in diagnostics as expressed sequence tags for identifying expressing in diagnostics as expressed sequence tags for identifying expression of generating antibodies against it, detecting or quantity useful for generating antibodies against it, detecting or quantity useful for generating antibodies against it, detecting or quantity useful for generating antibodies against it, detecting or quantity of supplement. (II) and its binding partners are useful in medical in of sites expressing (II). (I) and (II) are useful for treating dinvolving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodi

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diagnostics, forensics, gene mapping, identification of mutatior responsible for genetic disorders or other traits to assess biod and to produce other types of data and products dependent on DNF amino acid sequences. ABG00010-ABG30377 represent novel human diamino acid sequences of the invention. Note: The sequence data f patent did not appear in the printed specification, but was obtailectronic format directly from WIPO at electronic format directly from WIPO at fib.who.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                          .
0
                                                                                                                                               Length 633;
                                                                                                                                                                        0; Indels
                                                                                                                                              DB 4; Leng
                                                                                                                                           2.8%; Score 8; DB 4
100.0%; Pred. No. 2.4
vative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #28282.
                                                                                                                                                                                                                                                                                      ABG28291 standard; protein; 799 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT;
                                                                                                                                                                                                                                                                                                                                       18-FEB-2002 (first entry)
                                                                                                                                                                       8; Conservative
                                                                                                                                                                                               61 LGLGLALA 68
                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                       44 LGLGLALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS92478.
                                                                                                                    Sequence 633 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2001.
                                                                                                                                                                                                                                                                                                             ABG28291;
                                                                                                                                            Query Match
                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                           RESULT 72
                                                                                                                                                                                                                                                                          ABG2829
    88888888888888
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e.other types of data and products dependent on DNA and quences. ABG00010-ABG30377 represent novel human diagnostic quences of the invention. Note: The sequence data for this t appear in the printed specification, but was obtained in trat directly from WIPO at out. gub/published\_pct\_sequences

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Gaps . 0 2.8%; Score 8; DB 4; Length 799; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels onservative

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63

SLAL 294

lard; protein; 842 AA.

(useful for identifying genetic disorders) #630.

vel protein; tissue marker; molecular weight marker; ker; genetic disorder,

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002WO-US039555

001US-0339453P. 001US-0339739P.

002US-0365384P. 002US-0372381P. 002US-0372615P.

002US-0376045P

W, Ren F, Zhang J, Zhao QA, Weng G, Zhou P, Drmanac RT, Boyle BJ; Goodrich RW, (, Wehrman T, W di V,

Wang J; Wang Z;

35/53.

tides, useful for expressing recombinant proteins for acterization or therapeutic use, or as markers for tissues orresponding protein is preferentially expressed.

ID NO 1541; 1177pp; English

comprises the amino acid and coding sequences of novel DNA and protein sequences of the invention are useful as: ssues in which the corresponding protein is preferentially molecular weight markers on gels, as chromosome markers or iff thromosomes or to map related gene positions, and to ndogenous DNA sequences in patients to identify potential ers. The present amino acid sequence represents a protein

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                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug d
                                         ..
     Length 842;
                                                                                                                                                                                                                                                                                             Protein encoded by Prokaryotic essential gene #2232.
     DB 7; Le
                     100.0%; Pred. No. 3.1 cive 0; Mismatches
     2.8%; Score 8;
                                                                                                                                                                                          ABU16705 standard; protein; 1032 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                             (first entry)
Query Match 2.8<sup>1</sup>
Best Local Similarity 100.<sup>1</sup>
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Acinetobacter baumannii.
                                                                                                    441 ALLVPLAL 448
                                                                      61
                                                                      54 ALLVPLAL
                                                                                                                                                                                                                                                                                                                                                                                                    WO200277183-A2.
                                                                                                                                                                                                                                                             19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                      03-OCT-2002
                                                                                                                                                                                                                         ABU16705;
                                                                                                                                                      RESULT 74
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Haselbeck R, Yamamoto R, Malone C, Carr GJ, (ELIT-) ELITRA PHARM INC Zamudio C, Trawick JD, WPI; 2003-029926/02. N-PSDB; ACA20575. Wang L, Wall D, 

06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P

Zyskind Xu HH;

Ohlsen KL, Forsyth RA,

New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 44629; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any composition where exproceed the 6213 antisense sequences given in the specification where exproceed the 6213 antisense sequences given in the specification where expression of the nucleic acid (12) a vector comprising a promoter operably linked to the nucleic modelic acid, (2) a host cell containing the vector; (3) an isolate polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically bit polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically bit proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity encounted for proliferation, or that inhibits cellular proliferation identifying a gene required for cellular proliferation or the biol pathway in which a proliferation required gene or its gene product or a gene not which the test compound that inhibits proliferation or a gene on which the test compound that inhibits proliferation or a gene on which the test compound that inhibits proliferation or a gene on which the test compound that inhibits proliferation or a gene on which the test compound that inhibits proliferation or a gene on which the test compound that inhibits proliferation or a gene on which the test compound that inhibits proliferation or a gene or which the pass of the product or a gene or which the test compound that inhibits proliferation or a gene or which the test compound that the control or pathway in which the test compound that inhibits proliferation or proved the control or pathway in which the test compound that inhibits proliferation or proved the control or pathway in which the test compound that inhibits proliferation or the product or a gene or which the test compound that inhibits proliferation or the product or a gene or which the pass or the product or a gene or which the pass or the product or the organism acts; (1) a culture comprising strains in which the product is overexpressed or underexpressed; (12) determining the to which each of the strains is present in a culture or collection strains; or (13) identifying the target of a compound that inhibit prolliferation of an organism. The antisense nucleic acids are usef identifying proteins or screening for homologous nucleic acids required.

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ry programs, or for screening homologous nucleic acids proliferation in cells other than S. aureus, S. typhimurium, e or P. aeruginosa. The present sequence is encoded by rokaryotic essential genes. Note: The sequence data for this of form part of the printed specification, but was obtained /pub/published_pct_sequences
proliferation to isolate candidate molecules for rational
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2 AA;

0 Gaps 0; Length 1032; Indels 0 2.8%; Score 8; DB 6; Ler 100.0%; Pred. No. 3.8e+02; tive 0; Mismatches 0; Conservative

ALGLG 64

ALGLG 981

ndard; protein; 1033 AA.

(first entry)

r baumannii protein #1012.

r baumannii; bacterial disease; antibacterial; vaccine;

crol agent.

r baumannii.

99US-00328352.

98US-0088701P.

AE THERAPEUTICS CORP.

ish D;

3092/54.

1725.

octer baumanii proteins and nucleic acids, useful as reagents 1g a bacterial disease, as components of antibacterial targets for antibacterial drugs, or as biocontrol agents for

ID NO 5138; 328pp; English.

I relates to isolated Acinetobacter baumannii nucleic acids.

Ini nucleic acids and polypeptides are useful as reagents of abacterial disease, as components of antibacterial targets for antibacterial drugs, to detect the presence of and other Acinetobacter species in a sample, in screening the ability to interfere with the A. baumannii life cycle A. baumannii life cycle A. baumannii life cycle as biocontrol agents for present sequence represents the amino acid sequence of an A. tein.

AA;

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o;
                               Gaps
                                ;
0
2.8%; Score 8; DB 6; Length 1033; 100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0; Indels
             arity 100.
Conservative
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975 VPLALGLG 982 57 VPLALGLG 64 셤 ∂

Search completed: April 7, 2004, 17:57:27 Job time : 65 secs